



United States
Environmental Protection Agency

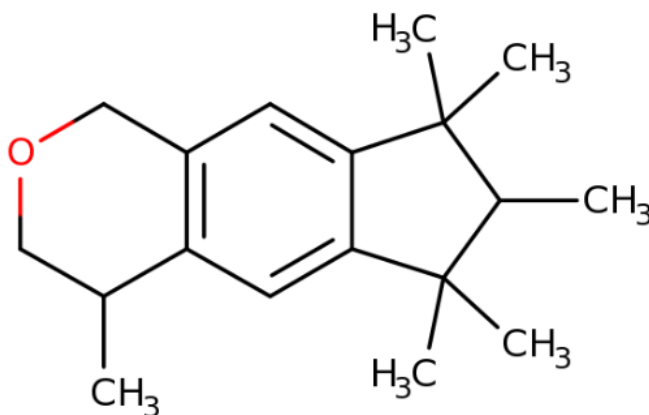
March 2026
Office of Chemical Safety and
Pollution Prevention

**Draft Benchmark Dose Modeling Results for 1,3,4,6,7,8-
Hexahydro-4,6,6,7,8,8-hexamethylcyclopenta [g]-2-
benzopyran (HHCB)**

Supplemental File Folder:

**Supplemental Information on Benchmark Dose Modeling in
the Human Health Hazard Assessment**

CASRN 1222-05-5



March 2026

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1 Benchmark Dose Modeling Approach

This benchmark dose (BMD) modeling supplemental file is in support of the *Draft Risk Evaluation for 1,3,4,6,7,8-Hexahydro-4,6,6,7,8,8-hexamethylcyclopenta [g]-2-benzopyran (HHCB)* ([U.S. EPA, 2026b](#)).

The extended one generation reproduction toxicity study of HHCB by the oral route (dietary administration) in Wistar rats ([IFF, 2021](#)), which adheres to [OECD Test Guideline No. 443](#), supports a no-observed adverse effect level (NOAEL) of 26.8 mg/kg-day and a lowest-observed adverse effect level (LOAEL) of 45.6 mg/kg-day based on reduced body weights and body weight gains in F1 and F2 offspring. This NOAEL and LOAEL are supported by the attached data evaluation record ([U.S. EPA, 2026a](#)). The magnitude of the effect of HHCB on offspring body weight at the LOAEL was a statistically significant decrease ranging from 6 to 11 percent in F1 males and 4 to 7 percent in F1 females relative to control males and females, respectively, depending on the time of measurement. EPA conducted BMD modeling of decreased F1 offspring bodyweight to refine the LOAEL. EPA BMD modeled bodyweight for both sexes combined on postnatal day (PND) 1, PND 4, PND 7, PND 14, and PND 21. EPA also BMD modeled bodyweight for F1 males and F1 females separately at sexual maturation (average age was PND 51 for males based on preputial separation and PND 32 for females based on vaginal opening) and on treatment days 50 and 72.

All BMD modeling was conducted with EPA's 2025 web-based version of BMD software (BMDS Online version 25.1) ([U.S. EPA, 2025](#)). EPA modeled all datasets using standard continuous models included in BMDS. EPA's continuous modeling approach and results are detailed in Sections 1.1 and 2, respectively.

Ideally, a nested continuous model would be used for pre-weaning datasets to reflect the complex study design of pups nested within litters. This is because nested models account for any intra-litter correlation, or the tendency of pups within the same litter to respond more similarly to one another relative to other litters in a dose group. However, nested continuous models are not currently available in EPA's BMDS. Therefore, in addition to standard continuous modeling, EPA modeled pre-weaning datasets using a nested dichotomous modeling approach by dichotomizing F1 pup continuous bodyweight data as described further in Section 1.2. Although nested dichotomous modeling accounts for litter effects, EPA's Benchmark Dose Technical Guidance ([U.S. EPA, 2012](#)) advises against dichotomizing continuous endpoints such as bodyweight, because of the resulting loss of information. EPA's nested dichotomous modeling approach and results for pre-weaning datasets are described in Sections 1.2 and 3, respectively. Overall, results between the two models were similar and yielded less than a two-fold difference in BMD and BMDL (95% lower confidence limit on the BMD) estimates. Therefore, although the results of both modeling approaches are presented in this supplement, EPA considered results from continuous modeling when identifying BMDLs for use as the point of departure (POD).

1.1 Continuous Modeling

Continuous modeling was used for all timepoints (*i.e.*, PNDs 1, 4, 7, 14, 21; sexual maturation; treatment day 50; treatment day 72). Although individual pup data were available, EPA chose to BMD model litter level data (*i.e.*, litter means and standard deviations) for pre-weaning timepoints (*i.e.*, PND 1, 4, 7, 14, and 21). Modeling in this manner is consistent with the study's methods section, which indicates that statistical analyses were performed on a per litter basis for these timepoints.

Continuous Models

All standard BMDS 25.1 continuous models that use maximum likelihood (MLE) estimation and profile likelihood-based confidence intervals were used in this analysis. Standard forms of these models (defined below) were run so that auto-generated model selection recommendations accurately reflect current EPA model selection procedures in EPA's Benchmark Dose Technical Guidance ([U.S. EPA, 2012](#)).

Standard BMDS 25.1 models applied to continuous endpoints in this supplemental file include:

- Exponential 3-restricted (exp3-r);
- Exponential 5-restricted (exp5-r);
- Hill-restricted (hil-r);
- Polynomial Degree 3-restricted (ply3-r);
- Polynomial Degree 2-restricted (ply2-r);
- Power-restricted (pow-r); and
- Linear-unrestricted (lin-ur).

Benchmark Response Levels

Consistent with EPA's Benchmark Dose Technical Guidance ([U.S. EPA, 2012](#)), EPA evaluated benchmark response (BMR) levels of 1 control standard deviation (1 SD) for all datasets to provide a standard BMR for comparison. For early postnatal and pup lifestages (*i.e.*, PND 1, 4, 7, 14, 21), EPA additionally evaluated a BMR of 5 percent relative deviation (RD); for adult F1 offspring (*i.e.*, F1 offspring at sexual maturation and treatment days 50 and 72), a BMR of 10 percent RD was evaluated. BMRs of 5 percent and 10 percent RD were included because EPA considers these BMRs to be biologically relevant for pre -and post-weaning body weight changes, respectively, in a developmental study.

Model Fit and Selection

Model fit was judged consistent with EPA's Benchmark Dose Technical Guidance ([U.S. EPA, 2012](#)). An adequate fit was judged based on the χ^2 goodness-of-fit p-value ($p > 0.1$), magnitude of the scaled residuals in the vicinity of the BMR, and visual inspection of the model fit. In addition to these three criteria for judging adequacy of model fit, a determination was made as to whether the variance across dose groups was constant. If a constant variance model was deemed appropriate based on the statistical test provided in BMDS (*i.e.*, Test 2; p-value > 0.05 [note: this is a change from previous versions of BMDS, which required variance p-value > 0.10 for adequate fit]), the final BMD results were estimated from a constant variance model. If the test for homogeneity of variance was rejected (*i.e.*, p-value < 0.05), the model was run again while modeling the variance as a power function of the mean to account for this nonconstant variance. If this nonconstant variance model did not adequately fit the data (*i.e.*, Test 3; p-value < 0.05), the data set was considered unsuitable for BMD modeling. Across all bodyweight datasets analyzed, the constant variance model was deemed appropriate and nonconstant variance models were not run.

Among all models providing adequate fit, the lowest BMDL was selected if the BMDLs estimated from different adequately fitting models varied greater than 3-fold; otherwise, the BMDL from the model with the lowest Akaike Information Criterion (AIC) was selected. Across all bodyweight datasets analyzed, BMDLs from different models were within 3-fold of one another, and the BMDL from the model with the lowest AIC was selected.

267 Table 1-1 summarizes the continuous BMD model results for the analysis presented in this supplemental
268 file. As recommended by EPA's Benchmark Dose Technical Guidance ([U.S. EPA, 2012](#)), if a BMD or
269 BMDL was outside of the observable range of tested doses, it was not considered for use as the POD.
270 This is because extrapolation to a BMD level below the experimental data range introduces more
271 uncertainty than staying within the observed dose range.

272 **Table 1-1. Summary of Continuous BMD Modeling of Decreased F1 Rat Bodyweight from (IFF, 2021)^a**

Data Set (Section with BMD Modeling Results)	Variance	BMR = 1 SD			BMR = 5% RD			BMR = 10% RD		
		Best Fitting Model	BMD _{1SD} (mg/kg-d)	BMDL _{1SD} (mg/kg-d)	Best Fitting Model	BMD ₅ (mg/kg-d)	BMDL ₅ (mg/kg-d)	Best Fitting Model	BMD ₁₀ (mg/kg-d)	BMDL ₁₀ (mg/kg-d)
F1 BW – PND 1 (Sections 2.1.1–2.1.2)	Constant	Exponential 3	133	78	Exponential 3	57	35	–	–	–
F1 BW – PND 4 (Pre- Culling) (Sections 2.1.3–2.1.4)	Constant	Linear	144	84	Linear	51	30	–	–	–
F1 BW – PND 4 (Post- Culling) (Sections 2.1.5–2.1.6)	Constant	Linear	147	85	Linear	52	31	–	–	–
F1 BW – PND 7 (Sections 2.1.7–2.1.8)	Constant	Exponential 3	116	71	Exponential 3	48	31	–	–	–
F1 BW – PND 14 (Sections 2.1.9–2.1.10)	Constant	Exponential 3	61	45	Exponential 3	40	30	–	–	–
F1 BW – PND 21 (Sections 2.1.11–2.1.12)	Constant	Linear	56	43	Linear	42	33	–	–	–
Male F1 BW – At sexual maturation (~PND 51) (Sections 2.2.1–2.2.2)	Constant	Linear	142	97	–	–	–	Linear	107	75
Male F1 BW – Treatment day 50 (Sections 2.3.1– 2.3.2)	Constant	Hill	52	31	–	–	–	Hill	57	36
Male F1 BW – Treatment day 72 (Sections 2.3.3– 2.3.4)	Constant	Exponential 3	44	33	–	–	–	Exponential 3	48	38
Female F1 BW – At sexual maturation (~PND 32) (Sections 2.2.3–2.2.4)	Constant	Linear	150	101	–	–	–	Linear	145	99
Female F1 BW – Treatment day 50 (Sections 2.3.5–2.3.6)	Constant	Exponential 3	123	87	–	–	–	Exponential 3	156	112
Female F1 BW – Treatment day 72 (Sections 2.3.7–2.3.8)	Constant	Exponential 3	93	59	–	–	–	Exponential 3	108	71
Abbreviations: ‘–’ = BMR not evaluated for this dataset; BMD = benchmark dose; BMDL = 95% lower confidence limit of BMD; BMR = benchmark response; BW = bodyweight; PND = postnatal day; RD = relative deviation; SD = standard deviation										

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1.2 Nested Dichotomous Modeling

Nested dichotomous modeling was conducted for early postnatal and pup lifestages (*i.e.*, PND 1, 4, 7, 14, 21) to consider the within-dam grouping of pup weight observations as well as litter size. To apply this model, the individual male and female weights were dichotomized using the 5th percentile of the control pup weight distribution as the cutoff value for each corresponding lifestage. All individual pup weights were binned by litter to determine the number of offspring in each litter with body weights below each percentile cutoff. Total litter size (number of live male and female fetuses on PND 1) was used as the litter specific covariate using the default “Overall Mean” option (averaged across all dose groups).

Nested Dichotomous Models

All standard BMDS 25.1 nested dichotomous models that use maximum likelihood (MLE) estimation and profile likelihood-based confidence intervals were used in this analysis. Standard forms of these models (defined below) were run so that auto-generated model selection recommendations accurately reflect current EPA model selection procedures in EPA’s Benchmark Dose Technical Guidance ([U.S. EPA, 2012](#)). Each model was applied with and without the litter-specific covariate (lsc) to determine whether the litter-specific covariate contributes to a better explanation of the observation. The model was also run with and without intralitter correlation (ilc) to estimate the degree to which observations within the same litter are correlated.

Standard BMDS 25.1 models applied to nested dichotomous endpoints in this supplemental file include:

- Nested Logistic-restricted without lsc and ilc (lsc-ilc-);
- Nested Logistic-restricted without lsc and with ilc (lsc-ilc+);
- Nested Logistic-restricted with lsc and without ilc (lsc+ilc-);
- Nested Logistic-restricted with lsc and ilc (lsc+ilc+)
- NCTR-restricted without lsc and ilc (lsc-ilc-);
- NCTR-restricted without lsc and with ilc (lsc-ilc+);
- NCTR-restricted with lsc and without ilc (lsc+ilc-); and
- NCTR-restricted with lsc and ilc (lsc+ilc+)

Benchmark Response Levels

EPA’s Benchmark Dose Technical Guidance ([U.S. EPA, 2012](#)) recommends calculating 10 percent extra risk (ER) for quantal data to compare modeling results across endpoints. This BMR was lowered to five percent ER because EPA considers that BMR to be biologically relevant for changes of pup body weights in a developmental study.

Model Fit and Selection

Model fit was judged consistent with EPA’s benchmark Dose Technical Guidance ([U.S. EPA, 2012](#)). An adequate fit was judged based on the χ^2 goodness-of-fit p-value ($p > 0.1$), magnitude of the scaled residuals in the vicinity of the BMR, and visual inspection of the model fit.

Among all models providing adequate fit, the lowest BMDL was selected if the BMDLs estimated from different adequately fitting models varied greater than 3-fold; otherwise, the BMDL from the model with the lowest AIC was selected. Across all bodyweight datasets analyzed, BMDLs from different models were within 3-fold of one another, and the BMDL from the model with the lowest AIC was selected.

321 Table 1-2 summarizes the nested dichotomous BMD model results for the analysis presented in this
322 supplemental file.

323 **Table 1-2. Summary of Nested Dichotomous BMD Modeling of Decreased F1 Rat Bodyweight from (IFF, 2021)^a**

Data Set (Section with BMD Modeling Results)	BMR = 5% ER		
	Best Fitting Model	BMD ₅ (mg/kg-d)	BMDL ₅ (mg/kg-d)
F1 BW – PND 1 (Section 3.1.1)	Nested Logistic (lsc+ilc+)	30	17
F1 BW – PND 4 Pre-Culling (Section 3.1.2)	Nested Logistic (lsc+ilc+)	93	48
F1 BW – PND 4 Post-Culling (Section 3.1.3)	NCTR (lsc-ilc+)	66	33
F1 BW – PND 7 (Section 3.1.4)	NCTR (lsc-ilc+)	43	22
F1 BW – PND 14 (Section 3.1.5)	NCTR (lsc-ilc+)	30	15
F1 BW – PND 21 (Sections 3.1.6)	NCTR (lsc-ilc+)	30	15
Abbreviations: BMD = benchmark dose; BMDL = 95% lower confidence limit of BMD; BMR = benchmark response; BW = bodyweight; ER = Extra Risk; PND = postnatal day			

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2 Continuous Modeling Results

2.1 Continuous Modeling of F1 Male and Female PND 1, 4, 7, 14, 21 Bodyweight (Sexes Combined)

Report Generated: 2025-Oct-17 21:10 UTC

Analysis URL: [View](#)

BMDS Online Version: 25.1 (pybmds 25.1; bmdscore 25.1)

2.1.1 Bodyweight on PND 1, BMR = 1 SD

2.1.1.1 Dataset

Name: P1

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
0	25	6.631	0.844
26.8	24	6.397	0.554
45.6	25	6.27	0.739
91.7	25	6.103	0.83

Test 1 Dose Response: 0.0715

Test 2 Homogeneity of Variance: 0.1729

Test 3 Variance Model Selection: 0.1729

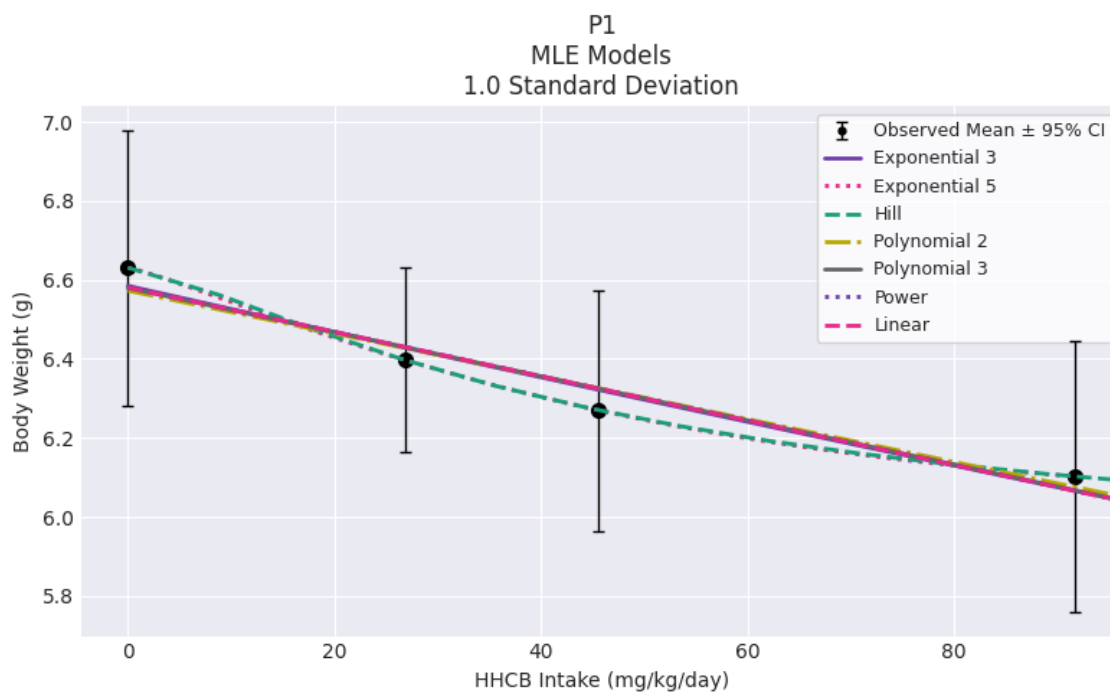
2.1.1.2 Settings

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

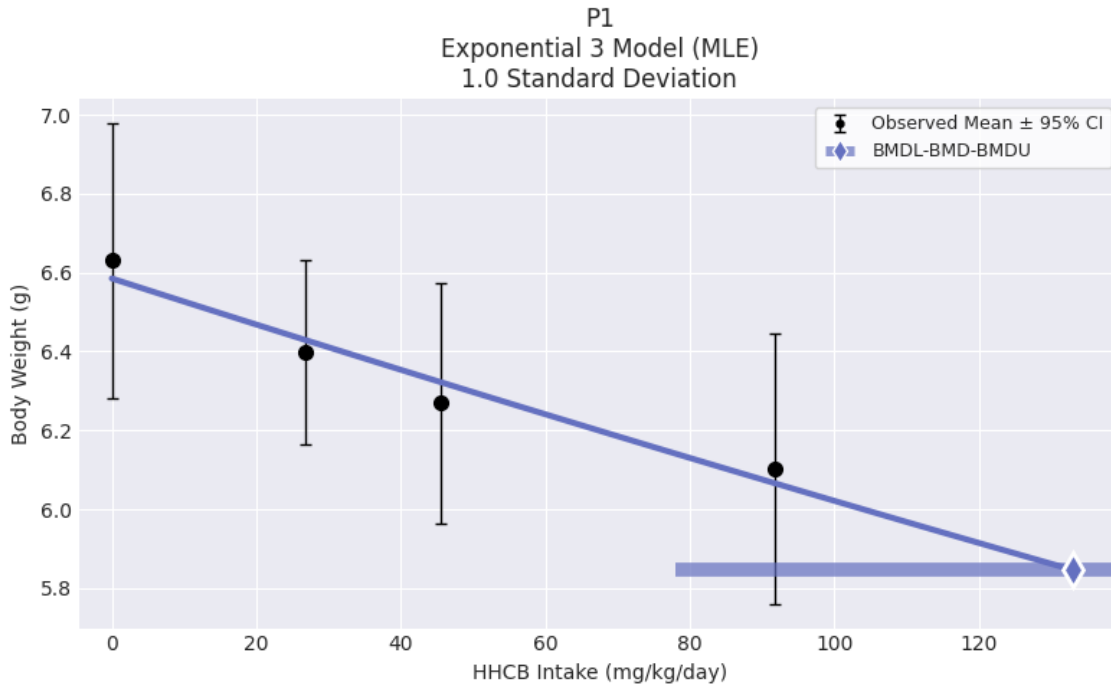
2.1.1.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 ^{ab}	78.006	132.933	398.032	0.85	226.871	0.311	0.245	Recommended - Lowest AIC BMD/highest dose ratio > 1.0
Exponential 5	-	-	-	-	230.547	-0.	-	Unusable Did not successfully execute.
Hill	55.04	880.313	-	-	230.547	<0.001	-0.	Questionable Zero degrees of freedom; saturated

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
								model BMD/highest dose ratio > 1.0 BMD/BMDL ratio > 3.0
Polynomial 2	79.26	136.471	385.497	0.831	226.917	0.394	0.179	Viable BMD/highest dose ratio > 1.0
Polynomial 3	79.318	132.275	384.375	0.834	226.909	0.348	0.236	Viable BMD/highest dose ratio > 1.0
Power	79.327	131.521	384.354	0.834	226.909	0.339	0.247	Viable BMD/highest dose ratio > 1.0
Linear	79.327	131.521	384.355	0.834	226.909	0.339	0.247	Viable BMD/highest dose ratio > 1.0
^a BMDS recommended best fitting model								
^b User selected best fitting model								



2.1.1.4 Selected Model: Exponential 3



Exponential 3 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	100
b	0	0	100
c	0	-20	0
d	1	1	18
log-alpha	0	-18	18

Modeling Summary:

BMD	132.933
BMDL	78.0056
BMDU	398.032
AIC	226.871
Log-Likelihood	-110.435
P-Value	0.850455
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	6.58496	no	0.119228
b	0.000894544	no	0.000353155

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d	1	yes	Not Reported
log-alpha	-0.60686	no	0.142132

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	25	6.63091	6.58496	0.311213
26.8	24	6.39726	6.42897	-0.210423
45.6	25	6.27013	6.32175	-0.349652
91.7	25	6.10254	6.06636	0.245049

Dose	N	Sample SD	Model Fitted SD
0	25	0.844483	0.738282
26.8	24	0.553706	0.738282
45.6	25	0.738621	0.738282
91.7	25	0.829759	0.738282

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-110.273	5	230.547
A2	-107.781	8	231.562
A3	-110.273	5	230.547
fitted	-110.435	3	226.871
reduced	-113.581	2	231.162

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	11.6003	6	0.0715029
Test 2	4.98498	3	0.172901
Test 3	4.98498	3	0.172901
Test 4	0.323967	2	0.850455

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.1.2 Bodyweight on PND 1, BMR = 5% RD

2.1.2.1 Dataset

Name: P1

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
0	25	6.631	0.844
26.8	24	6.397	0.554

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Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
45.6	25	6.27	0.739
91.7	25	6.103	0.83

Test 1 Dose Response: 0.0715

Test 2 Homogeneity of Variance: 0.1729

Test 3 Variance Model Selection: 0.1729

2.1.2.2 Settings

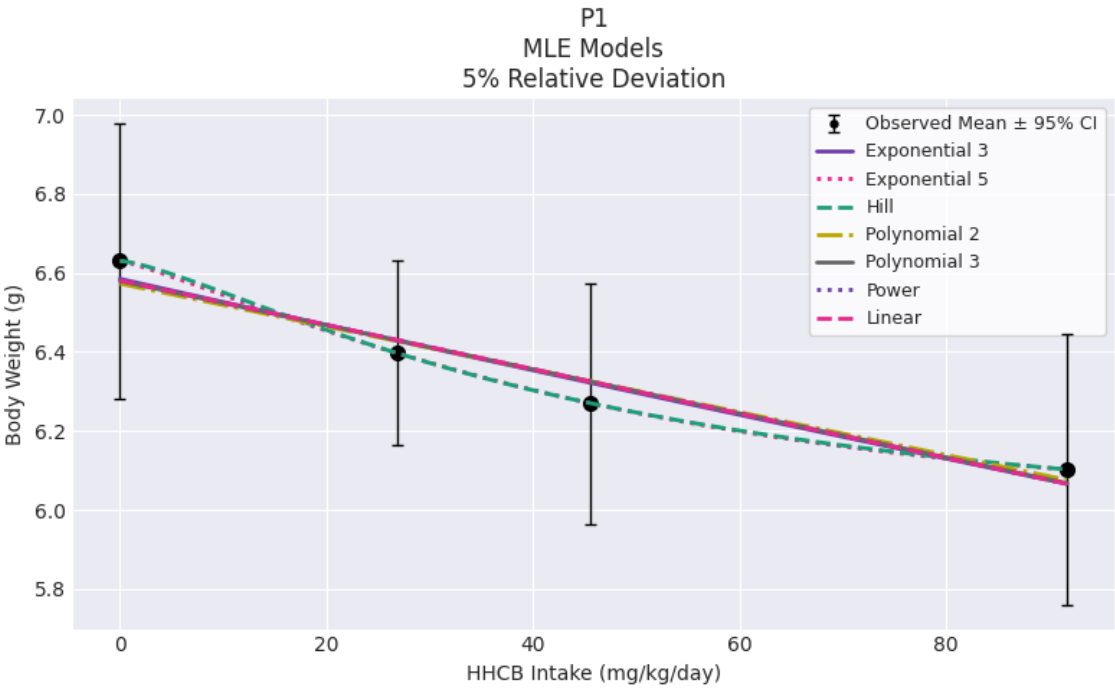
Setting	Value
BMR	5% Relative Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.1.2.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 ^{ab}	34.606	57.34	164.379	0.955	226.871	0.311	-0.35	Recommended - Lowest AIC
Exponential 5	1.973	40.687	295.595	-	230.547	-0.	<0.001	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 Zero degrees of freedom; saturated model BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0
Hill	0.068	40.595	-	-	230.547	<0.001	<0.001	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 Zero degrees of freedom; saturated model BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0
Polynomial 2	36.248	60.674	164.987	0.831	226.917	0.394	-0.376	Viable

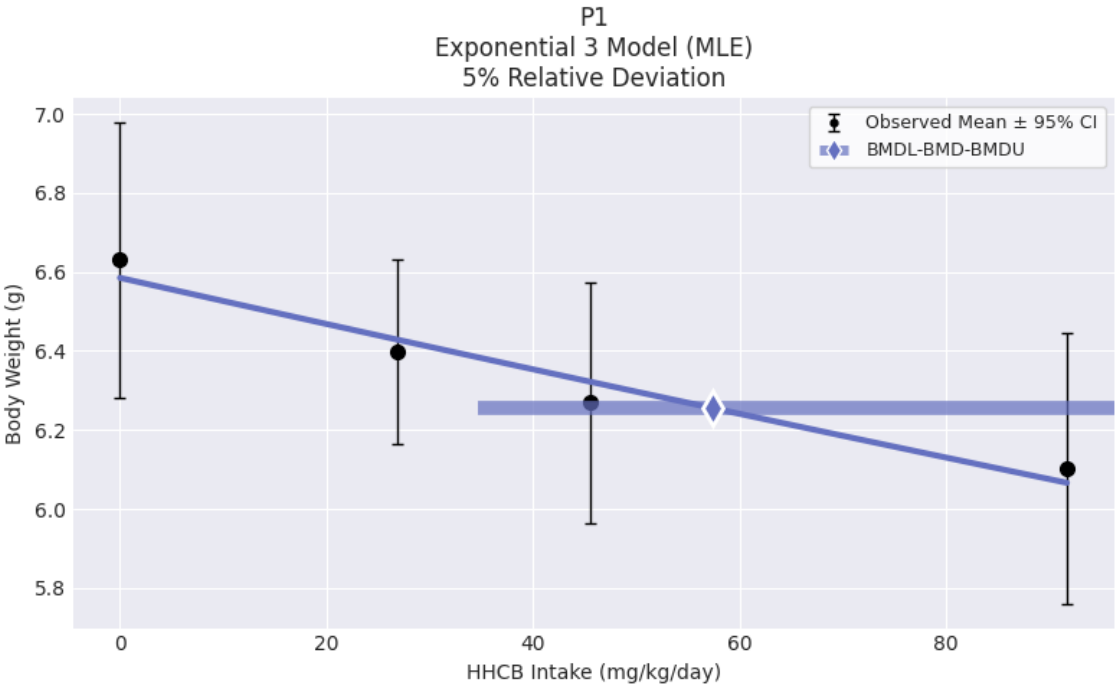
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Polynomial 3	36.271	58.931	164.532	0.834	226.909	0.348	-0.372	Viable
Power	36.275	58.606	164.51	0.834	226.909	0.339	-0.371	Viable
Linear	36.275	58.606	164.519	0.834	226.909	0.339	-0.371	Viable

^a BMDs recommended best fitting model
^b User selected best fitting model



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2.1.2.4 Selected Model: Exponential 3



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Exponential 3 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	5% Relative Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	100
b	0	0	100
c	0	-20	0
d	1	1	18
log-alpha	0	-18	18

Modeling Summary:

BMD	57.3401
BMDL	34.6055
BMDU	164.379
AIC	226.871
Log-Likelihood	-110.435
P-Value	0.95546
Model d.f.	3

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	6.58496	no	0.119228

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b	0.000894544	no	0.000353155
d	1	yes	Not Reported
log-alpha	-0.60686	no	0.142132

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	25	6.63091	6.58496	0.311213
26.8	24	6.39726	6.42897	-0.210423
45.6	25	6.27013	6.32175	-0.349652
91.7	25	6.10254	6.06636	0.245049

Dose	N	Sample SD	Model Fitted SD
0	25	0.844483	0.738282
26.8	24	0.553706	0.738282
45.6	25	0.738621	0.738282
91.7	25	0.829759	0.738282

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-110.273	5	230.547
A2	-107.781	8	231.562
A3	-110.273	5	230.547
fitted	-110.435	2	224.871
reduced	-113.581	2	231.162

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	11.6003	6	0.0715029
Test 2	4.98498	3	0.172901
Test 3	4.98498	3	0.172901
Test 4	0.323967	3	0.95546

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.1.3 Bodyweight on PND 4 (Pre-Culling), BMR = 1 SD

2.1.3.1 Dataset

Name: P4pr

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
0	25	10.188	1.724

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
26.8	23	10.087	1.058
45.6	25	9.655	1.656
91.7	25	9.313	1.368

Test 1 Dose Response: 0.0603
Test 2 Homogeneity of Variance: 0.0899
Test 3 Variance Model Selection: 0.0899

2.1.3.2 Settings

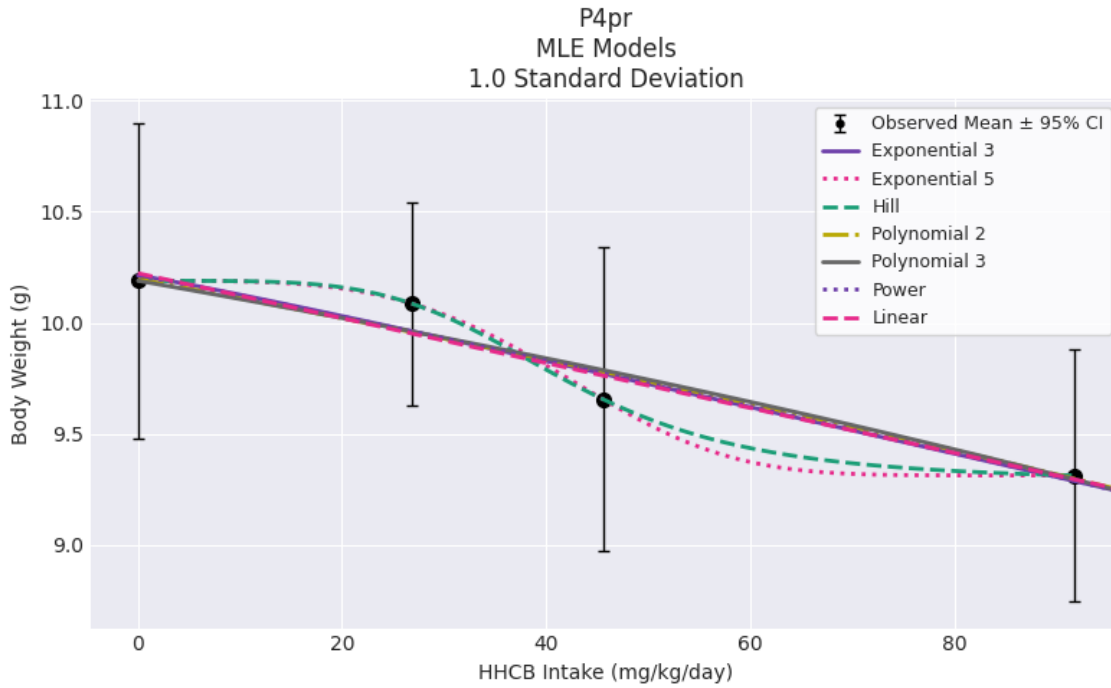
Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.1.3.3 Maximum Likelihood Approach

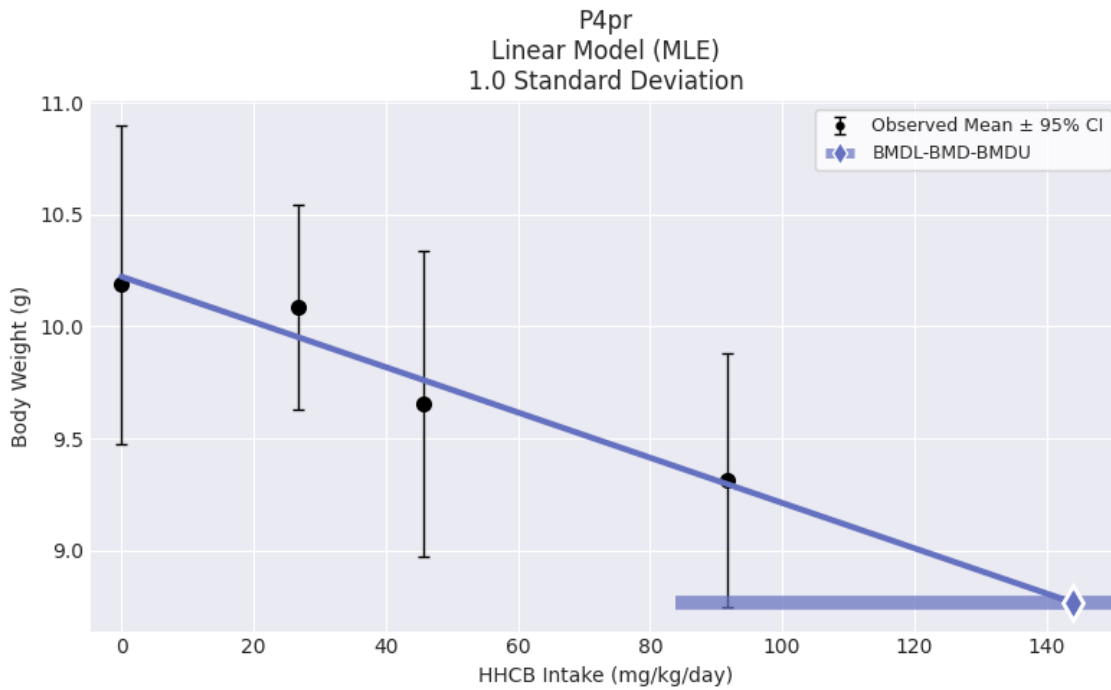
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	83.008	142.779	544.691	0.844	359.602	-0.082	0.084	Viable BMD/highest dose ratio > 1.0
Exponential 5	-	-	-	-	361.264	-0.	-	Unusable Did not successfully execute.
Hill	-	-	-	-	361.264	<0.001	-	Unusable Did not successfully execute.
Polynomial 2	83.653	139.177	142.058	0.546	359.628	-0.027	0.048	Viable BMD/highest dose ratio > 1.0
Polynomial 3	83.563	135.05	137.846	0.538	359.643	-0.002	0.057	Viable BMD/highest dose ratio > 1.0
Power	83.769	140.95	511.479	0.557	359.608	-0.081	0.082	Viable BMD/highest dose ratio > 1.0
Linear ^{a b}	83.742	143.996	512.62	0.84	357.613	-0.117	0.058	Recommended - Lowest AIC BMD/highest dose ratio > 1.0

^a BMDS recommended best fitting model

^b User selected best fitting model



2.1.3.4 Selected Model: Linear



Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR Distribution	1.0 Standard Deviation Normal + Constant variance
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Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-1e+06	1e+06
b1	0	-1e+06	1e+06
alpha	0	-18	18

Modeling Summary:

BMD	143.996
BMDL	83.7423
BMDU	512.62
AIC	357.613
Log-Likelihood	-175.806
P-Value	0.839843
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	10.2226	no	0.232437
b1	-0.0101044	no	0.00435839
alpha	2.11702	no	0.640201

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	25	10.1884	10.2226	-0.117394
26.8	23	10.0865	9.95179	0.444131
45.6	25	9.65526	9.76183	-0.366206
91.7	25	9.31278	9.29602	0.0576044

Dose	N	Sample SD	Model Fitted SD
0	25	1.72378	1.455
26.8	23	1.05847	1.455
45.6	25	1.65641	1.455
91.7	25	1.36809	1.455

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-175.632	5	361.264
A2	-172.386	8	360.771
A3	-175.632	5	361.264
fitted	-175.806	3	357.613
reduced	-178.423	2	360.845

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	12.0743	6	0.0603308
Test 2	6.49276	3	0.0899484

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Test 3	6.49276	3	0.0899484
Test 4	0.34908	2	0.839843

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.1.4 Bodyweight on PND 4 (Pre-Culling), BMR = 5% RD

2.1.4.1 Dataset

Name: P4pr

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
0	25	10.188	1.724
26.8	23	10.087	1.058
45.6	25	9.655	1.656
91.7	25	9.313	1.368

Test 1 Dose Response: 0.0603

Test 2 Homogeneity of Variance: 0.0899

Test 3 Variance Model Selection: 0.0899

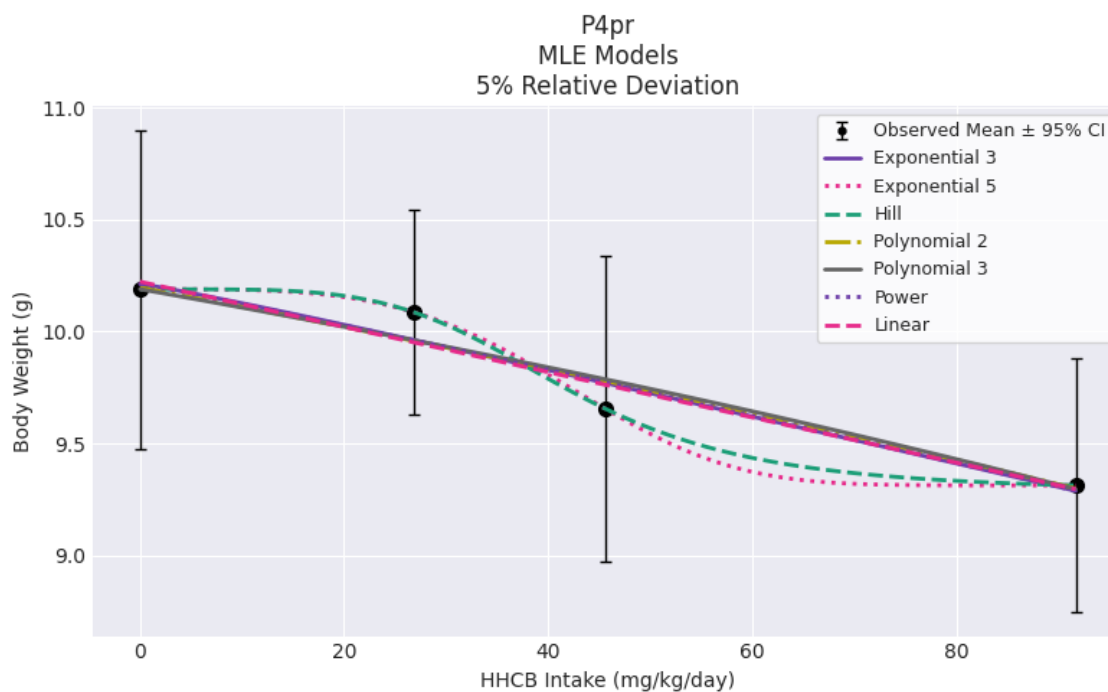
2.1.4.2 Settings

Setting	Value
BMR	5% Relative Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

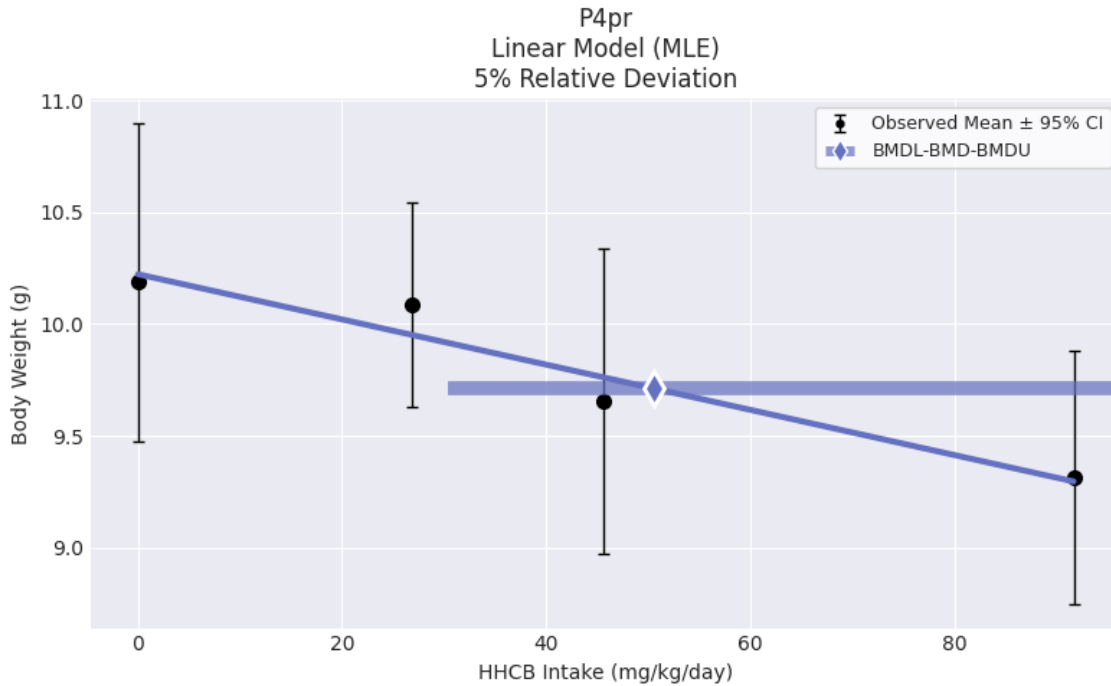
2.1.4.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	28.71	52.219	173.103	0.844	359.602	-0.082	-0.395	Viable
Exponential 5	14.676	44.723	148.792	-	361.264	-0.	-0.	Questionable Zero degrees of freedom; saturated model BMD/BMDL ratio > 3.0

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	21.895	44.534	-	-	361.264	<0.001	<0.001	Questionable Zero degrees of freedom; saturated model
Polynomial 2	30.304	54.974	173.207	0.546	359.628	-0.027	-0.427	Viable
Polynomial 3	30.271	56.481	174.393	0.538	359.643	-0.002	-0.452	Viable
Power	30.348	52.405	171.612	0.557	359.608	-0.081	-0.399	Viable
Linear ^{a b}	30.342	50.585	171.991	0.84	357.613	-0.117	-0.366	Recommended - Lowest AIC
^a BMDS recommended best fitting model								
^b User selected best fitting model								



2.1.4.4 Selected Model: Linear



Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	5% Relative Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (\downarrow)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-1e+06	1e+06
b1	0	-1e+06	1e+06
alpha	0	-18	18

Modeling Summary:

BMD	50.5848
BMDL	30.3424
BMDU	171.991
AIC	357.613
Log-Likelihood	-175.806
P-Value	0.839843
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error

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g	10.2226	no	0.232437
b1	-0.0101044	no	0.00435839
alpha	2.11702	no	0.640201

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	25	10.1884	10.2226	-0.117394
26.8	23	10.0865	9.95179	0.444131
45.6	25	9.65526	9.76183	-0.366206
91.7	25	9.31278	9.29602	0.0576044

Dose	N	Sample SD	Model Fitted SD
0	25	1.72378	1.455
26.8	23	1.05847	1.455
45.6	25	1.65641	1.455
91.7	25	1.36809	1.455

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-175.632	5	361.264
A2	-172.386	8	360.771
A3	-175.632	5	361.264
fitted	-175.806	3	357.613
reduced	-178.423	2	360.845

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	12.0743	6	0.0603308
Test 2	6.49276	3	0.0899484
Test 3	6.49276	3	0.0899484
Test 4	0.34908	2	0.839843

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.1.5 Bodyweight on PND 4 (Post-Culling), BMR = 1 SD

2.1.5.1 Dataset

Name: P4po

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
0	25	10.168	1.742
26.8	23	10.118	1.037
45.6	25	9.709	1.645
91.7	25	9.318	1.378

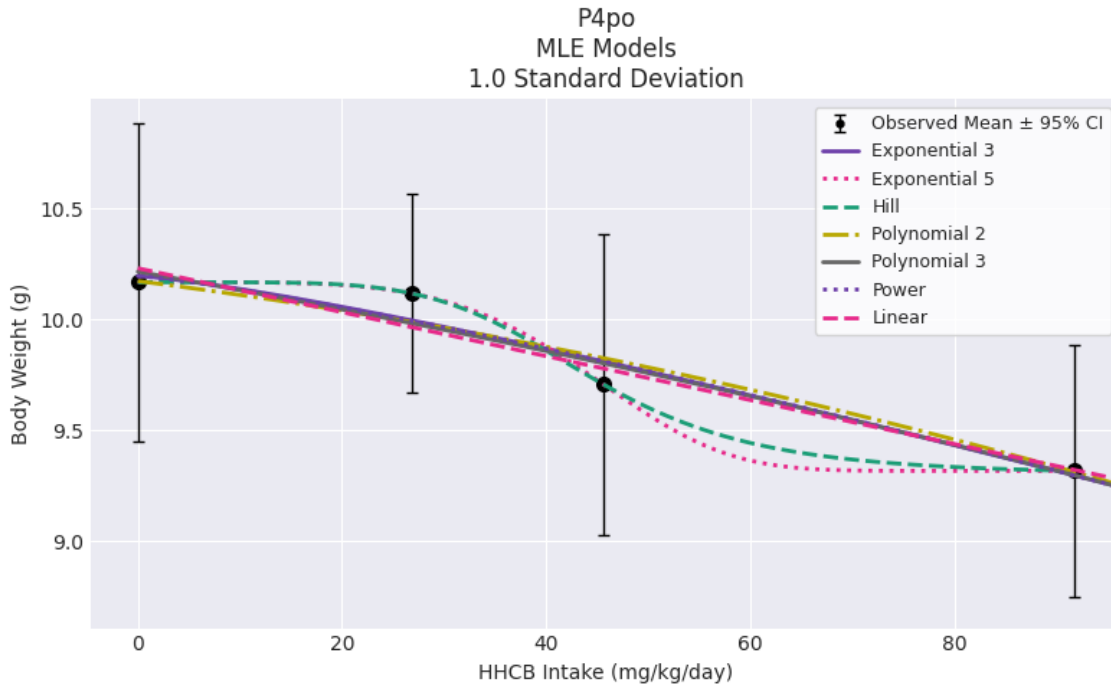
Test 1 Dose Response: 0.0536
 Test 2 Homogeneity of Variance: 0.0713
 Test 3 Variance Model Selection: 0.0713

2.1.5.2 Settings

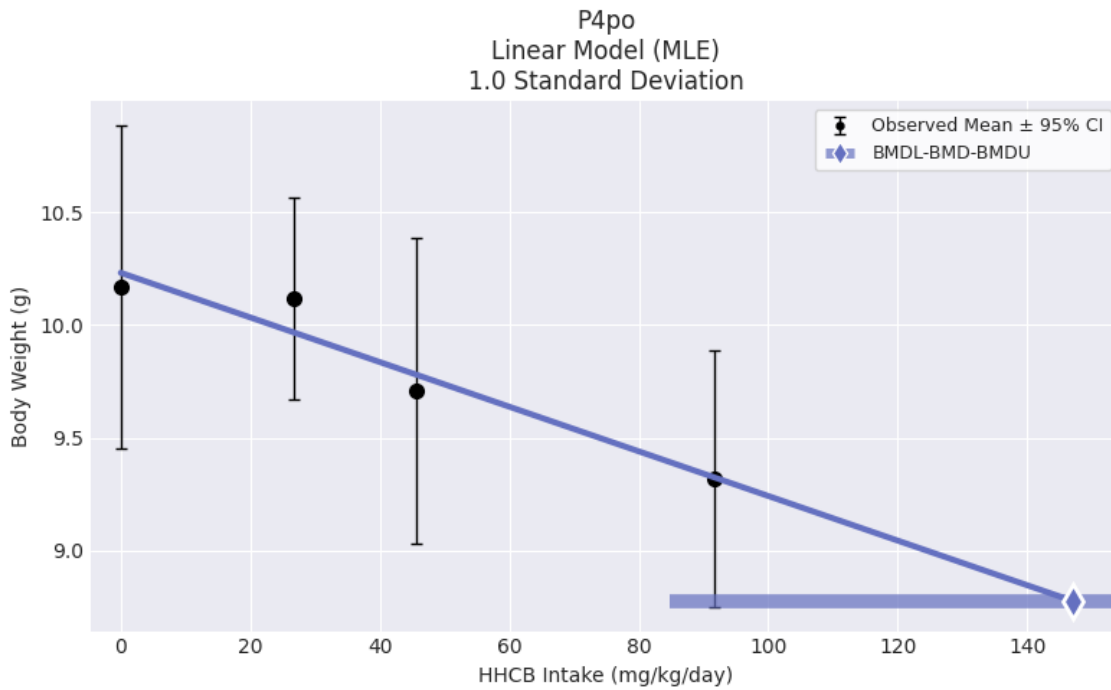
Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.1.5.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	84.737	138.192	572.676	0.861	359.673	-0.097	0.067	Viable BMD/highest dose ratio > 1.0
Exponential 5	-	-	-	-	361.373	-0.	-	Unusable Did not successfully execute.
Hill	-	-	-	-	361.373	<0.001	-	Unusable Did not successfully execute.
Polynomial 2	84.874	132.894	135.645	0.556	359.719	-0.018	0.015	Viable BMD/highest dose ratio > 1.0
Polynomial 3	84.96	134.023	545.175	0.564	359.706	-0.164	0.064	Viable BMD/highest dose ratio > 1.0
Power	85.129	136.437	537.687	0.58	359.678	-0.096	0.066	Viable BMD/highest dose ratio > 1.0
Linear ^{ab}	84.791	147.022	552.333	0.836	357.732	-0.217	-0.019	Recommended - Lowest AIC BMD/highest dose ratio > 1.0
^a BMDS recommended best fitting model								
^b User selected best fitting model								



2.1.5.4 Selected Model: Linear



Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR Distribution	1.0 Standard Deviation Normal + Constant variance
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Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-1e+06	1e+06
b1	0	-1e+06	1e+06
alpha	0	-18	18

Modeling Summary:

BMD	147.022
BMDL	84.7914
BMDU	552.333
AIC	357.732
Log-Likelihood	-175.866
P-Value	0.835756
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	10.2316	no	0.232559
b1	-0.00990247	no	0.00436044
alpha	2.11959	no	0.641757

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	25	10.1685	10.2316	-0.216772
26.8	23	10.1183	9.96623	0.500799
45.6	25	9.70871	9.78007	-0.245047
91.7	25	9.31817	9.32356	-0.0185301

Dose	N	Sample SD	Model Fitted SD
0	25	1.74181	1.45588
26.8	23	1.03711	1.45588
45.6	25	1.64478	1.45588
91.7	25	1.37775	1.45588

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-175.686	5	361.373
A2	-172.176	8	360.353
A3	-175.686	5	361.373
fitted	-175.866	3	357.732
reduced	-178.378	2	360.756

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	12.4034	6	0.0535511
Test 2	7.01985	3	0.0712678
Test 3	7.01985	3	0.0712678
Test 4	0.358837	2	0.835756

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.1.6 Bodyweight on PND 4 (Post-Culling), BMR = 5% RD

2.1.6.1 Dataset

Name: P4po

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
0	25	10.168	1.742
26.8	23	10.118	1.037
45.6	25	9.709	1.645
91.7	25	9.318	1.378

Test 1 Dose Response: 0.0536

Test 2 Homogeneity of Variance: 0.0713

Test 3 Variance Model Selection: 0.0713

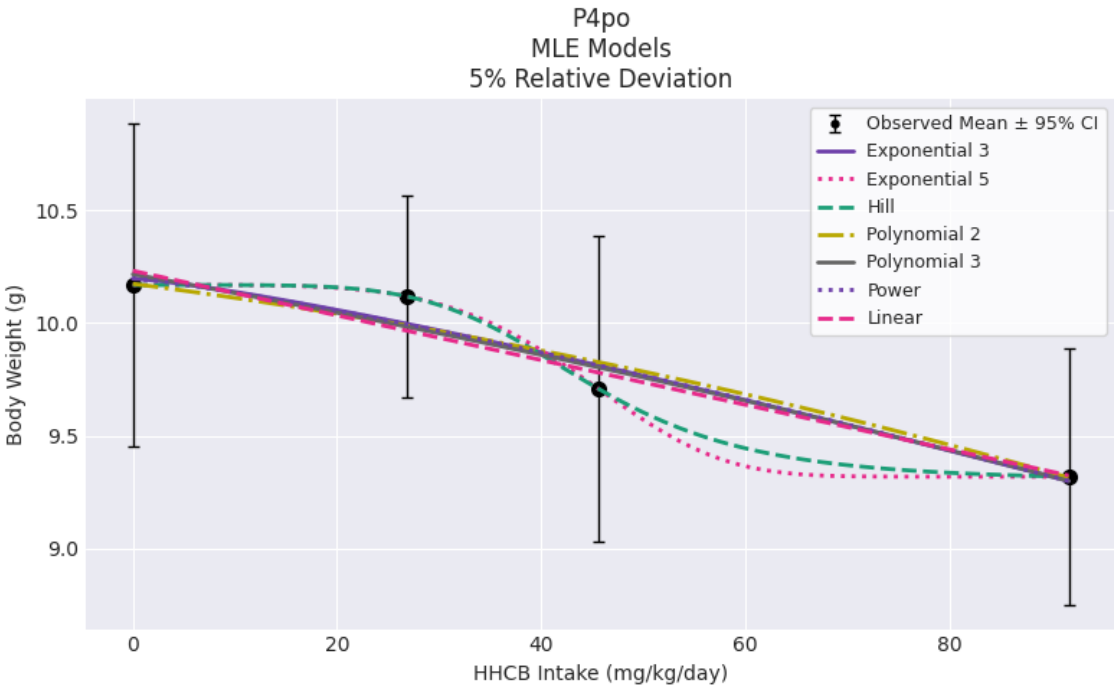
2.1.6.2 Settings

Setting	Value
BMR	5% Relative Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

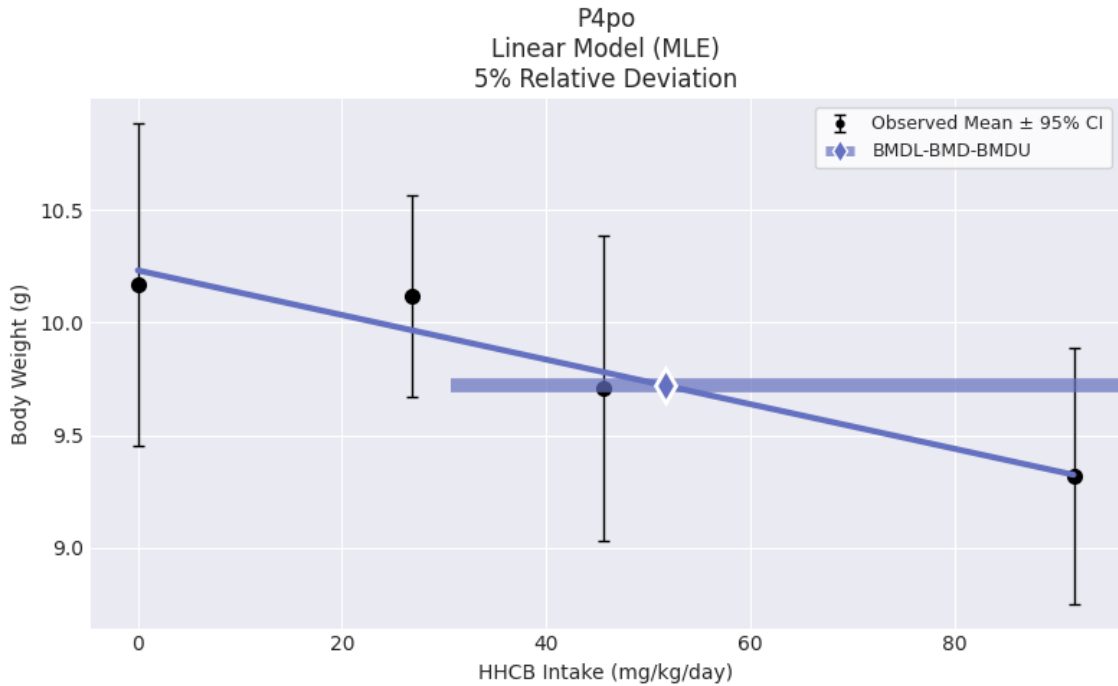
2.1.6.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	29.294	57.378	182.201	0.584	359.673	-0.097	-0.354	Viable
Exponential 5	16.98	47.126	241.216	-	361.373	-0.	<0.001	Questionable Zero degrees of freedom; saturated model

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	24.313	47.537	-	-	361.373	<0.001	<0.001	Questionable Zero degrees of freedom; saturated model
Polynomial 2	30.743	61.786	184.263	0.556	359.719	-0.018	-0.405	Viable
Polynomial 3	30.78	55.229	56.373	0.564	359.706	-0.164	-0.325	Viable
Power	30.837	57.605	180.57	0.58	359.678	-0.096	-0.358	Viable
Linear ^{ab}	30.715	51.662	185.396	0.836	357.732	-0.217	-0.245	Recommended - Lowest AIC
^a BMDS recommended best fitting model ^b User selected best fitting model								



2.1.6.4 Selected Model: Linear



Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	5% Relative Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-1e+06	1e+06
b1	0	-1e+06	1e+06
alpha	0	-18	18

Modeling Summary:

BMD	51.6619
BMDL	30.7146
BMDU	185.396
AIC	357.732
Log-Likelihood	-175.866
P-Value	0.835756
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	10.2316	no	0.232559
b1	-0.00990247	no	0.00436044

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alpha	2.11959	no	0.641757
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Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	25	10.1685	10.2316	-0.216772
26.8	23	10.1183	9.96623	0.500799
45.6	25	9.70871	9.78007	-0.245047
91.7	25	9.31817	9.32356	-0.0185301

Dose	N	Sample SD	Model Fitted SD
0	25	1.74181	1.45588
26.8	23	1.03711	1.45588
45.6	25	1.64478	1.45588
91.7	25	1.37775	1.45588

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-175.686	5	361.373
A2	-172.176	8	360.353
A3	-175.686	5	361.373
fitted	-175.866	3	357.732
reduced	-178.378	2	360.756

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	12.4034	6	0.0535511
Test 2	7.01985	3	0.0712678
Test 3	7.01985	3	0.0712678
Test 4	0.358837	2	0.835756

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.1.7 Bodyweight on PND 7, BMR = 1 SD

2.1.7.1 Dataset

Name: P7

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
0	25	16.698	2.136
26.8	23	16.284	1.337
45.6	24	15.791	1.967
91.7	25	15.18	2.24

Test 1 Dose Response: 0.0205

Test 2 Homogeneity of Variance: 0.082

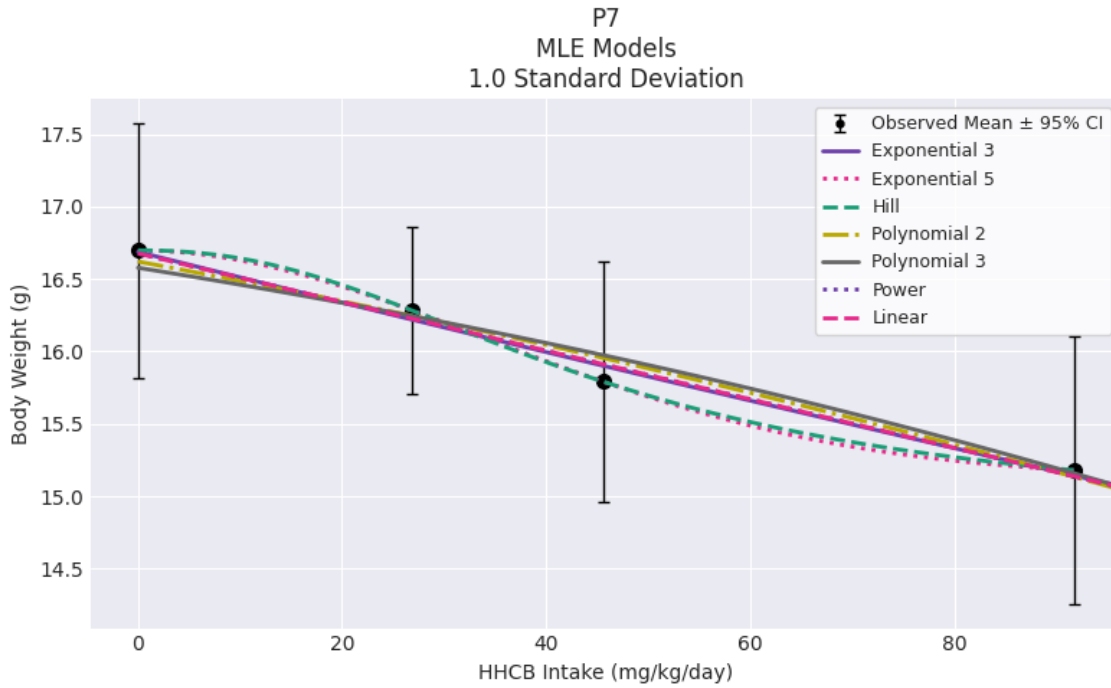
Test 3 Variance Model Selection: 0.082

2.1.7.2 Settings

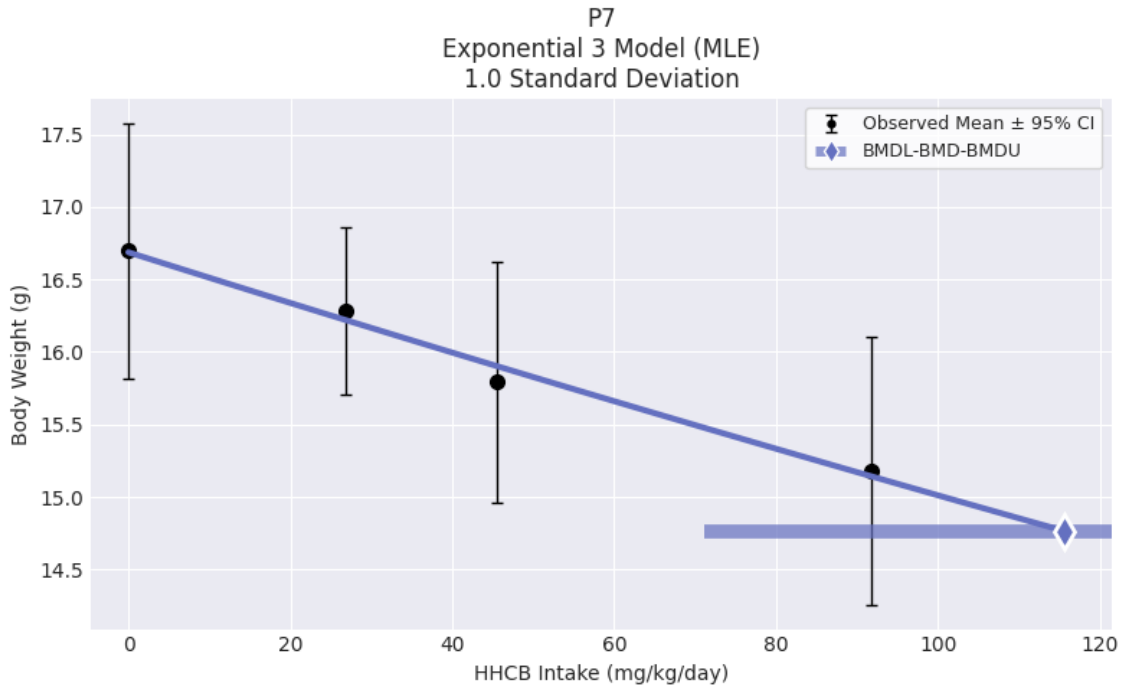
Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.1.7.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 ^{a b}	71.196	115.599	281.369	0.99	408.118	0.027	0.095	Recommended - Lowest AIC BMD/highest dose ratio > 1.0
Exponential 5	-	-	-	-	412.005	<0.001	-	Unusable Did not successfully execute.
Hill	-	-	-	-	412.005	0	-	Unusable Did not successfully execute.
Polynomial 2	72.144	113.474	115.823	0.627	410.241	0.201	0.117	Viable BMD/highest dose ratio > 1.0
Polynomial 3	71.595	114.29	116.656	0.555	410.354	0.315	0.054	Viable BMD/highest dose ratio > 1.0
Power	72.658	114.572	270.654	0.937	408.134	0.055	0.11	Viable BMD/highest dose ratio > 1.0
Linear	72.657	114.572	270.654	0.937	408.134	0.055	0.11	Viable BMD/highest dose ratio > 1.0
^a BMDS recommended best fitting model								
^b User selected best fitting model								



2.1.7.4 Selected Model: Exponential 3



Exponential 3 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR Distribution	1.0 Standard Deviation Normal + Constant variance
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Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	100
b	0	0	100
c	0	-20	0
d	1	1	18
log-alpha	0	-18	18

Modeling Summary:

BMD	115.599
BMDL	71.1955
BMDU	281.369
AIC	408.118
Log-Likelihood	-201.059
P-Value	0.990225
Model d.f.	3

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	16.6877	no	0.312739
b	0.00105906	no	0.000365813
d	1	yes	Not Reported
log-alpha	1.30767	no	0.143591

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	25	16.698	16.6877	0.0267614
26.8	23	16.2842	16.2207	0.158255
45.6	24	15.7912	15.901	-0.279506
91.7	25	15.18	15.1433	0.0954778

Dose	N	Sample SD	Model Fitted SD
0	25	2.1359	1.9229
26.8	23	1.33739	1.9229
45.6	24	1.96694	1.9229
91.7	25	2.24	1.9229

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-201.003	5	412.005
A2	-197.651	8	411.301
A3	-201.003	5	412.005
fitted	-201.059	2	406.118
reduced	-205.136	2	414.272

Tests of Mean and Variance Fits:

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Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	14.9705	6	0.0204877
Test 2	6.70383	3	0.0819613
Test 3	6.70383	3	0.0819613
Test 4	0.113067	3	0.990225

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.1.8 Bodyweight on PND 7, BMR = 5% RD

2.1.8.1 Dataset

Name: P7

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
0	25	16.698	2.136
26.8	23	16.284	1.337
45.6	24	15.791	1.967
91.7	25	15.18	2.24

Test 1 Dose Response: 0.0205

Test 2 Homogeneity of Variance: 0.082

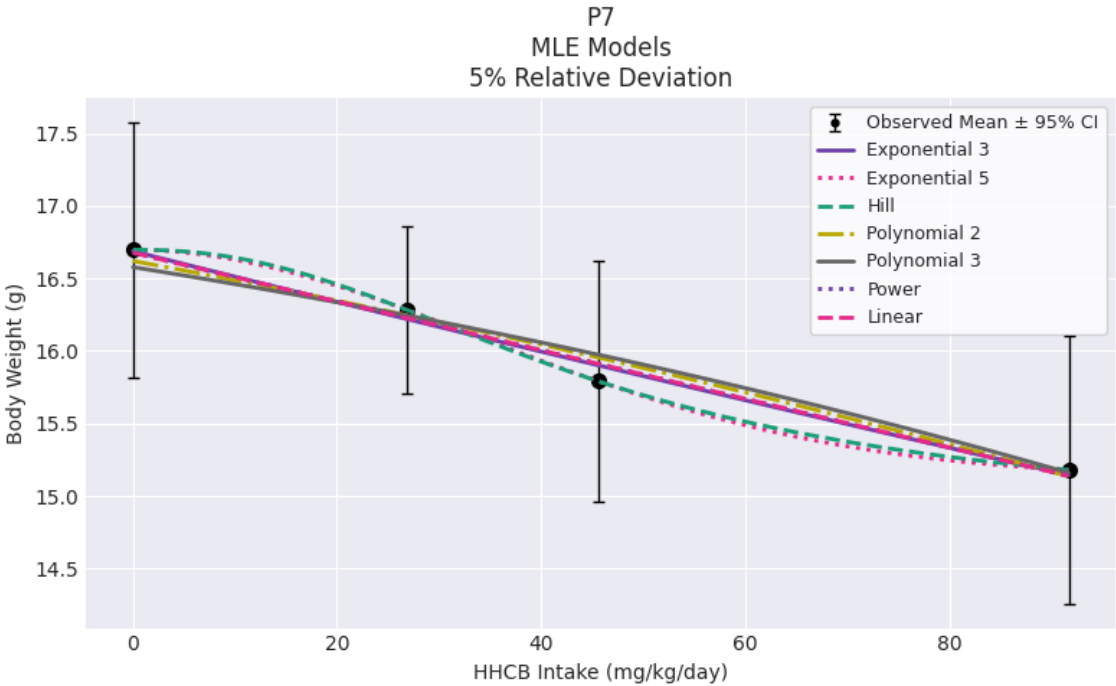
Test 3 Variance Model Selection: 0.082

2.1.8.2 Settings

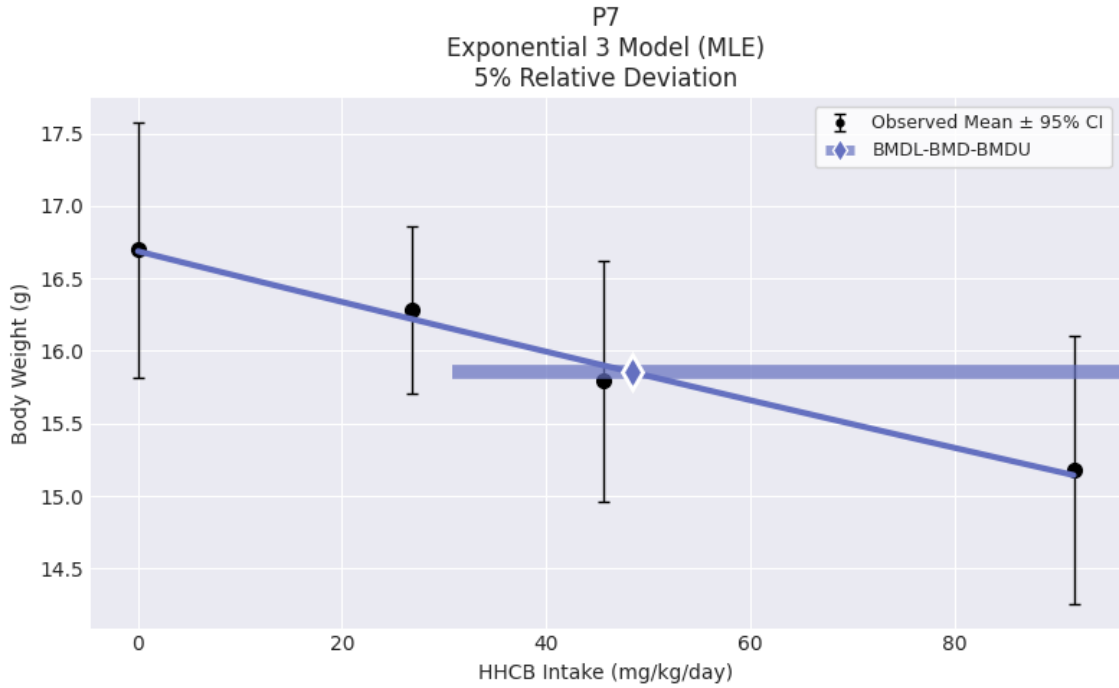
Setting	Value
BMR	5% Relative Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.1.8.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 ^{a b}	30.751	48.433	112.542	0.945	408.118	0.027	-0.28	Recommended - Lowest AIC
Exponential 5	14.768	42.722	223.689	-	412.005	<0.001	<0.001	Questionable Zero degrees of freedom; saturated model
Hill	11.813	42.56	25013.952	-	412.005	0	<0.001	Questionable Zero degrees of freedom; saturated model BMD/BMDL ratio > 3.0
Polynomial 2	32.176	55.57	115.391	0.627	410.241	0.201	-0.416	Viable
Polynomial 3	31.954	59.688	118.636	0.555	410.354	0.315	-0.471	Viable
Power	32.404	49.679	112.435	0.937	408.134	0.055	-0.307	Viable
Linear	32.404	49.679	112.44	0.937	408.134	0.055	-0.307	Viable
^a BMDS recommended best fitting model								
^b User selected best fitting model								



2.1.8.4 Selected Model: Exponential 3



Exponential 3 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	5% Relative Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	100
b	0	0	100
c	0	-20	0
d	1	1	18
log-alpha	0	-18	18

Modeling Summary:

BMD	48.433
BMDL	30.7513
BMDU	112.542
AIC	408.118
Log-Likelihood	-201.059
P-Value	0.945035
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	16.6877	no	0.312739

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b	0.00105906	no	0.000365813
d	1	yes	Not Reported
log-alpha	1.30767	no	0.143591

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	25	16.698	16.6877	0.0267614
26.8	23	16.2842	16.2207	0.158255
45.6	24	15.7912	15.901	-0.279506
91.7	25	15.18	15.1433	0.0954778

Dose	N	Sample SD	Model Fitted SD
0	25	2.1359	1.9229
26.8	23	1.33739	1.9229
45.6	24	1.96694	1.9229
91.7	25	2.24	1.9229

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-201.003	5	412.005
A2	-197.651	8	411.301
A3	-201.003	5	412.005
fitted	-201.059	3	408.118
reduced	-205.136	2	414.272

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	14.9705	6	0.0204877
Test 2	6.70383	3	0.0819613
Test 3	6.70383	3	0.0819613
Test 4	0.113067	2	0.945035

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.1.9 Bodyweight on PND 14, BMR = 1 SD

2.1.9.1 Dataset

Name: P14

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
0	25	33.764	3.112

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
26.8	23	32.298	2.025
45.6	24	31.645	2.997
91.7	25	29.939	2.079

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.0566

Test 3 Variance Model Selection: 0.0566

2.1.9.2 Settings

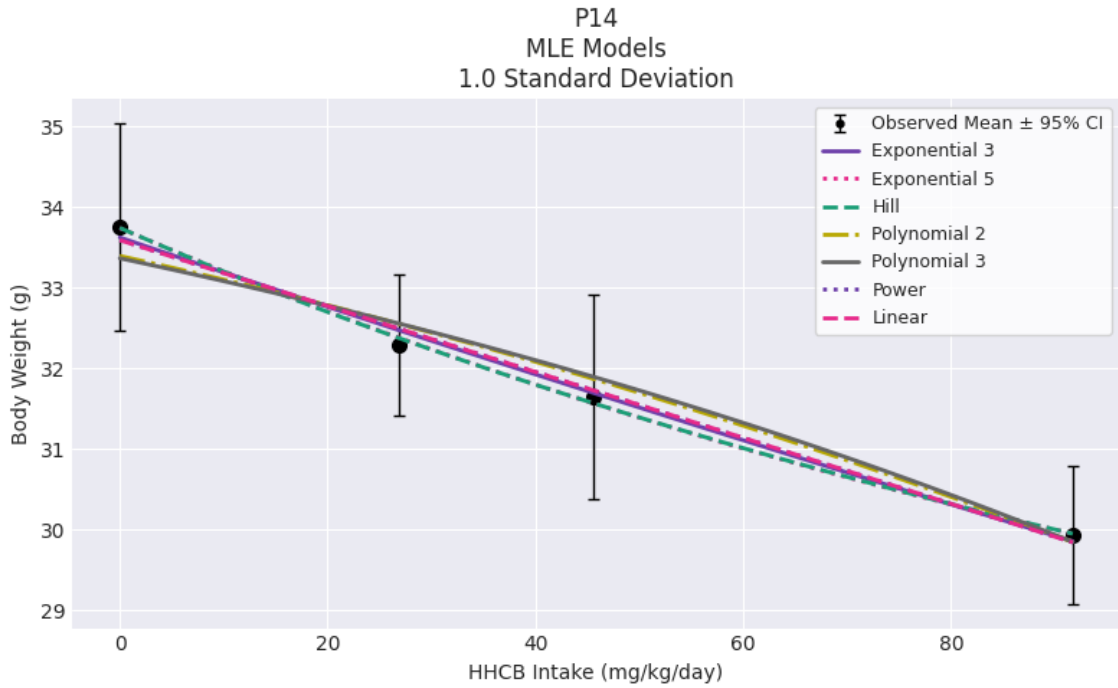
Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.1.9.3 Maximum Likelihood Approach

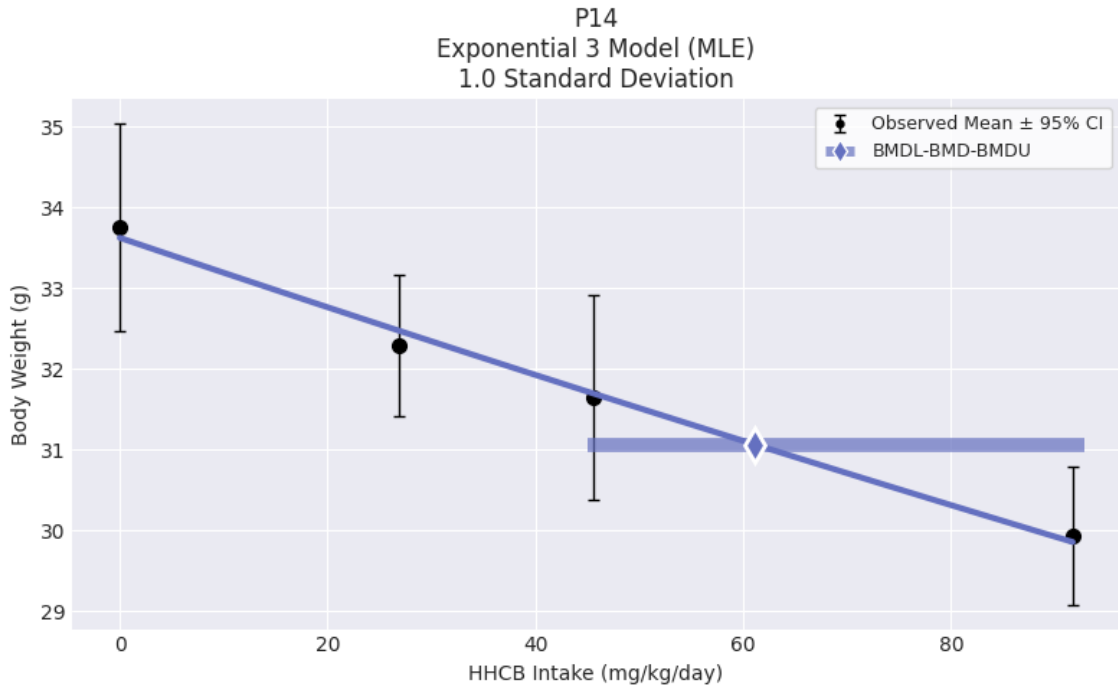
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 ^{a b}	45.056	61.068	92.778	0.895	463.446	0.269	-0.101	Recommended - Lowest AIC
Exponential 5	30.252	55.269	91.589	0.822	465.275	0.041	0.145	Viable
Hill	29.579	55.304	91.769	0.828	465.271	0.036	0.143	Viable
Polynomial 2	45.732	70.816	72.282	0.325	466.192	0.713	0.173	Viable
Polynomial 3	45.494	72.138	73.631	0.294	466.325	0.769	0.173	Viable
Power	47.039	62.61	93.468	0.856	463.536	0.334	-0.162	Viable
Linear	47.039	62.61	93.468	0.856	463.536	0.334	-0.162	Viable

^a BMDS recommended best fitting model

^b User selected best fitting model



2.1.9.4 Selected Model: Exponential 3



Exponential 3 Model

Version: pybmds 25.1 (bmdscore 25.1)

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Input Summary:

BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	100
b	0	0	100
c	0	-20	0
d	1	1	18
log-alpha	0	-18	18

Modeling Summary:

BMD	61.068
BMDL	45.056
BMDU	92.7778
AIC	463.446
Log-Likelihood	-228.723
P-Value	0.895198
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	33.626	no	0.417539
b	0.00129536	no	0.000244729
d	1	yes	Not Reported
log-alpha	1.87806	no	0.14359

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	25	33.7635	33.626	0.268782
26.8	23	32.2981	32.4787	-0.338592
45.6	24	31.6447	31.6973	-0.100737
91.7	25	29.9393	29.8599	0.155342

Dose	N	Sample SD	Model Fitted SD
0	25	3.11219	2.5575
26.8	23	2.02496	2.5575
45.6	24	2.99748	2.5575
91.7	25	2.07857	2.5575

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-228.612	5	467.224
A2	-224.844	8	465.688
A3	-228.612	5	467.224
fitted	-228.723	3	463.446
reduced	-241.232	2	486.464

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	32.7763	6	1.15778e-05
Test 2	7.53654	3	0.056627
Test 3	7.53654	3	0.056627
Test 4	0.22142	2	0.895198

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.1.10 Bodyweight on PND 14, BMR = 5% RD

2.1.10.1 Dataset

Name: P14

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
0	25	33.764	3.112
26.8	23	32.298	2.025
45.6	24	31.645	2.997
91.7	25	29.939	2.079

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.0566

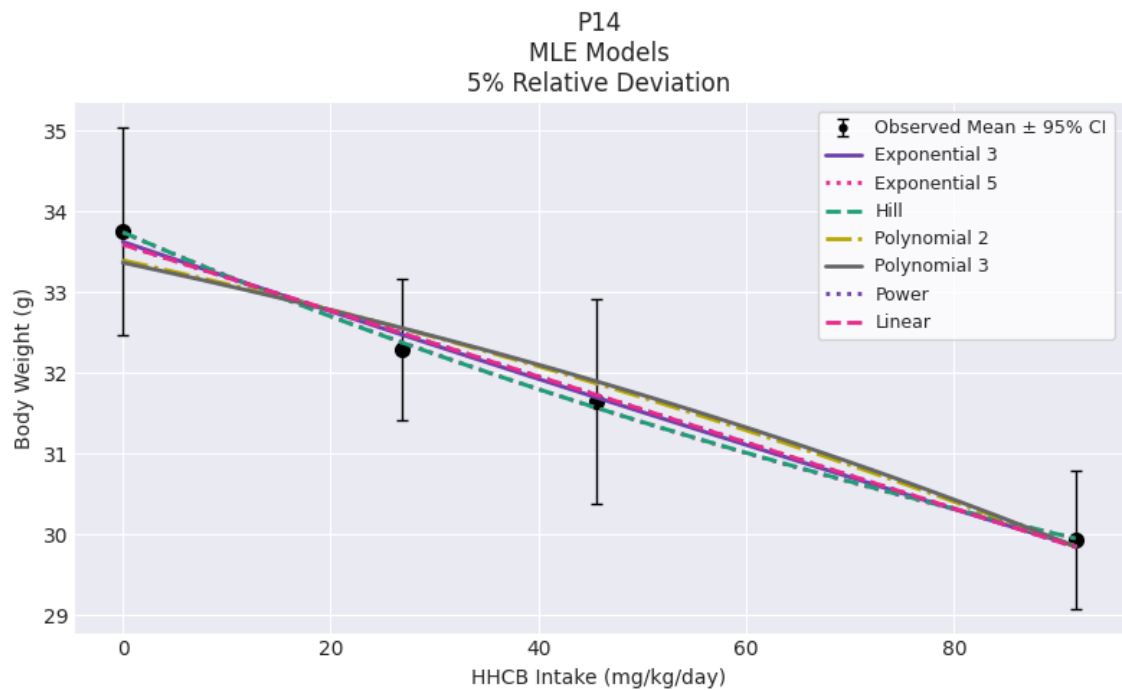
Test 3 Variance Model Selection: 0.0566

2.1.10.2 Settings

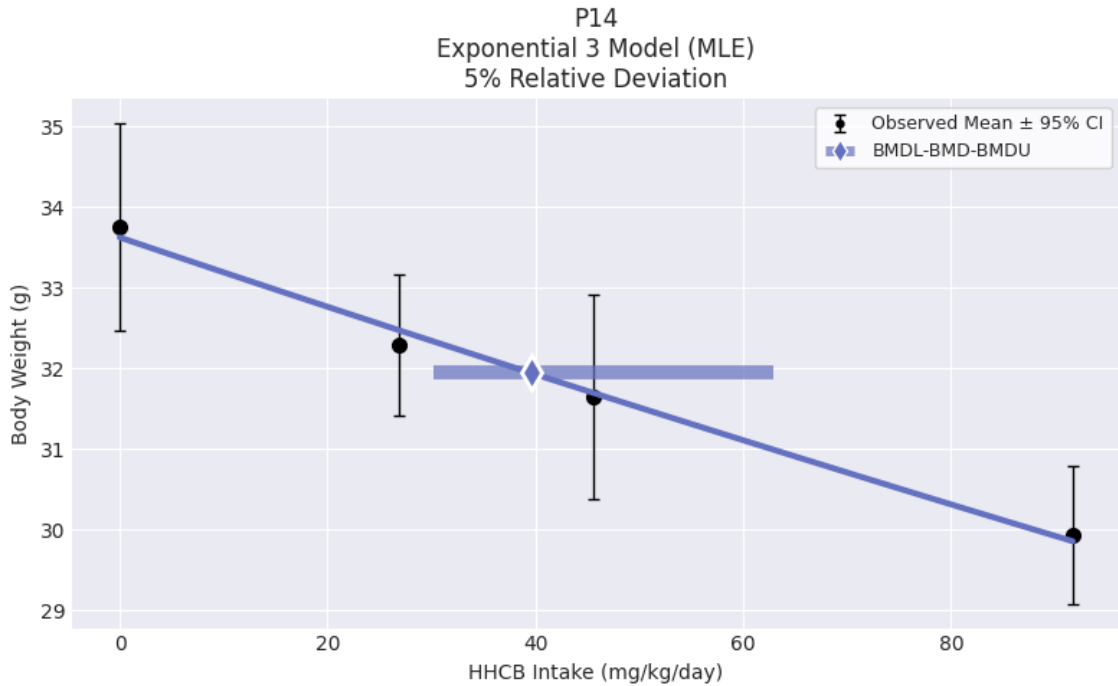
Setting	Value
BMR	5% Relative Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.1.10.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 ^{a b}	30.123	39.598	62.829	0.974	463.446	0.269	-0.101	Recommended - Lowest AIC
Exponential 5	17.587	34.119	61.862	0.822	465.275	0.041	-0.164	Viable
Hill	16.286	34.013	61.011	0.828	465.271	0.036	-0.156	Viable
Polynomial 2	31.02	49.304	67.859	0.325	466.192	0.713	-0.432	Viable
Polynomial 3	30.861	50.761	70.487	0.294	466.325	0.769	-0.482	Viable
Power	31.833	41.1	63.554	0.856	463.536	0.334	-0.162	Viable
Linear	31.833	41.1	58.727	0.856	463.536	0.334	-0.162	Viable
^a BMDS recommended best fitting model ^b User selected best fitting model								



2.1.10.4 Selected Model: Exponential 3



Exponential 3 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	5% Relative Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	100
b	0	0	100
c	0	-20	0
d	1	1	18
log-alpha	0	-18	18

Modeling Summary:

BMD	39.5977
BMDL	30.1226
BMDU	62.8289
AIC	463.446
Log-Likelihood	-228.723
P-Value	0.974059
Model d.f.	3

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	33.626	no	0.417539
b	0.00129536	no	0.000244729

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d	1	yes	Not Reported
log-alpha	1.87806	no	0.14359

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	25	33.7635	33.626	0.268782
26.8	23	32.2981	32.4787	-0.338592
45.6	24	31.6447	31.6973	-0.100737
91.7	25	29.9393	29.8599	0.155342

Dose	N	Sample SD	Model Fitted SD
0	25	3.11219	2.5575
26.8	23	2.02496	2.5575
45.6	24	2.99748	2.5575
91.7	25	2.07857	2.5575

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-228.612	5	467.224
A2	-224.844	8	465.688
A3	-228.612	5	467.224
fitted	-228.723	2	461.446
reduced	-241.232	2	486.464

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	32.7763	6	1.15778e-05
Test 2	7.53654	3	0.056627
Test 3	7.53654	3	0.056627
Test 4	0.22142	3	0.974059

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.1.11 Bodyweight on PND 21, BMR = 1 SD

2.1.11.1 Dataset

Name: P21

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
0	25	55.038	4.465

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Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
26.8	23	53.561	2.761
45.6	24	52.212	4.236
91.7	25	49.06	3.187

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.0641

Test 3 Variance Model Selection: 0.0641

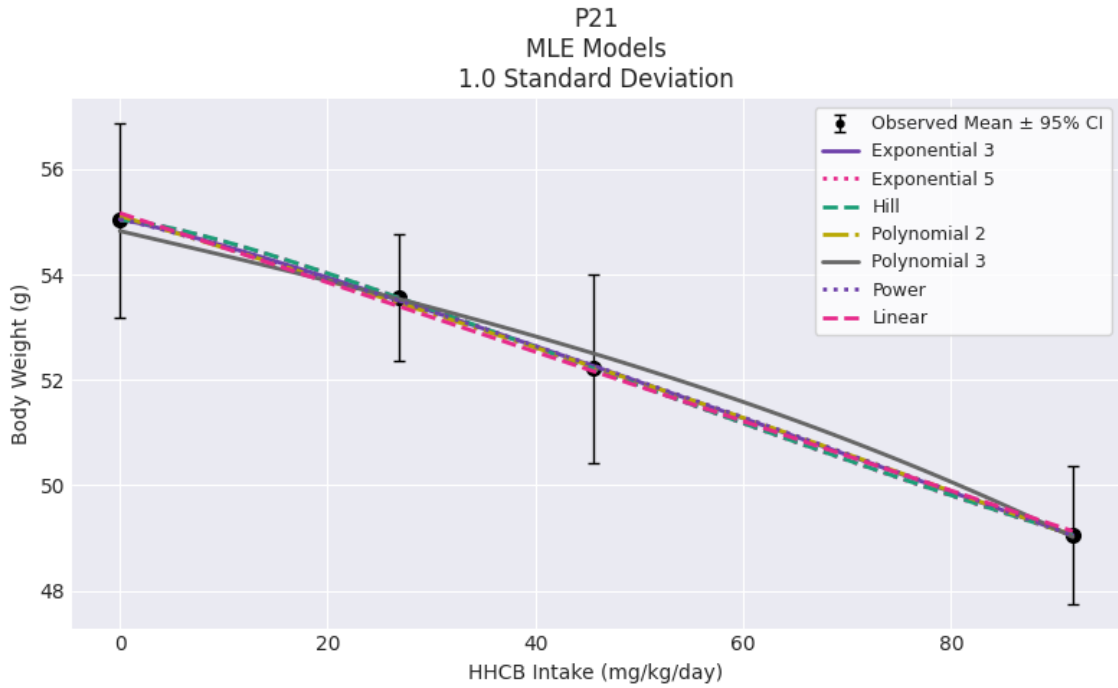
2.1.11.2 Settings

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

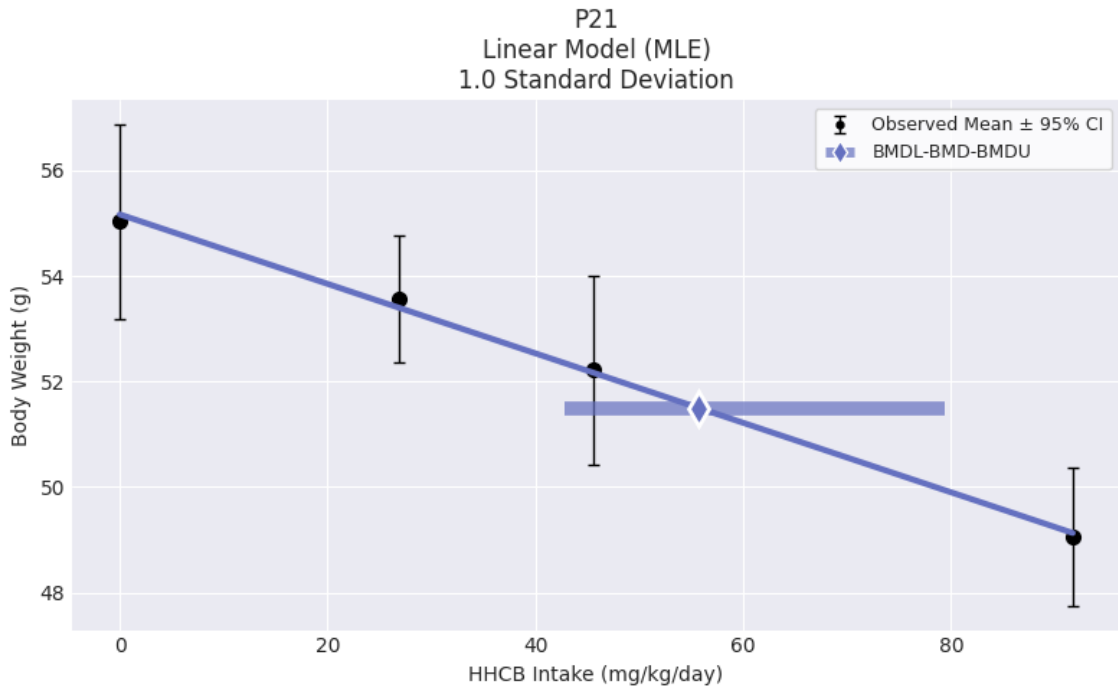
2.1.11.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	41.473	58.374	83.169	0.996	535.24	-0.014	-0.064	Viable
Exponential 5	35.767	57.198	83.075	-	537.231	-0.	-0.	Questionable Zero degrees of freedom; saturated model
Hill	51.759	57.246	83.006	-	537.231	-0.	<0.001	Questionable Zero degrees of freedom; saturated model
Polynomial 2	42.942	57.427	58.615	0.863	535.26	-0.101	-0.045	Viable
Polynomial 3	42.575	66.028	85.105	-	537.467	0.289	-0.384	Questionable Zero degrees of freedom; saturated model
Power	42.985	58.595	83.278	0.911	535.243	-0.016	-0.076	Viable
Linear ^{a b}	42.841	55.674	79.366	0.957	533.318	-0.175	0.066	Recommended - Lowest AIC

^a BMDS recommended best fitting model^b User selected best fitting model



2.1.11.4 Selected Model: Linear



Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR

1.0 Standard Deviation

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Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-1e+06	1e+06
b1	0	-1e+06	1e+06
alpha	0	-18	18

Modeling Summary:

BMD	55.6744
BMDL	42.8415
BMDU	79.3665
AIC	533.318
Log-Likelihood	-263.659
P-Value	0.957482
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	55.1655	no	0.586531
b1	-0.0658532	no	0.0109824
alpha	13.442	no	25.945

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	25	55.0375	55.1655	-0.174505
26.8	23	53.5607	53.4006	0.209492
45.6	24	52.2116	52.1626	0.065559
91.7	25	49.0602	49.1267	-0.0906676

Dose	N	Sample SD	Model Fitted SD
0	25	4.46515	3.66634
26.8	23	2.76113	3.66634
45.6	24	4.23617	3.66634
91.7	25	3.18685	3.66634

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-263.615	5	537.231
A2	-259.986	8	535.971
A3	-263.615	5	537.231
fitted	-263.659	3	533.318
reduced	-278.948	2	561.897

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	37.9254	6	1.1617e-06

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Test 2	7.25957	3	0.0640687
Test 3	7.25957	3	0.0640687
Test 4	0.0868963	2	0.957482

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.1.12 Bodyweight on PND 21, BMR = 5% RD

2.1.12.1 Dataset

Name: P21

Dose (mg/kg/day)	N	Mean (g)	Std. Dev. (g)
0	25	55.038	4.465
26.8	23	53.561	2.761
45.6	24	52.212	4.236
91.7	25	49.06	3.187

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.0641

Test 3 Variance Model Selection: 0.0641

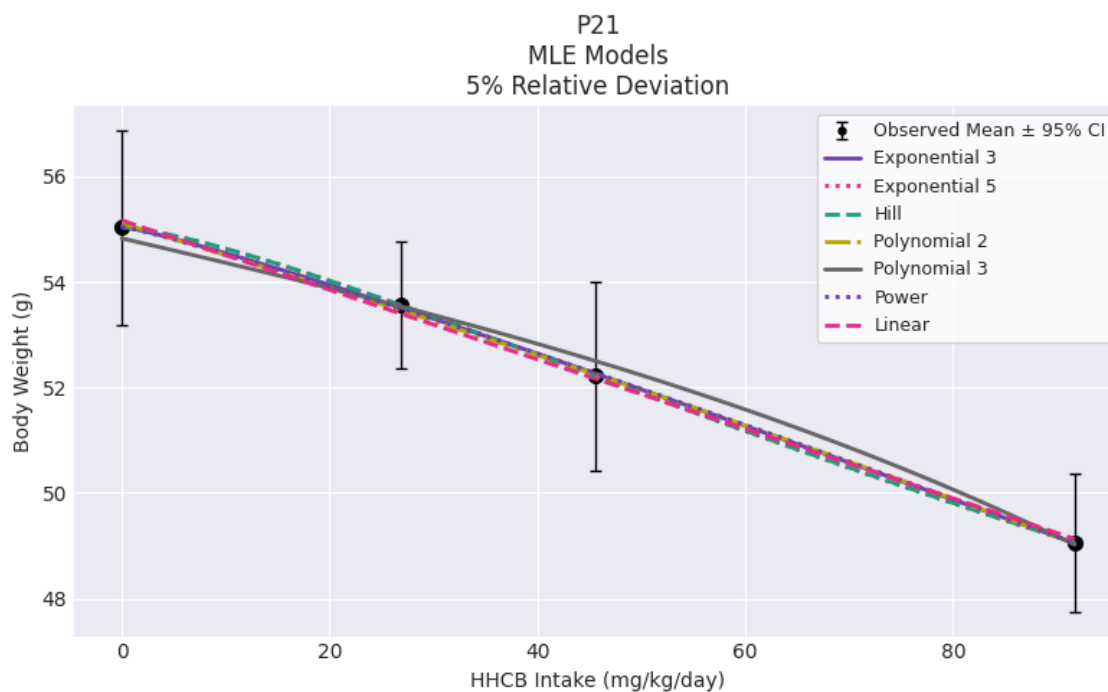
2.1.12.2 Settings

Setting	Value
BMR	5% Relative Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

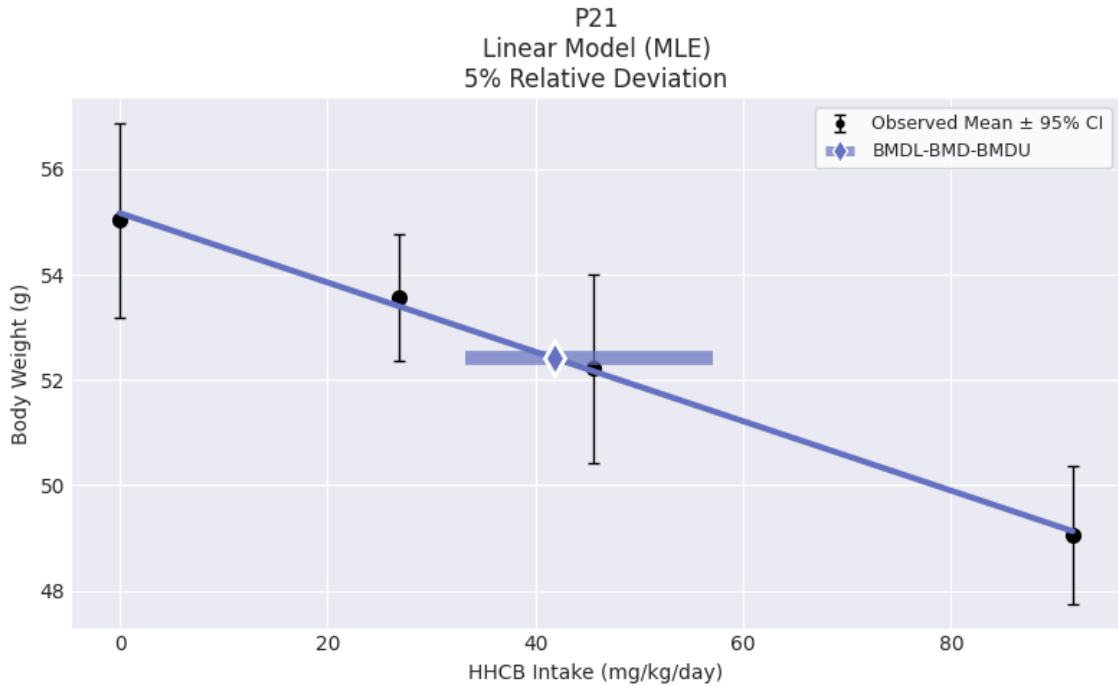
2.1.12.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	31.902	45.074	69.118	0.996	535.24	-0.014	-0.064	Viable
Exponential 5	25.756	44.583	69.086	-	537.231	-0.	-0.	Questionable Zero degrees of freedom; saturated model

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	25.442	44.58	67.871	-	537.231	-0.	<0.001	Questionable Zero degrees of freedom; saturated model
Polynomial 2	33.331	43.924	44.833	0.863	535.26	-0.101	-0.045	Viable
Polynomial 3	33.063	52.349	72.265	-	537.467	0.289	-0.384	Questionable Zero degrees of freedom; saturated model
Power	33.351	45.174	69.354	0.911	535.243	-0.016	-0.076	Viable
Linear ^{a b}	33.251	41.885	57.123	0.957	533.318	-0.175	0.066	Recommended - Lowest AIC
^a BMDS recommended best fitting model ^b User selected best fitting model								



2.1.12.4 Selected Model: Linear



Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	5% Relative Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-1e+06	1e+06
b1	0	-1e+06	1e+06
alpha	0	-18	18

Modeling Summary:

BMD	41.8852
BMDL	33.2506
BMDU	57.123
AIC	533.318
Log-Likelihood	-263.659
P-Value	0.957482
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	55.1655	no	0.586531
b1	-0.0658532	no	0.0109824

alpha	13.442	no	25.945
-------	--------	----	--------

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	25	55.0375	55.1655	-0.174505
26.8	23	53.5607	53.4006	0.209492
45.6	24	52.2116	52.1626	0.065559
91.7	25	49.0602	49.1267	-0.0906676

Dose	N	Sample SD	Model Fitted SD
0	25	4.46515	3.66634
26.8	23	2.76113	3.66634
45.6	24	4.23617	3.66634
91.7	25	3.18685	3.66634

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-263.615	5	537.231
A2	-259.986	8	535.971
A3	-263.615	5	537.231
fitted	-263.659	3	533.318
reduced	-278.948	2	561.897

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	37.9254	6	1.1617e-06
Test 2	7.25957	3	0.0640687
Test 3	7.25957	3	0.0640687
Test 4	0.0868963	2	0.957482

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.2 Continuous Modeling of F1 Male and Female Bodyweight at Sexual Maturation

Report Generated: 2025-Apr-23 20:04 UTC

Analysis URL: [View](#)

BMDS Online Version: 24.1 (pybmds 24.1; bmdscore 24.1)

2.2.1 Male Bodyweight at Sexual Maturation, BMR = 1 SD**2.2.1.1 Dataset****Name:** Male maturation EOGRTS IFF

Dose (mg/kg-d)	N	Mean (Grams)	Std. Dev. (Grams)
0	60	235.25	33.68
26.8	60	235.84	32.11
45.6	60	231.42	34.7
91.7	60	216.13	25.27

Test 1 Dose Response: 0.0012

Test 2 Homogeneity of Variance: 0.0767

Test 3 Variance Model Selection: 0.0767

2.2.1.2 Settings

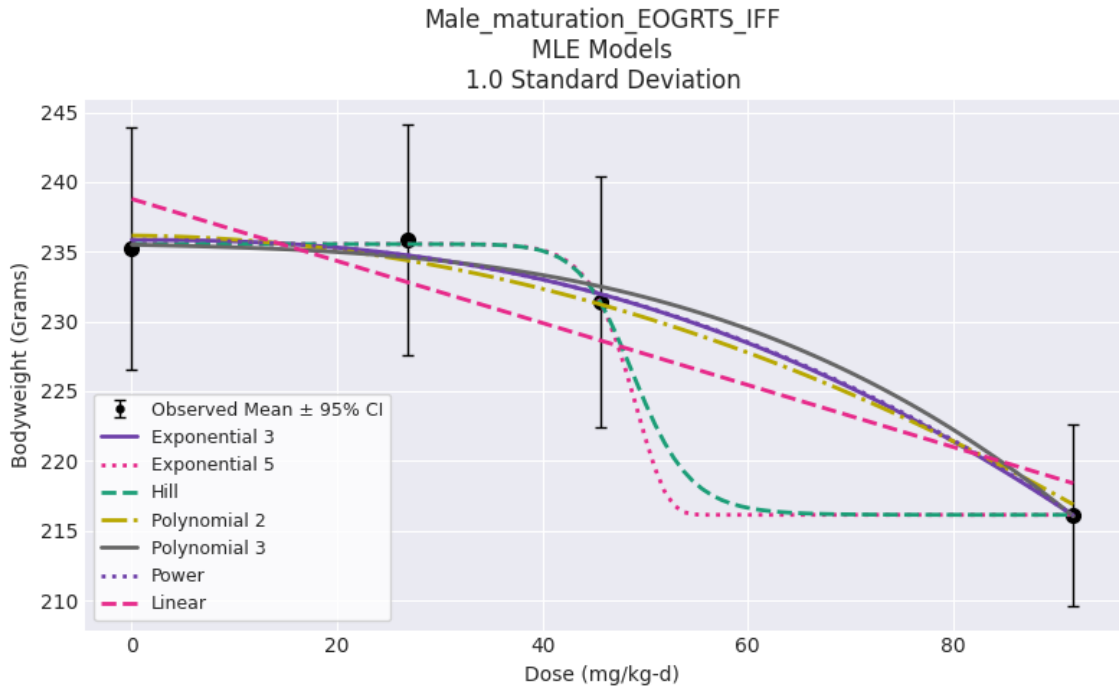
Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.2.1.3 Maximum Likelihood Approach

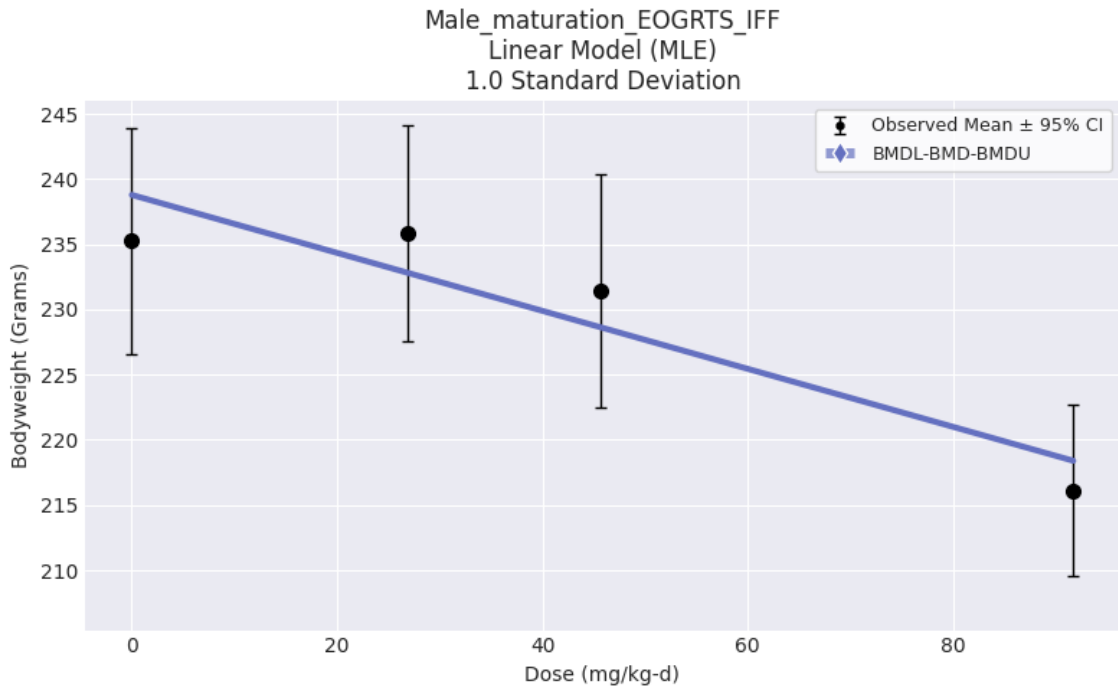
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	94.154	112.641	117.198	0.945	2343.514	-0.146	0.012	Viable BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Exponential 5	-	-	-	0.918	2343.412	-0.073	-	Unusable Did not successfully execute.
Hill	-	-	-	0.918	2343.412	-0.073	-	Unusable Did not successfully execute.
Polynomial 2	95.709	117.421	189.923	0.643	2343.616	-0.224	-0.182	Viable BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Polynomial 3	95.077	108.401	110.645	-	2345.572	-0.063	0.024	Questionable Zero degrees of freedom; saturated model BMDL/highest dose ratio > 1.0

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
								BMD/highest dose ratio > 1.0
Power	91.874	111.784	186.755	0.733	2343.517	-0.146	0.012	Viable BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Linear ^{a b}	97.364	141.793	260.799	0.352	2343.487	-0.868	-0.556	Recommended - Lowest AIC BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0

^a BMDS recommended best fitting model
^b User selected best fitting model



2.2.1.4 Selected Model: Linear



Linear Model

Version: pybmds 24.1 (bmdscore 24.1)

Input Summary:

BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-1e+06	1e+06
b1	0	-1e+06	1e+06
alpha	0	-18	18

Modeling Summary:

BMD	141.793
BMDL	97.3638
BMDU	260.799
AIC	2343.49
Log-Likelihood	-1168.74
P-Value	0.35236
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	238.782	no	3.22071
b1	-0.222342	no	0.0608492
alpha	993.916	no	90179.9

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Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	60	235.25	238.782	-0.867698
26.8	60	235.84	232.823	0.741316
45.6	60	231.42	228.643	0.682355
91.7	60	216.13	218.393	-0.555972

Dose	N	Sample SD	Model Fitted SD
0	60	33.68	31.5264
26.8	60	32.11	31.5264
45.6	60	34.7	31.5264
91.7	60	25.27	31.5264

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-1167.7	5	2345.4
A2	-1164.27	8	2344.55
A3	-1167.7	5	2345.4
fitted	-1168.74	3	2343.49
reduced	-1175.24	2	2354.48

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	21.9333	6	0.00124501
Test 2	6.85271	3	0.0767436
Test 3	6.85271	3	0.0767436
Test 4	2.0862	2	0.35236

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.2.2 Male Bodyweight at Sexual Maturation, BMR = 10% RD

2.2.2.1 Dataset

Name: Male maturation EOGRTS IFF

Dose (mg/kg-d)	N	Mean (Grams)	Std. Dev. (Grams)
0	60	235.25	33.68
26.8	60	235.84	32.11
45.6	60	231.42	34.7
91.7	60	216.13	25.27

Test 1 Dose Response: 0.0012

1878 Test 2 Homogeneity of Variance: 0.0767

1879 Test 3 Variance Model Selection: 0.0767

1880 **2.2.2.2 Settings**

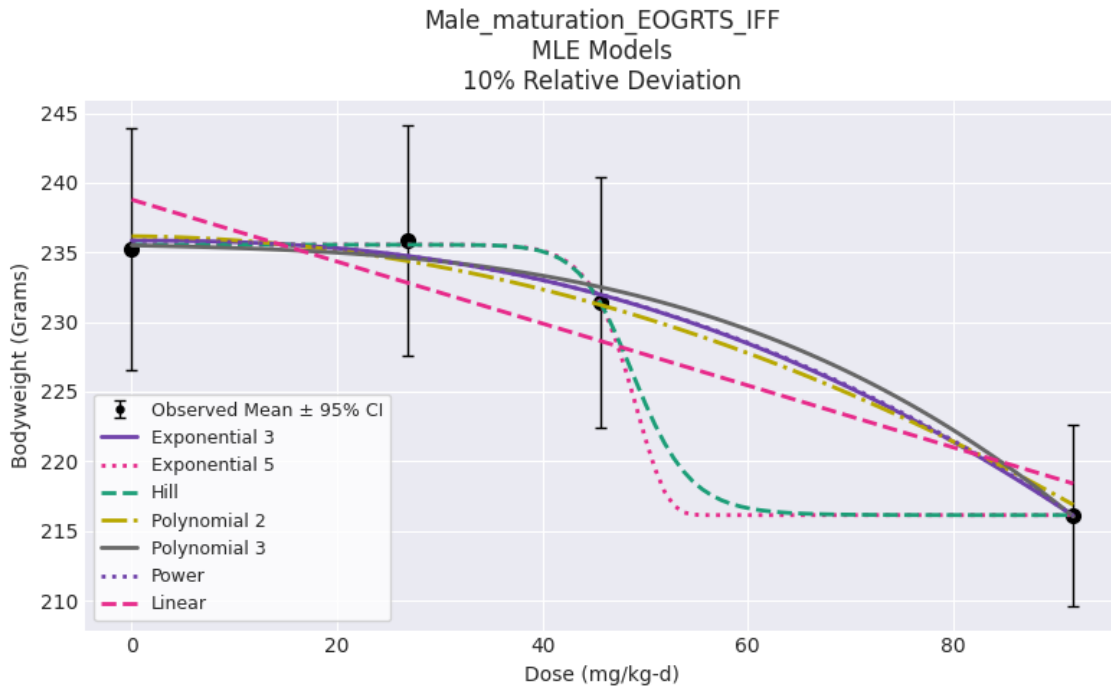
1881

Setting	Value
BMR	10% Relative Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

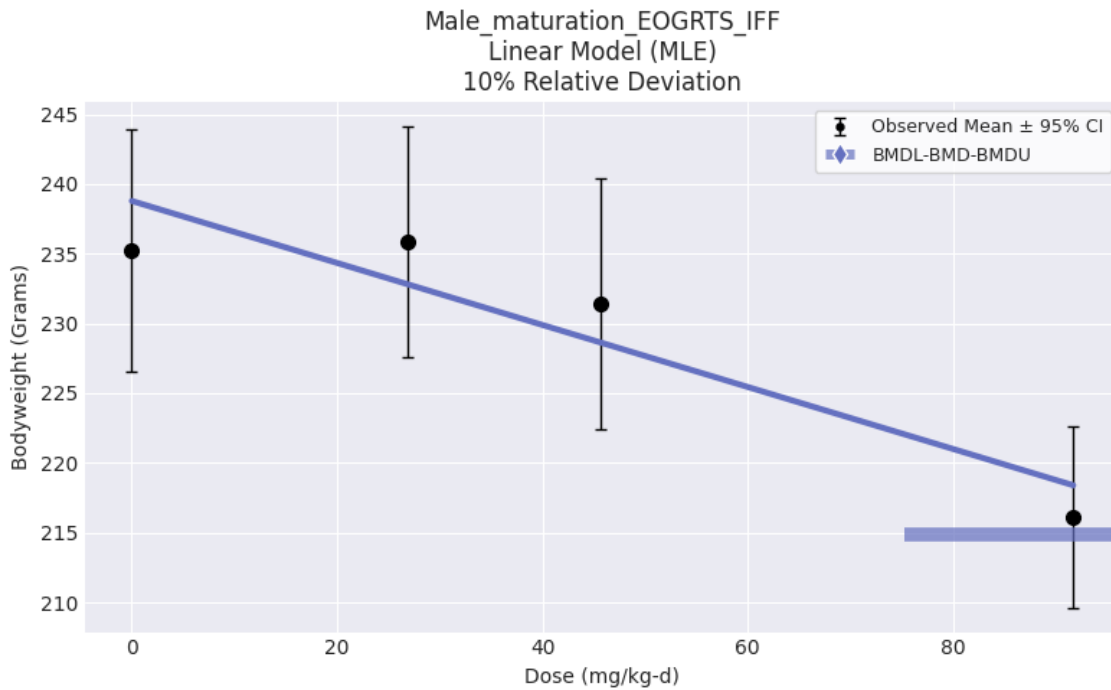
1882 **2.2.2.3 Maximum Likelihood Approach**

1883

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	81.222	99.129	144.391	0.945	2343.514	-0.146	0.012	Viable BMD/highest dose ratio > 1.0
Exponential 5	-	-	-	0.918	2343.412	-0.073	-	Unusable Did not successfully execute.
Hill	-	-	-	0.918	2343.412	-0.073	-	Unusable Did not successfully execute.
Polynomial 2	81.534	101.624	141.857	0.643	2343.616	-0.224	-0.182	Viable BMD/highest dose ratio > 1.0
Polynomial 3	82.785	98.044	100.074	-	2345.572	-0.063	0.024	Questionable Zero degrees of freedom; saturated model BMD/highest dose ratio > 1.0
Power	81.348	98.906	142.943	0.733	2343.517	-0.146	0.012	Viable BMD/highest dose ratio > 1.0
Linear ^{a b}	75.242	107.394	192.408	0.352	2343.487	-0.868	-0.556	Recommended - Lowest AIC BMD/highest dose ratio > 1.0
^a BMDS recommended best fitting model								
^b User selected best fitting model								



2.2.2.4 Selected Model: Linear



Linear Model

Version: pybmds 24.1 (bmdscore 24.1)

Input Summary:

BMR	10% Relative Deviation
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Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-1e+06	1e+06
b1	0	-1e+06	1e+06
alpha	0	-18	18

Modeling Summary:

BMD	107.394
BMDL	75.2423
BMDU	192.408
AIC	2343.49
Log-Likelihood	-1168.74
P-Value	0.35236
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	238.782	no	3.22071
b1	-0.222342	no	0.0608492
alpha	993.916	no	90179.9

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	60	235.25	238.782	-0.867698
26.8	60	235.84	232.823	0.741316
45.6	60	231.42	228.643	0.682355
91.7	60	216.13	218.393	-0.555972

Dose	N	Sample SD	Model Fitted SD
0	60	33.68	31.5264
26.8	60	32.11	31.5264
45.6	60	34.7	31.5264
91.7	60	25.27	31.5264

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-1167.7	5	2345.4
A2	-1164.27	8	2344.55
A3	-1167.7	5	2345.4
fitted	-1168.74	3	2343.49
reduced	-1175.24	2	2354.48

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	21.9333	6	0.00124501

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Test 2	6.85271	3	0.0767436
Test 3	6.85271	3	0.0767436
Test 4	2.0862	2	0.35236

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.2.3 Female Bodyweight at Sexual Maturation, BMR = 1 SD

2.2.3.1 Dataset

Name: Female maturation EOGRTS IFF

Dose (mg/kg-d)	N	Mean (Grams)	Std. Dev. (Grams)
0	60	107.91	11.48
26.8	60	105.43	11.54
45.6	60	104.87	12.4
91.7	60	100.92	9.34

Test 1 Dose Response: 0.0098

Test 2 Homogeneity of Variance: 0.1699

Test 3 Variance Model Selection: 0.1699

2.2.3.2 Settings

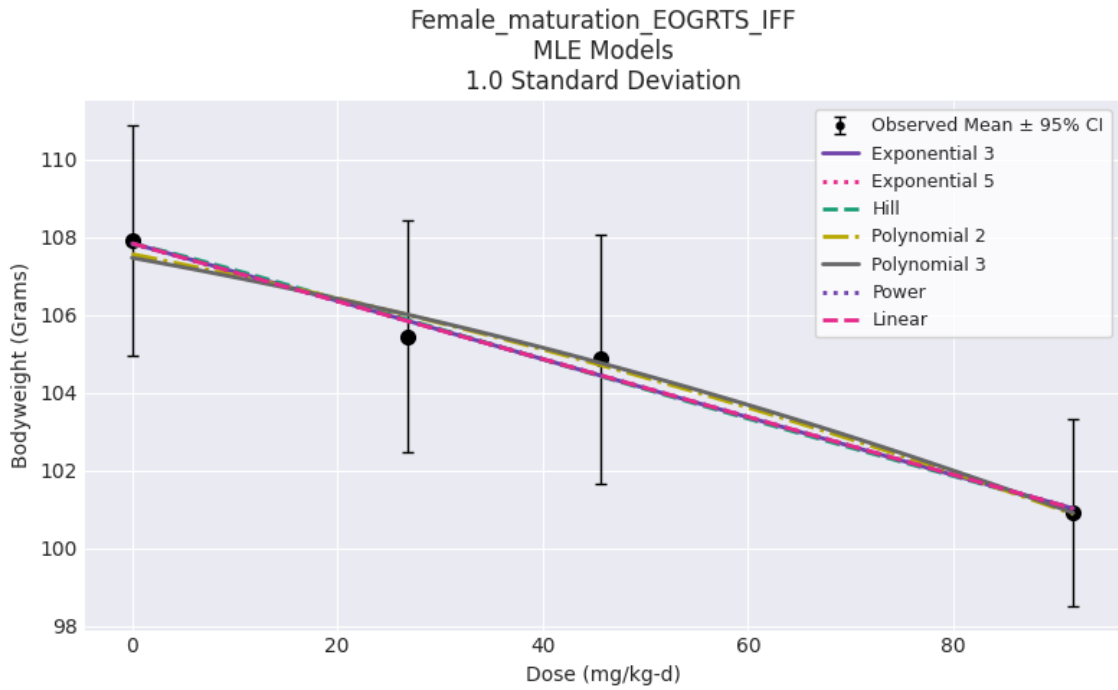
Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.2.3.3 Maximum Likelihood Approach

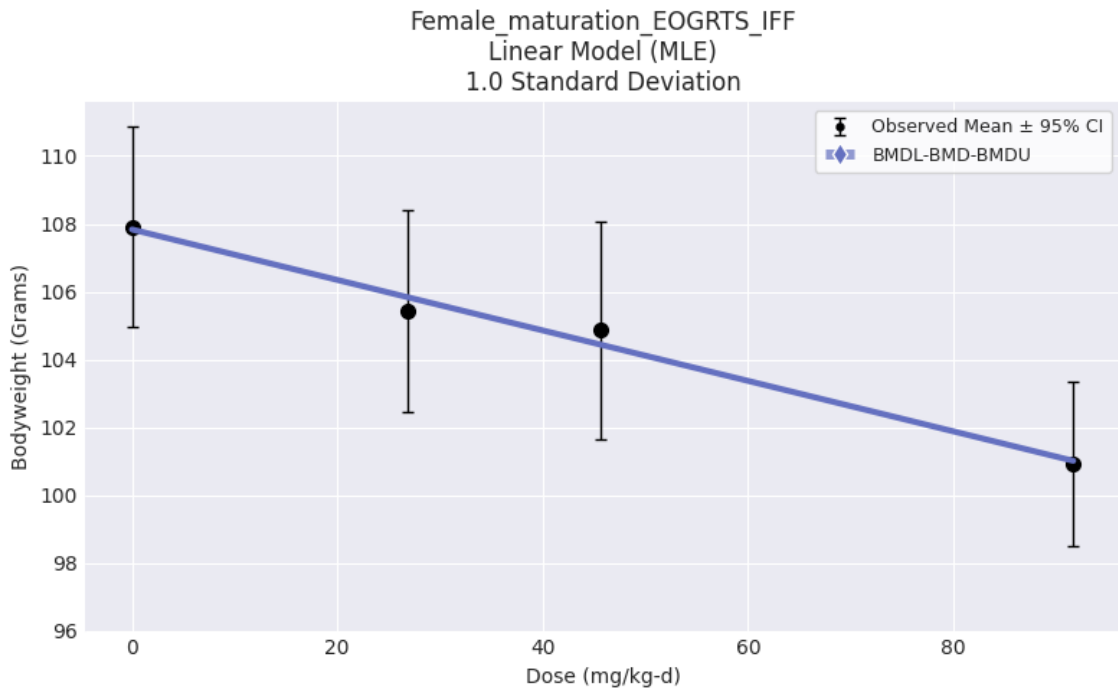
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	101.49	151.67	300.859	0.67	1846.876	0.055	-0.066	Viable BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Exponential 5	101.418	151.667	300.41	-	1848.876	0.055	-0.066	Questionable Zero degrees of

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Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
								freedom; saturated model BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Hill	102.09	158.648	-	-	1848.895	0.065	-0.067	Questionable Zero degrees of freedom; saturated model BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Polynomial 2	100.082	134.872	137.664	0.632	1846.924	0.245	0.035	Viable BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Polynomial 3	98.934	133.854	136.625	0.609	1846.957	0.31	0.014	Viable BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Power	101.087	149.671	289.507	0.674	1846.871	0.057	-0.061	Viable BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Linear ^{a b}	101.162	149.974	289.504	0.916	1844.871	0.052	-0.064	Recommended - Lowest AIC BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
^a BMDS recommended best fitting model ^b User selected best fitting model								



2.2.3.4 Selected Model: Linear



Linear Model

Version: pybmds 24.1 (bmdscore 24.1)

Input Summary:

BMR	1.0 Standard Deviation
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Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-1e+06	1e+06
b1	0	-1e+06	1e+06
alpha	0	-18	18

Modeling Summary:

BMD	149.974
BMDL	101.162
BMDU	289.504
AIC	1844.87
Log-Likelihood	-919.436
P-Value	0.915527
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	107.834	no	1.13953
b1	-0.0743913	no	0.0215264
alpha	124.473	no	1414.35

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	60	107.91	107.834	0.0524846
26.8	60	105.43	105.841	-0.285155
45.6	60	104.87	104.442	0.297044
91.7	60	100.92	101.013	-0.0643733

Dose	N	Sample SD	Model Fitted SD
0	60	11.48	11.1567
26.8	60	11.54	11.1567
45.6	60	12.4	11.1567
91.7	60	9.34	11.1567

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-919.347	5	1848.69
A2	-916.834	8	1849.67
A3	-919.347	5	1848.69
fitted	-919.436	3	1844.87
reduced	-925.26	2	1854.52

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	16.8515	6	0.00984485
Test 2	5.02664	3	0.169857
Test 3	5.02664	3	0.169857
Test 4	0.176512	2	0.915527

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.2.4 Female Bodyweight at Sexual Maturation, BMR = 10% RD

2.2.4.1 Dataset

Name: Female maturation EOGRTS IFF

Dose (mg/kg-d)	N	Mean (Grams)	Std. Dev. (Grams)
0	60	107.91	11.48
26.8	60	105.43	11.54
45.6	60	104.87	12.4
91.7	60	100.92	9.34

Test 1 Dose Response: 0.0098

Test 2 Homogeneity of Variance: 0.1699

Test 3 Variance Model Selection: 0.1699

2.2.4.2 Settings

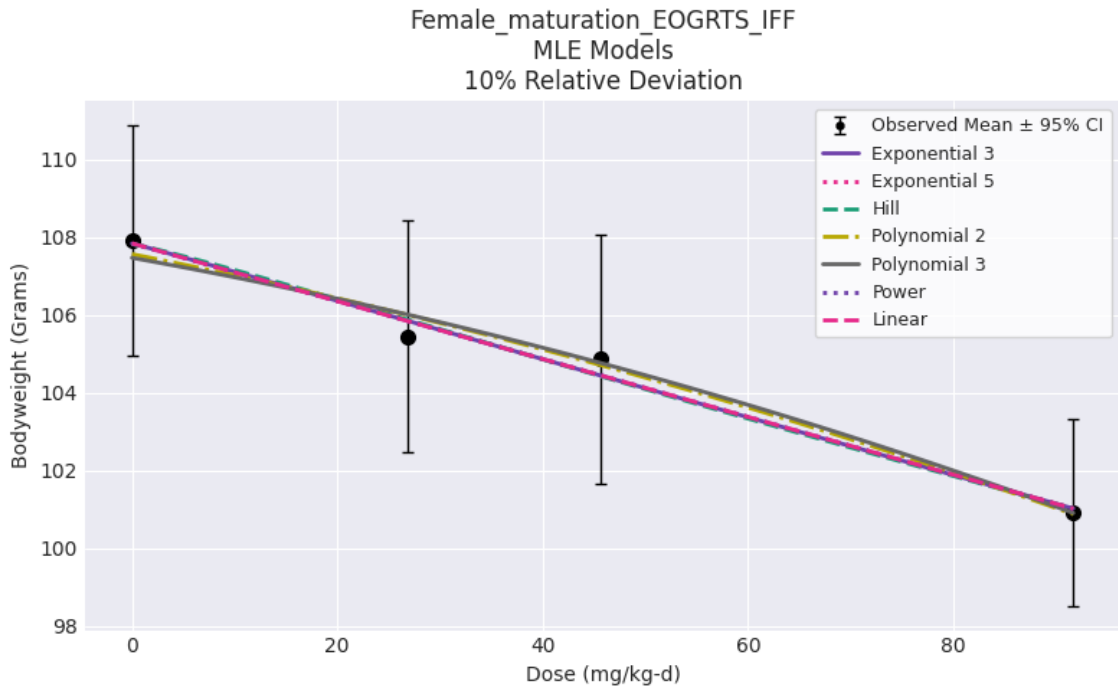
Setting	Value
BMR	10% Relative Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.2.4.3 Maximum Likelihood Approach

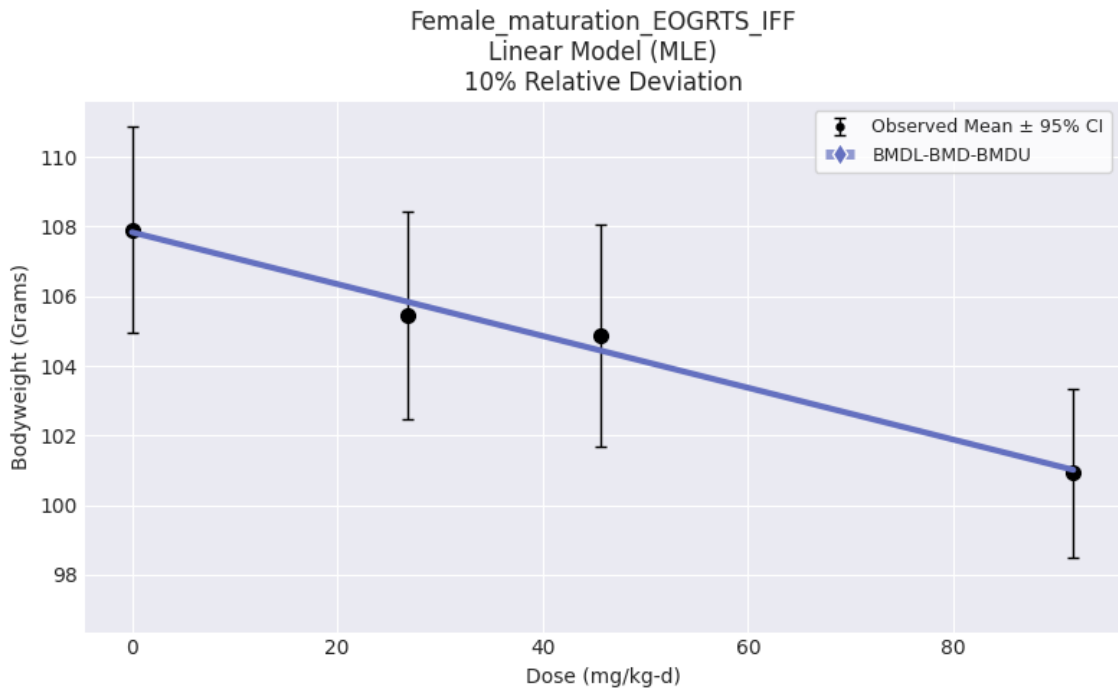
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	99.561	146.426	283.479	0.67	1846.876	0.055	-0.066	Viable BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Exponential 5	99.561	146.424	283.483	-	1848.876	0.055	-0.066	Questionable Zero degrees of freedom; saturated model

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Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
								BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Hill	100.384	152.408	-	-	1848.895	0.065	-0.067	Questionable Zero degrees of freedom; saturated model BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Polynomial 2	98.439	131.321	134.039	0.632	1846.924	0.245	0.035	Viable BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Polynomial 3	97.428	130.418	133.117	0.609	1846.957	0.31	0.014	Viable BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Power	99.35	144.678	273.667	0.674	1846.871	0.057	-0.061	Viable BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Linear ^{a b}	99.421	144.956	273.67	0.916	1844.871	0.052	-0.064	Recommended - Lowest AIC BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
^a BMDS recommended best fitting model ^b User selected best fitting model								



2.2.4.4 Selected Model: Linear



Linear Model

Version: pybmds 24.1 (bmddscore 24.1)

Input Summary:

BMR	10% Relative Deviation
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Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-1e+06	1e+06
b1	0	-1e+06	1e+06
alpha	0	-18	18

Modeling Summary:

BMD	144.956
BMDL	99.4211
BMDU	273.67
AIC	1844.87
Log-Likelihood	-919.436
P-Value	0.915527
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	107.834	no	1.13953
b1	-0.0743913	no	0.0215264
alpha	124.473	no	1414.35

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	60	107.91	107.834	0.0524846
26.8	60	105.43	105.841	-0.285155
45.6	60	104.87	104.442	0.297044
91.7	60	100.92	101.013	-0.0643733

Dose	N	Sample SD	Model Fitted SD
0	60	11.48	11.1567
26.8	60	11.54	11.1567
45.6	60	12.4	11.1567
91.7	60	9.34	11.1567

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-919.347	5	1848.69
A2	-916.834	8	1849.67
A3	-919.347	5	1848.69
fitted	-919.436	3	1844.87
reduced	-925.26	2	1854.52

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	16.8515	6	0.00984485
Test 2	5.02664	3	0.169857
Test 3	5.02664	3	0.169857
Test 4	0.176512	2	0.915527

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.3 Continuous Modeling of F1 Male and Female Post-Maturation Bodyweight

Report Generated: 2025-Apr-21 18:04 UTC

Analysis URL: [View](#)

BMDS Online Version: 24.1 (pybmds 24.1; bmdscore 24.1)

2.3.1 Male Bodyweight on Treatment Day 50, BMR = 1 SD

2.3.1.1 Dataset

Name: Male treatment day 50 EOGRTS IFF

Dose (mg/kg-d)	N	Mean (Grams)	Std. Dev. (Grams)
0	60	340.47	31.91
26.8	60	316.17	34.41
45.6	60	313.77	31.03
91.7	60	296.09	32.1

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.8713

Test 3 Variance Model Selection: 0.8713

2.3.1.2 Settings

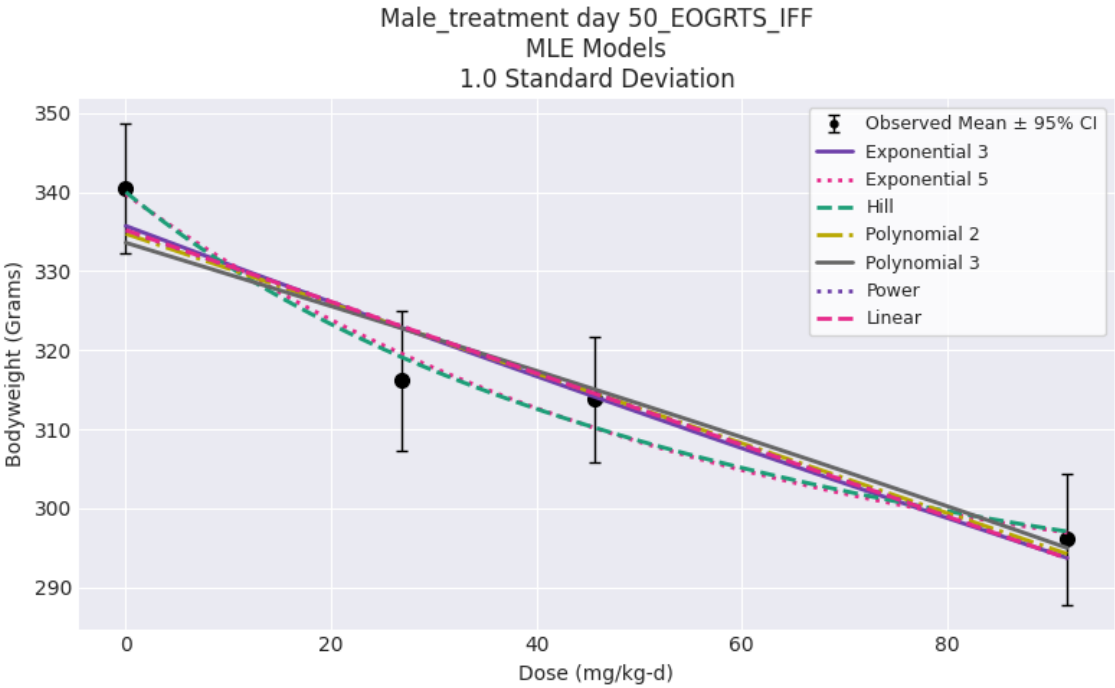
Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.3.1.3 Maximum Likelihood Approach

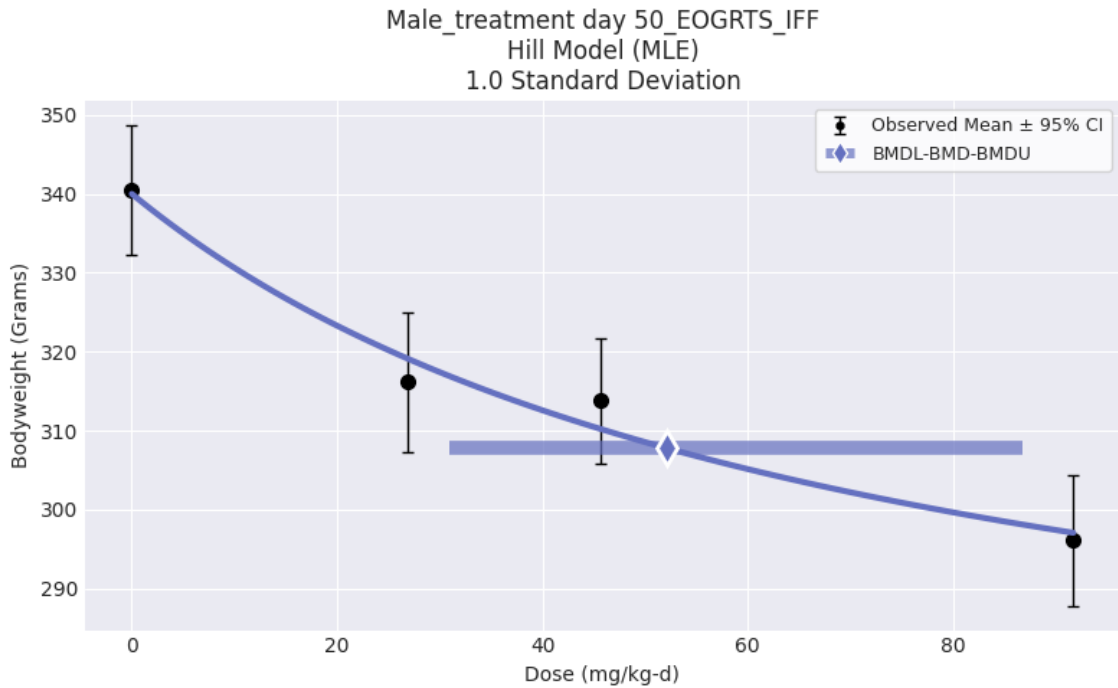
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	55.334	69.64	93.019	0.239	2356.587	1.133	0.563	Viable
Exponential 5	32.23	52.304	87.11	0.222	2355.865	0.171	0.857	Viable
Hill ^{a b}	30.882	52.075	86.806	0.252	2355.685	0.111	0.847	Recommended - Lowest AIC
Polynomial 2	57.693	73.446	94.381	0.093	2357.114	1.368	0.441	Questionable Goodness of fit p-value < 0.1
Polynomial 3	56.411	78.086	79.703	-	2361.794	1.636	0.262	Questionable Zero degrees of

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
								freedom; saturated model
Power	57.758	71.644	94.203	0.095	2357.083	1.26	0.574	Questionable Goodness of fit p-value < 0.1
Linear	57.758	71.644	94.203	0.095	2357.083	1.26	0.574	Questionable Goodness of fit p-value < 0.1

^a BMDS recommended best fitting model
^b User selected best fitting model



2.3.1.4 Selected Model: Hill



Hill Model

Version: pybmds 24.1 (bmdscore 24.1)

Input Summary:

BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-100	100
v	0	-100	100
k	0	0	5
n	1	1	18
alpha	0	-18	18

Modeling Summary:

BMD	52.0751
BMDL	30.8818
BMDU	86.8055
AIC	2355.68
Log-Likelihood	-1173.84
P-Value	0.252336
Model d.f.	1

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	340.007	no	4.19261

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v	-76.3642	no	29.5006
k	71.4112	no	56.852
n	1	yes	Not Reported
alpha	1037.06	no	98178.1

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	60	340.47	340.007	0.111283
26.8	60	316.17	319.169	-0.721355
45.6	60	313.77	310.248	0.847219
91.7	60	296.09	297.076	-0.237146

Dose	N	Sample SD	Model Fitted SD
0	60	31.91	32.2034
26.8	60	34.41	32.2034
45.6	60	31.03	32.2034
91.7	60	32.1	32.2034

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-1173.19	5	2356.37
A2	-1172.83	8	2361.67
A3	-1173.19	5	2356.37
fitted	-1173.84	4	2355.68
reduced	-1199.2	2	2402.4

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	52.7322	6	1.3284e-09
Test 2	0.708204	3	0.871273
Test 3	0.708204	3	0.871273
Test 4	1.31033	1	0.252336

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.3.2 Male Bodyweight on Treatment Day 50, BMR = 10%

2.3.2.1 Dataset

Name: Male_treatment day 50_EOGRTS_IFF

Dose (mg/kg-d)	N	Mean (Grams)	Std. Dev. (Grams)
0	60	340.47	31.91
26.8	60	316.17	34.41
45.6	60	313.77	31.03
91.7	60	296.09	32.1

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.8713

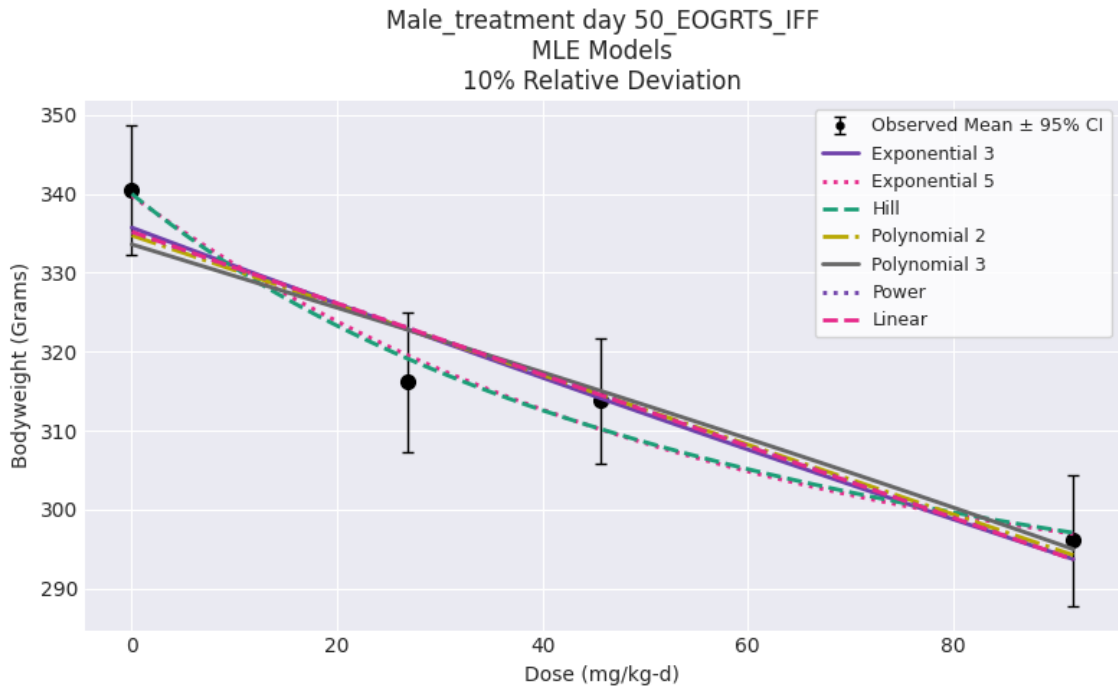
Test 3 Variance Model Selection: 0.8713

2.3.2.2 Settings

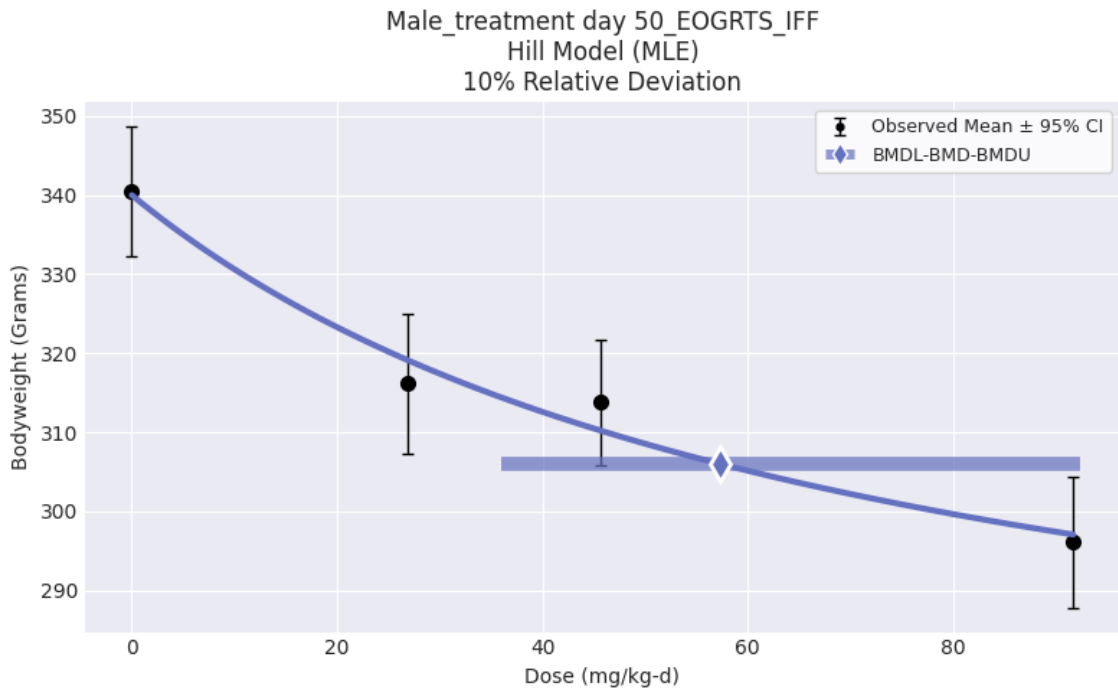
Setting	Value
BMR	10% Relative Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.3.2.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	58.768	72.302	93.79	0.122	2356.587	1.133	0.563	Viable
Exponential 5	36.791	57.218	93.169	0.222	2355.865	0.171	0.857	Viable
Hill ^{a b}	36.031	57.314	92.31	0.252	2355.685	0.111	0.847	Recommended - Lowest AIC
Polynomial 2	60.928	75.793	94.896	0.093	2357.114	1.368	0.441	Questionable Goodness of fit p-value < 0.1
Polynomial 3	59.687	80.069	81.725	-	2361.794	1.636	0.262	Questionable Zero degrees of freedom; saturated model
Power	60.991	74.046	94.73	0.095	2357.083	1.26	0.574	Questionable Goodness of fit p-value < 0.1
Linear	60.991	74.046	94.73	0.095	2357.083	1.26	0.574	Questionable Goodness of fit p-value < 0.1
^a BMDS recommended best fitting model								
^b User selected best fitting model								



2.3.2.4 Selected Model: Hill



Hill Model

Version: pybmds 24.1 (bmdscore 24.1)

Input Summary:

BMR	10% Relative Deviation
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Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-100	100
v	0	-100	100
k	0	0	5
n	1	1	18
alpha	0	-18	18

Modeling Summary:

BMD	57.3143
BMDL	36.0313
BMDU	92.3101
AIC	2355.68
Log-Likelihood	-1173.84
P-Value	0.252336
Model d.f.	1

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	340.007	no	4.19261
v	-76.3642	no	29.5006
k	71.4112	no	56.852
n	1	yes	Not Reported
alpha	1037.06	no	98178.1

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	60	340.47	340.007	0.111283
26.8	60	316.17	319.169	-0.721355
45.6	60	313.77	310.248	0.847219
91.7	60	296.09	297.076	-0.237146

Dose	N	Sample SD	Model Fitted SD
0	60	31.91	32.2034
26.8	60	34.41	32.2034
45.6	60	31.03	32.2034
91.7	60	32.1	32.2034

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-1173.19	5	2356.37
A2	-1172.83	8	2361.67
A3	-1173.19	5	2356.37
fitted	-1173.84	4	2355.68
reduced	-1199.2	2	2402.4

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Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	52.7322	6	1.3284e-09
Test 2	0.708204	3	0.871273
Test 3	0.708204	3	0.871273
Test 4	1.31033	1	0.252336

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.3.3 Male Bodyweight on Treatment Day 72, BMR = 1 SD

2.3.3.1 Dataset

Name: Male_treatment day 72_EOGRTS_IFF

Dose (mg/kg-d)	N	Mean (Grams)	Std. Dev. (Grams)
0	20	406.12	40.18
26.8	20	375.13	34.65
45.6	20	364.09	43.97
91.7	20	331.8	28.76

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.2678

Test 3 Variance Model Selection: 0.2678

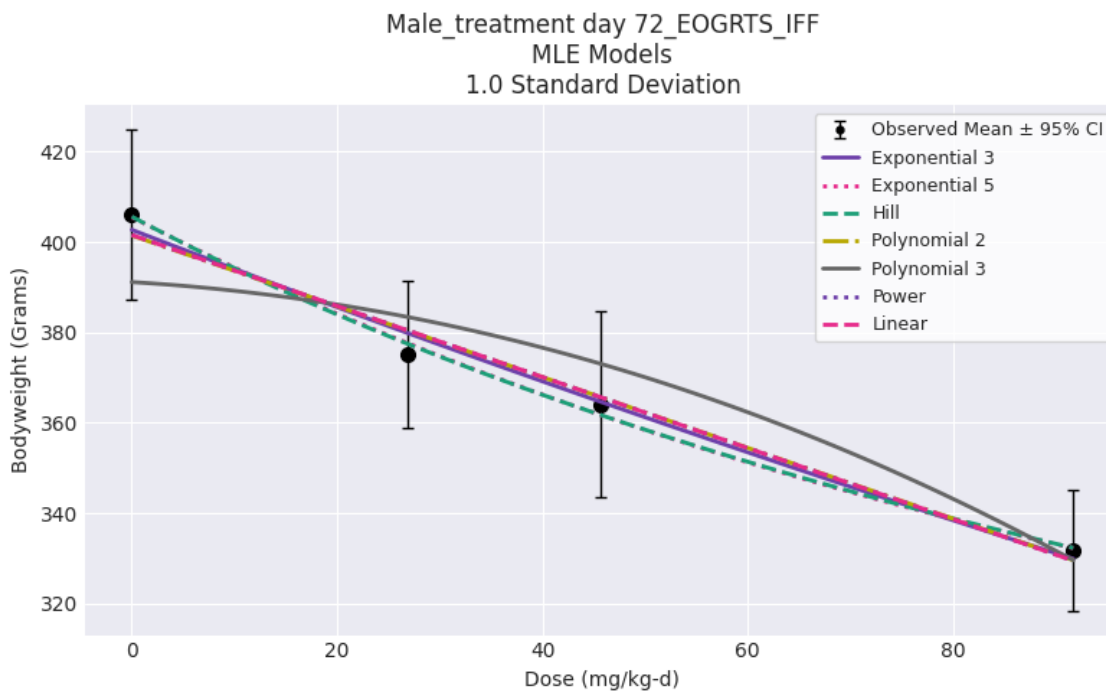
2.3.3.2 Settings

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.3.3.3 Maximum Likelihood Approach

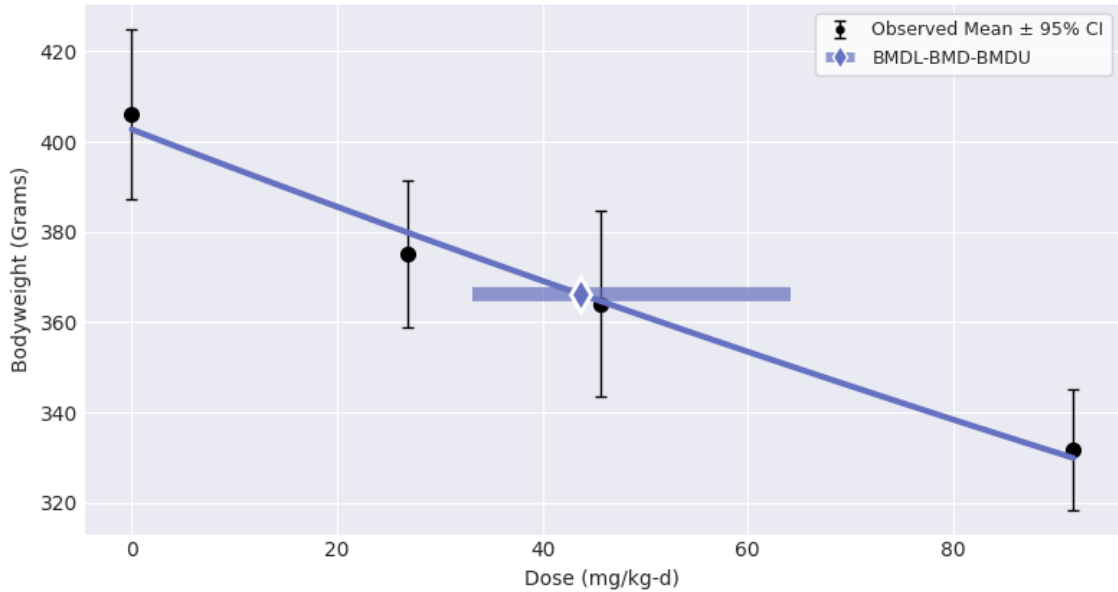
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 ^{a b}	33.144	43.72	64.1	0.901	808.693	0.421	-0.071	Recommended - Lowest AIC
Exponential 5	20.938	36.574	62.06	0.663	810.305	0.077	0.289	Viable
Hill	19.696	36.352	61.556	0.675	810.29	0.065	0.287	Viable
Polynomial 2	36.137	46.704	66.844	0.649	808.981	0.573	-0.197	Viable
Polynomial 3	68.679	70.117	71.552	-	817.658	1.772	0.265	Questionable Zero degrees of freedom; saturated model
Power	36.143	46.537	65.971	0.649	808.98	0.56	-0.195	Viable
Linear	36.143	46.537	65.248	0.649	808.98	0.56	-0.195	Viable

^a BMDS recommended best fitting model
^b User selected best fitting model



2.3.3.4 Selected Model: Exponential 3

Male_treatment day 72_EOGRTS_IFF
Exponential 3 Model (MLE)
1.0 Standard Deviation



Exponential 3 Model

Version: pybmds 24.1 (bmdscore 24.1)

Input Summary:

BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	100
b	0	0	100
c	0	-20	0
d	0	1	18
log-alpha	0	-18	18

Modeling Summary:

BMD	43.7202
BMDL	33.1439
BMDU	64.0997
AIC	808.693
Log-Likelihood	-401.347
P-Value	0.901348
Model d.f.	3

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	402.682	no	6.6935

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b	0.00217461	no	0.000342455
d	1	yes	Not Reported
log-alpha	7.19579	no	0.158114

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	20	406.12	402.682	0.420947
26.8	20	375.13	379.885	-0.582257
45.6	20	364.09	364.667	-0.0707026
91.7	20	331.8	329.882	0.234828

Dose	N	Sample SD	Model Fitted SD
0	20	40.18	36.5213
26.8	20	34.65	36.5213
45.6	20	43.97	36.5213
91.7	20	28.76	36.5213

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-401.057	5	812.115
A2	-399.087	8	814.173
A3	-401.057	5	812.115
fitted	-401.347	2	806.693
reduced	-418.146	2	840.292

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	38.1191	6	1.06473e-06
Test 2	3.94179	3	0.267819
Test 3	3.94179	3	0.267819
Test 4	0.578448	3	0.901348

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.3.4 Male Bodyweight on Treatment Day 72, BMR = 10% RD

2.3.4.1 Dataset

Name: Male_treatment day 72_EOGRS_IFF

Dose (mg/kg-d)	N	Mean (Grams)	Std. Dev. (Grams)
0	20	406.12	40.18
26.8	20	375.13	34.65
45.6	20	364.09	43.97
91.7	20	331.8	28.76

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.2678

Test 3 Variance Model Selection: 0.2678

2.3.4.2 Settings

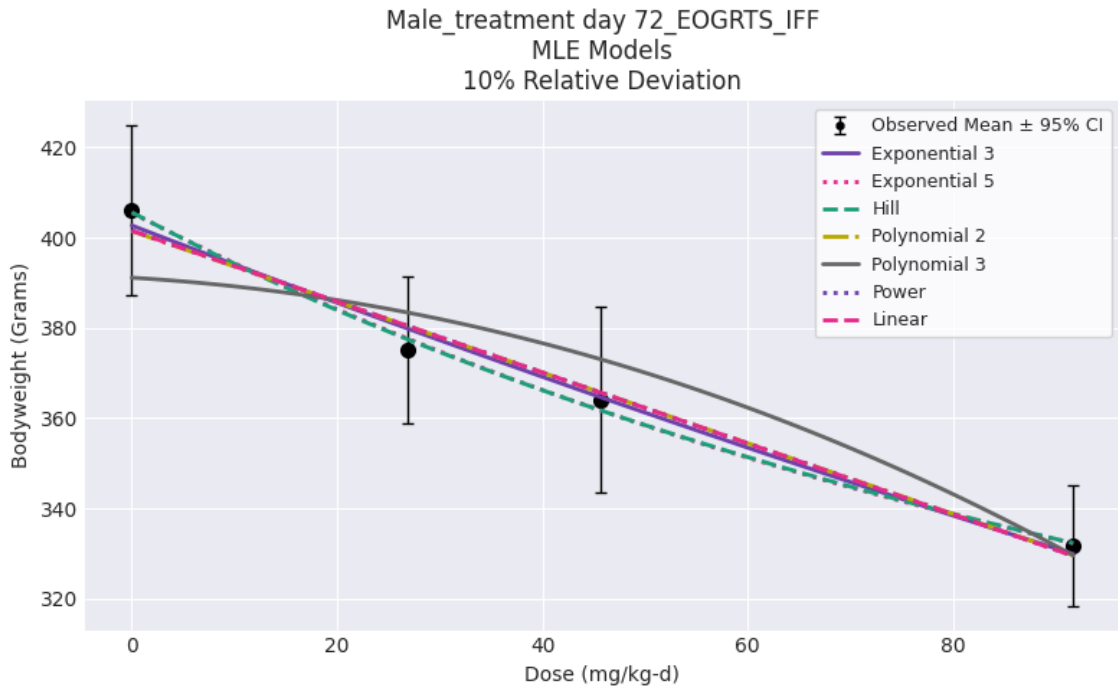
Setting	Value
BMR	10% Relative Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.3.4.3 Maximum Likelihood Approach

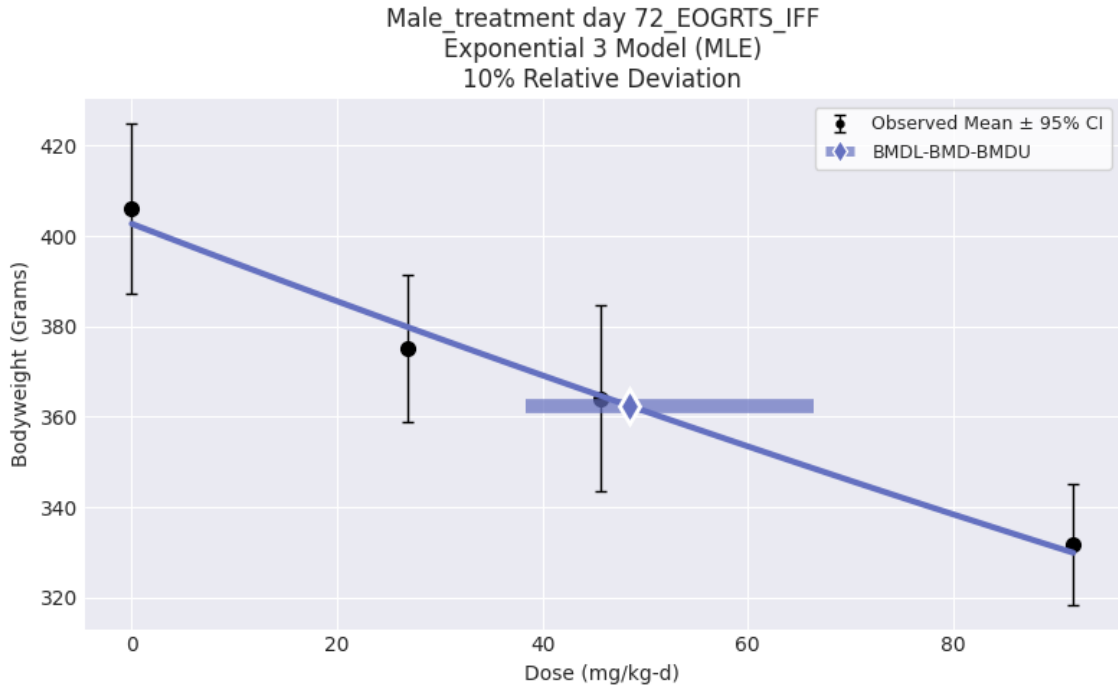
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 ^{a b}	38.359	48.45	66.396	0.901	808.693	0.421	-0.071	Recommended - Lowest AIC
Exponential 5	25.091	41.561	64.636	0.663	810.305	0.077	0.289	Viable
Hill	29.448	41.411	63.391	0.675	810.29	0.065	0.287	Viable
Polynomial 2	41.382	51.235	68.833	0.649	808.981	0.573	-0.197	Viable
Polynomial 3	69.913	71.376	72.837	-	817.658	1.772	0.265	Questionable Zero degrees of freedom; saturated model
Power	41.39	51.074	68.047	0.649	808.98	0.56	-0.195	Viable
Linear	41.39	51.074	67.461	0.649	808.98	0.56	-0.195	Viable

^a BMDS recommended best fitting model

^b User selected best fitting model



2.3.4.4 Selected Model: Exponential 3



Exponential 3 Model

Version: pybmds 24.1 (bmdscore 24.1)

March 2026

Input Summary:

BMR	10% Relative Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	100
b	0	0	100
c	0	-20	0
d	0	1	18
log-alpha	0	-18	18

Modeling Summary:

BMD	48.4502
BMDL	38.3595
BMDU	66.3959
AIC	808.693
Log-Likelihood	-401.347
P-Value	0.901348
Model d.f.	3

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	402.682	no	6.6935
b	0.00217461	no	0.000342455
d	1	yes	Not Reported
log-alpha	7.19579	no	0.158114

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	20	406.12	402.682	0.420947
26.8	20	375.13	379.885	-0.582257
45.6	20	364.09	364.667	-0.0707026
91.7	20	331.8	329.882	0.234828

Dose	N	Sample SD	Model Fitted SD
0	20	40.18	36.5213
26.8	20	34.65	36.5213
45.6	20	43.97	36.5213
91.7	20	28.76	36.5213

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-401.057	5	812.115
A2	-399.087	8	814.173
A3	-401.057	5	812.115
fitted	-401.347	2	806.693
reduced	-418.146	2	840.292

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	38.1191	6	1.06473e-06
Test 2	3.94179	3	0.267819
Test 3	3.94179	3	0.267819
Test 4	0.578448	3	0.901348

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.3.5 Female Bodyweight on Treatment Day 50, BMR = 1 SD

2.3.5.1 Dataset

Name: Female treatment day 50 EOGRTS IFF

Dose (mg/kg-d)	N	Mean (Grams)	Std. Dev. (Grams)
0	60	206.51	17.61
26.8	60	199.48	17.87
45.6	60	196.57	14.98
91.7	60	193.72	14.83

Test 1 Dose Response: 0.0007

Test 2 Homogeneity of Variance: 0.3031

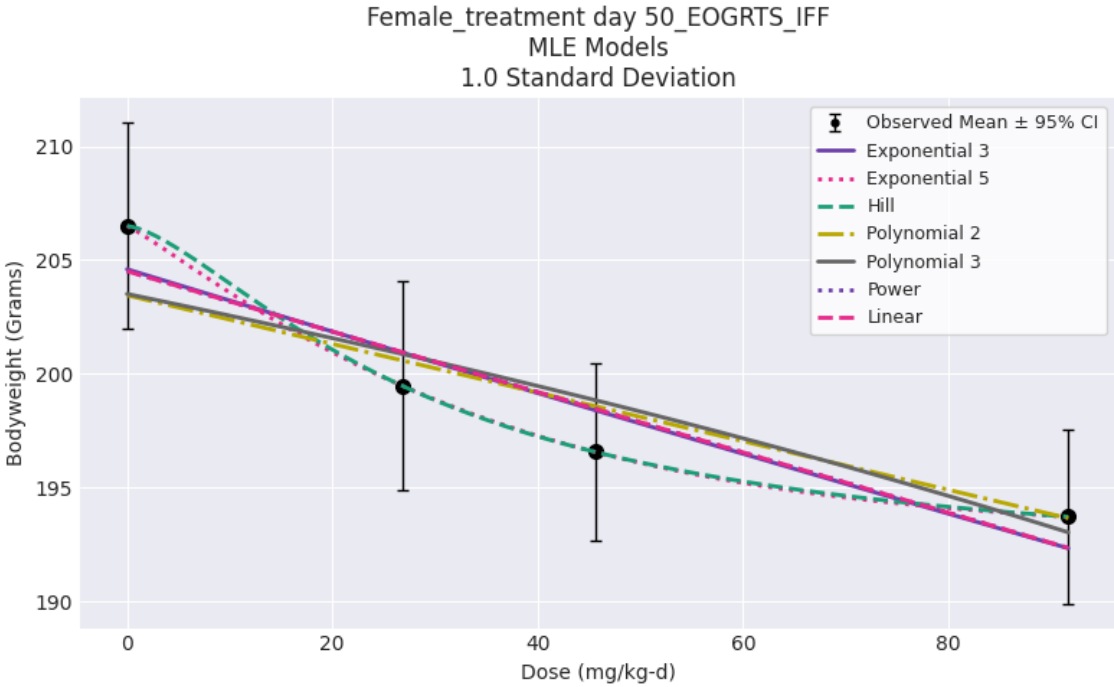
Test 3 Variance Model Selection: 0.3031

2.3.5.2 Settings

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

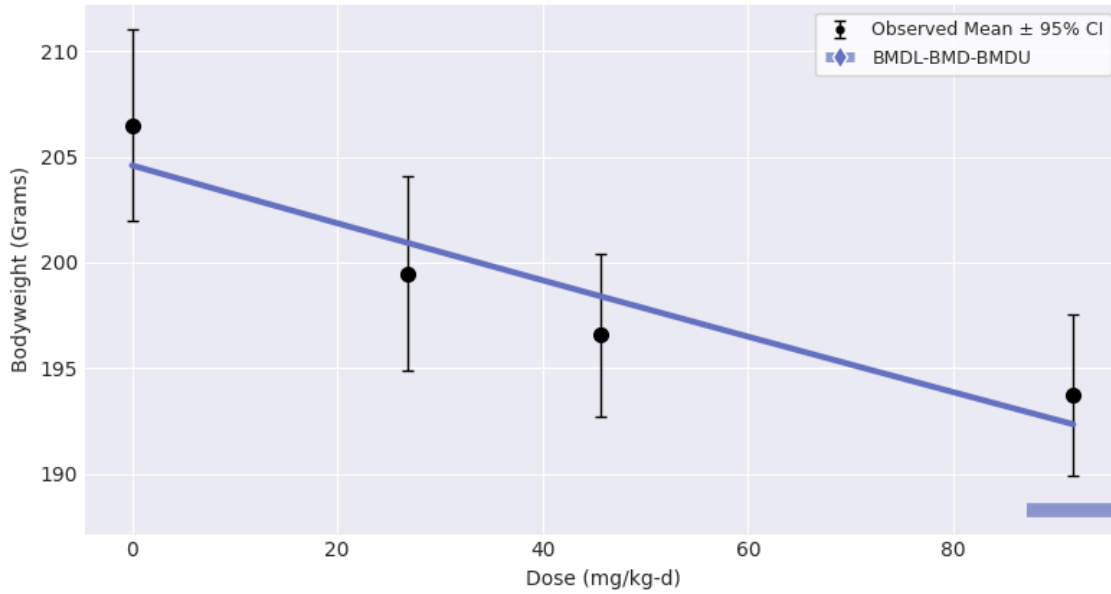
2.3.5.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 ^{a b}	87.161	123.364	207.172	0.475	2027.792	0.905	0.658	Recommended - Lowest AIC BMD/highest dose ratio > 1.0
Exponential 5	-	-	-	-	2029.291	-0.	-	Unusable Did not successfully execute.
Hill	-	-	-	-	2029.291	-0.	-	Unusable Did not successfully execute.
Polynomial 2	85.217	153.345	221.701	0.192	2028.593	1.444	0.031	Viable BMD/highest dose ratio > 1.0
Polynomial 3	83.597	129.522	132.203	0.053	2031.028	1.414	0.325	Questionable Goodness of fit p-value < 0.1 BMD/highest dose ratio > 1.0
Power	88.058	123.135	204.551	0.268	2027.923	0.947	0.651	Viable BMD/highest dose ratio > 1.0
Linear	88.058	123.135	204.551	0.268	2027.923	0.947	0.651	Viable BMD/highest dose ratio > 1.0
^a BMDS recommended best fitting model ^b User selected best fitting model								



2.3.5.4 Selected Model: Exponential 3

Female_treatment day 50_EOGRTS_1FF
Exponential 3 Model (MLE)
1.0 Standard Deviation



Exponential 3 Model

Version: pybmds 24.1 (bmdscore 24.1)

Input Summary:

BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	100
b	0	0	100
c	0	-20	0
d	0	1	18
log-alpha	0	-18	18

Modeling Summary:

BMD	123.364
BMDL	87.1609
BMDU	207.172
AIC	2027.79
Log-Likelihood	-1010.9
P-Value	0.475145
Model d.f.	3

Model Parameters:

Variable	Estimate	On Bound	Std Error
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March 2026

a	204.602	no	1.68995
b	0.000674342	no	0.000160376
d	1	yes	Not Reported
log-alpha	5.58626	no	0.0912869

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	60	206.51	204.602	0.904989
26.8	60	199.48	200.937	-0.691237
45.6	60	196.57	198.406	-0.870832
91.7	60	193.72	192.333	0.657772

Dose	N	Sample SD	Model Fitted SD
0	60	17.61	16.332
26.8	60	17.87	16.332
45.6	60	14.98	16.332
91.7	60	14.83	16.332

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-1009.65	5	2029.29
A2	-1007.83	8	2031.65
A3	-1009.65	5	2029.29
fitted	-1010.9	2	2025.79
reduced	-1019.5	2	2043.01

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	23.3538	6	0.000686246
Test 2	3.63967	3	0.303095
Test 3	3.63967	3	0.303095
Test 4	2.50081	3	0.475145

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.3.6 Female Bodyweight on Treatment Day 50, BMR = 10% RD

2.3.6.1 Dataset

Name: Female_treatment day 50_EOGRS_IFF

Dose (mg/kg-d)	N	Mean (Grams)	Std. Dev. (Grams)
0	60	206.51	17.61
26.8	60	199.48	17.87
45.6	60	196.57	14.98
91.7	60	193.72	14.83

Test 1 Dose Response: 0.0007

Test 2 Homogeneity of Variance: 0.3031

Test 3 Variance Model Selection: 0.3031

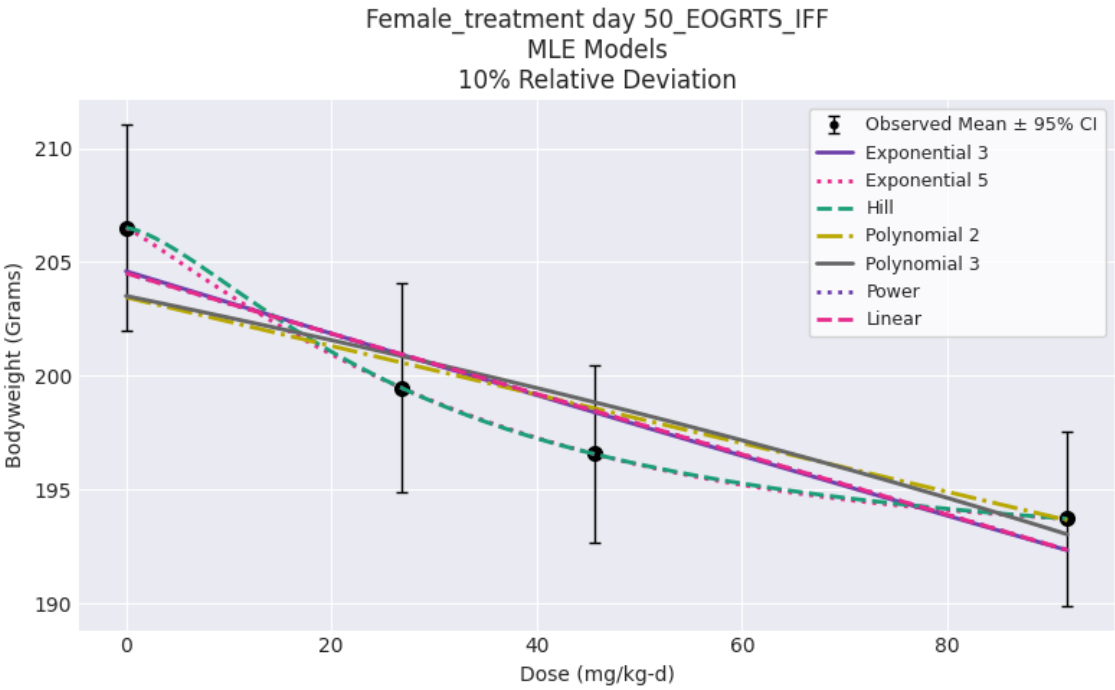
2.3.6.2 Settings

Setting	Value
BM	10% Relative Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.3.6.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 ^{ab}	112.146	156.242	256.802	0.286	2027.792	0.905	0.658	Recommended - Lowest AIC BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Exponential 5	-	-	-	-	2029.291	-0.	-	Unusable Did not successfully execute.
Hill	-	-	-	-	2029.291	-0.	-	Unusable Did not successfully execute.
Polynomial 2	108.388	190.342	271.256	0.192	2028.593	1.444	0.031	Viable BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Polynomial 3	106.798	151.185	158.135	0.053	2031.028	1.414	0.325	Questionable Goodness of fit p-value < 0.1 BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Power	111.832	154.151	250.91	0.268	2027.923	0.947	0.651	Viable BMDL/highest dose ratio > 1.0

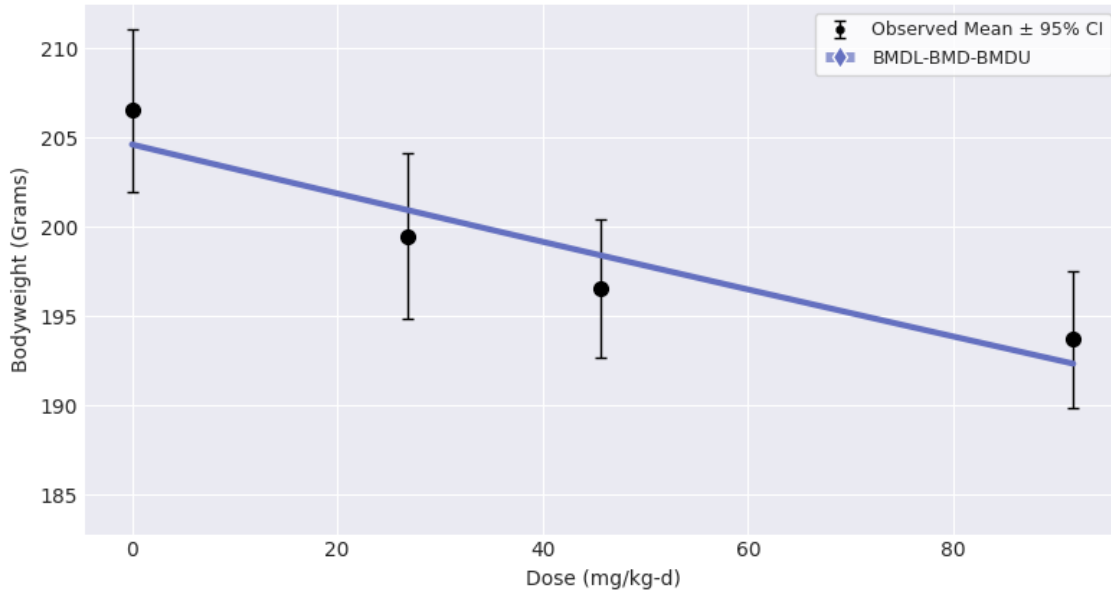
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
								BMD/highest dose ratio > 1.0
Linear	111.832	154.151	250.91	0.268	2027.923	0.947	0.651	Viable BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
^a BMDS recommended best fitting model								
^b User selected best fitting model								



2.3.6.4 Selected Model: Exponential 3

March 2026

Female_treatment day 50_EOGRTS_1FF
Exponential 3 Model (MLE)
10% Relative Deviation



Exponential 3 Model

Version: pybmds 24.1 (bmdscore 24.1)

Input Summary:

BMR	10% Relative Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	100
b	0	0	100
c	0	-20	0
d	0	1	18
log-alpha	0	-18	18

Modeling Summary:

BMD	156.242
BMDL	112.146
BMDU	256.802
AIC	2027.79
Log-Likelihood	-1010.9
P-Value	0.286389
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
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March 2026

a	204.602	no	1.68995
b	0.000674342	no	0.000160376
d	1	yes	Not Reported
log-alpha	5.58626	no	0.0912869

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	60	206.51	204.602	0.904989
26.8	60	199.48	200.937	-0.691237
45.6	60	196.57	198.406	-0.870832
91.7	60	193.72	192.333	0.657772

Dose	N	Sample SD	Model Fitted SD
0	60	17.61	16.332
26.8	60	17.87	16.332
45.6	60	14.98	16.332
91.7	60	14.83	16.332

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-1009.65	5	2029.29
A2	-1007.83	8	2031.65
A3	-1009.65	5	2029.29
fitted	-1010.9	3	2027.79
reduced	-1019.5	2	2043.01

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	23.3538	6	0.000686246
Test 2	3.63967	3	0.303095
Test 3	3.63967	3	0.303095
Test 4	2.50081	2	0.286389

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.3.7 Female Bodyweight on Treatment Day 72, BMR = 1 SD

2.3.7.1 Dataset

Name: Female_treatment day 72_EOGRS_IFF

March 2026

Dose (mg/kg-d)	N	Mean (Grams)	Std. Dev. (Grams)
0	20	234.11	21.62
26.8	20	223.33	23.74
45.6	20	221.56	20.25
91.7	20	213.16	16.56

Test 1 Dose Response: 0.0449

Test 2 Homogeneity of Variance: 0.4493

Test 3 Variance Model Selection: 0.4493

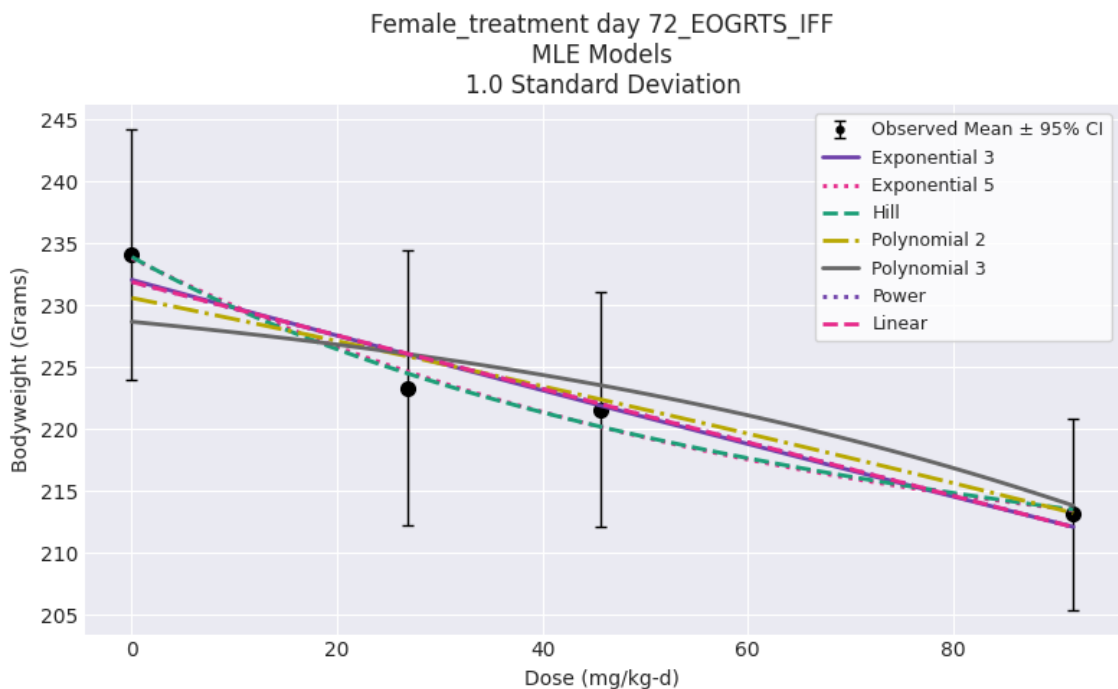
2.3.7.2 Settings

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

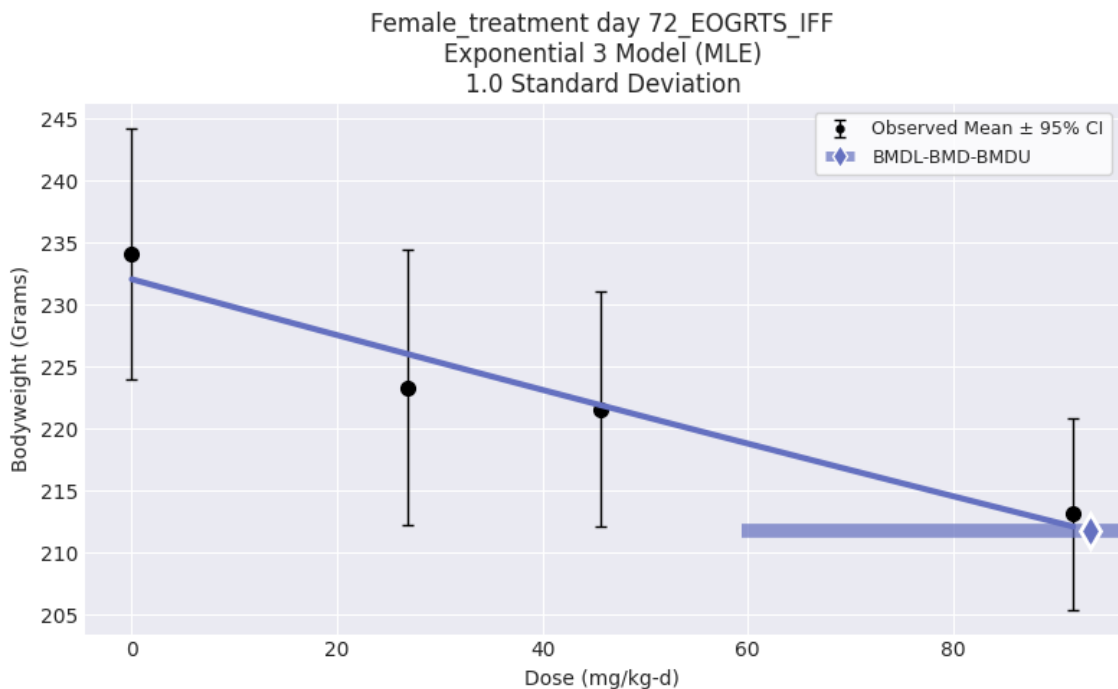
2.3.7.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 ^{a b}	59.445	93.27	203.993	0.891	714.436	0.452	0.229	Recommended - Lowest AIC BMD/highest dose ratio > 1.0
Exponential 5	31.928	90.258	-	0.664	715.999	0.065	-0.068	Viable
Hill	30.809	89.951	-	0.683	715.977	0.045	-0.078	Viable
Polynomial 2	60.217	105.947	108.14	0.327	716.772	0.769	-0.017	Viable BMD/highest dose ratio > 1.0
Polynomial 3	56.49	108.088	110.326	-	719.963	1.224	-0.153	Questionable Zero degrees of freedom; saturated model BMD/highest dose ratio > 1.0
Power	61.273	94.124	200.853	0.71	714.496	0.488	0.232	Viable BMD/highest dose ratio > 1.0
Linear	61.277	93.915	200.821	0.71	714.495	0.489	0.233	Viable BMD/highest dose ratio > 1.0

^a BMDS recommended best fitting model^b User selected best fitting model



2.3.7.4 Selected Model: Exponential 3



Exponential 3 Model

Version: pybmds 24.1 (bmdscore 24.1)

March 2026

Input Summary:

BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	100
b	0	0	100
c	0	-20	0
d	0	1	18
log-alpha	0	-18	18

Modeling Summary:

BMD	93.2696
BMDL	59.4446
BMDU	203.993
AIC	714.436
Log-Likelihood	-354.218
P-Value	0.890575
Model d.f.	3

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	232.061	no	3.6478
b	0.000979595	no	0.00030881
d	1	yes	Not Reported
log-alpha	6.01758	no	0.158114

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	20	234.11	232.061	0.452155
26.8	20	223.33	226.048	-0.599937
45.6	20	221.56	221.923	-0.0801976
91.7	20	213.16	212.124	0.228567

Dose	N	Sample SD	Model Fitted SD
0	20	21.62	20.2629
26.8	20	23.74	20.2629
45.6	20	20.25	20.2629
91.7	20	16.56	20.2629

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-353.905	5	717.811
A2	-352.582	8	721.164
A3	-353.905	5	717.811
fitted	-354.218	2	712.436
reduced	-359.024	2	722.047

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	12.8836	6	0.044922
Test 2	2.64728	3	0.44926
Test 3	2.64728	3	0.44926
Test 4	0.625482	3	0.890575

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

2.3.8 Female Bodyweight on Treatment Day 72, BMR = 10% RD

2.3.8.1 Dataset

Name: Female treatment day 72_EOGRTS_IFF

Dose (mg/kg-d)	N	Mean (Grams)	Std. Dev. (Grams)
0	20	234.11	21.62
26.8	20	223.33	23.74
45.6	20	221.56	20.25
91.7	20	213.16	16.56

Test 1 Dose Response: 0.0449

Test 2 Homogeneity of Variance: 0.4493

Test 3 Variance Model Selection: 0.4493

2.3.8.2 Settings

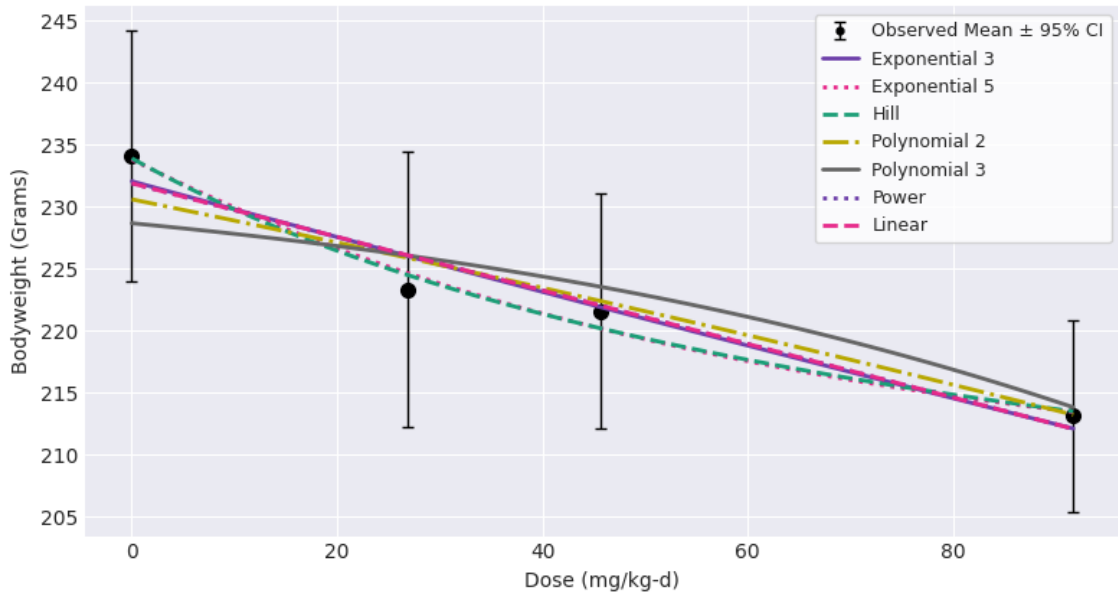
Setting	Value
BMR	10% Relative Deviation
Distribution	Normal + Constant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

2.3.8.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 ^{a b}	70.506	107.555	224.436	0.731	714.436	0.452	0.229	Recommended - Lowest AIC

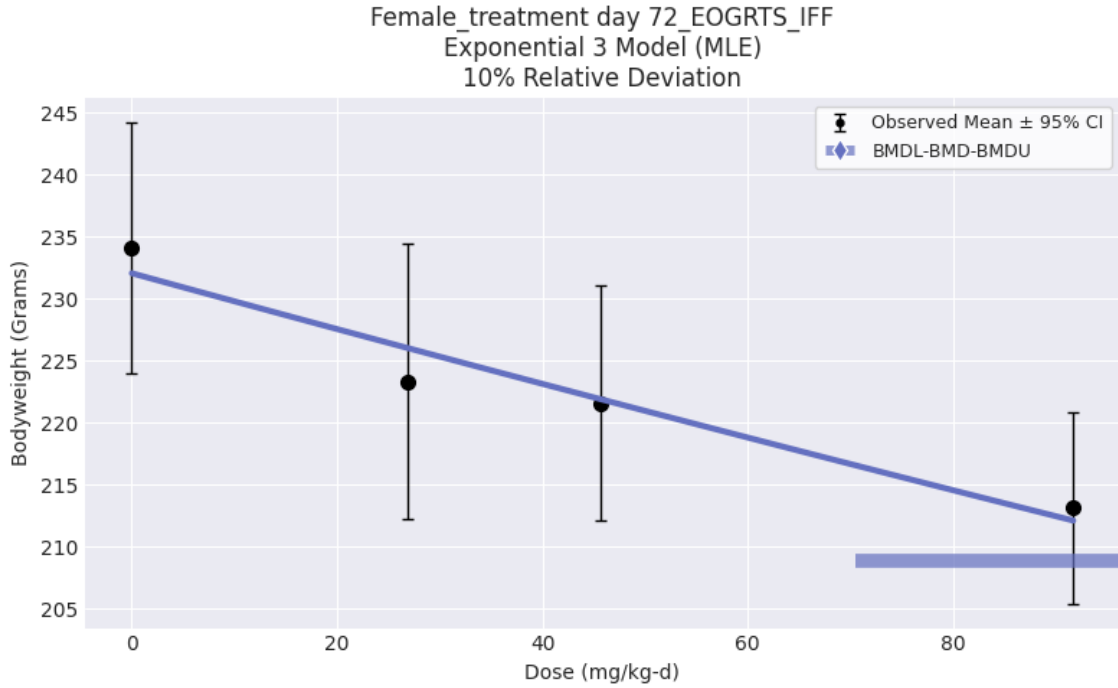
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
								BMD/highest dose ratio > 1.0
Exponential 5	47.626	132.829	638.224	0.664	715.999	0.065	-0.068	Viable BMD/highest dose ratio > 1.0
Hill	50.592	124.652	-	0.683	715.977	0.045	-0.078	Viable BMD/highest dose ratio > 1.0
Polynomial 2	70.849	118.225	120.672	0.327	716.772	0.769	-0.017	Viable BMD/highest dose ratio > 1.0
Polynomial 3	66.699	116.674	119.089	-	719.963	1.224	-0.153	Questionable Zero degrees of freedom; saturated model BMD/highest dose ratio > 1.0
Power	72.024	107.458	219.811	0.71	714.496	0.488	0.232	Viable BMD/highest dose ratio > 1.0
Linear	72.027	107.44	219.776	0.71	714.495	0.489	0.233	Viable BMD/highest dose ratio > 1.0
^a BMDS recommended best fitting model								
^b User selected best fitting model								

Female_treatment day 72_EOGRS_IFF
MLE Models
10% Relative Deviation



3090
3091

2.3.8.4 Selected Model: Exponential 3



Exponential 3 Model

Version: pybmds 24.1 (bmdscore 24.1)

Input Summary:

BMR	10% Relative Deviation
Distribution	Normal + Constant variance
Modeling Direction	Down (↓)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	100
b	0	0	100
c	0	-20	0
d	0	1	18
log-alpha	0	-18	18

Modeling Summary:

BMD	107.555
BMDL	70.5056
BMDU	224.436
AIC	714.436
Log-Likelihood	-354.218
P-Value	0.731439
Model d.f.	2

March 2026

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	232.061	no	3.6478
b	0.000979595	no	0.00030881
d	1	yes	Not Reported
log-alpha	6.01758	no	0.158114

Standard errors estimates are not generated for parameters estimated on corresponding bounds, although sampling error is present for all parameters, as a rule. Standard error estimates may not be reliable as a basis for confidence intervals or tests when one or more parameters are on bounds.

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	20	234.11	232.061	0.452155
26.8	20	223.33	226.048	-0.599937
45.6	20	221.56	221.923	-0.0801976
91.7	20	213.16	212.124	0.228567

Dose	N	Sample SD	Model Fitted SD
0	20	21.62	20.2629
26.8	20	23.74	20.2629
45.6	20	20.25	20.2629
91.7	20	16.56	20.2629

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-353.905	5	717.811
A2	-352.582	8	721.164
A3	-353.905	5	717.811
fitted	-354.218	3	714.436
reduced	-359.024	2	722.047

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	12.8836	6	0.044922
Test 2	2.64728	3	0.44926
Test 3	2.64728	3	0.44926
Test 4	0.625482	2	0.731439

Test 1: Test the null hypothesis that responses and variances don't differ among dose levels (A2 vs R). If this test fails to reject the null hypothesis (p-value > 0.05), there may not be a dose-response.

Test 2: Test the null hypothesis that variances are homogenous (A1 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), the simpler constant variance model may be appropriate.

Test 3: Test the null hypothesis that the variances are adequately modeled (A3 vs A2). If this test fails to reject the null hypothesis (p-value > 0.05), it may be inferred that the variances have been modeled appropriately.

Test 4: Test the null hypothesis that the model for the mean fits the data (Fitted vs A3). If this test fails to reject the null hypothesis (p-value > 0.1), the user has support for use of the selected model.

3 Nested Dichotomous Modeling Results

3.1 Nested Dichotomous Modeling of F1 Male and Female PND 1, 4, 7, 14, 21 Bodyweight (Sexes Combined)

Fixed at initial litter size

Report Generated: 2025-Sep-25 22:09 UTC

Analysis URL: [View](#)

BMDS Online Version: 25.1 (pybmds 25.1; bmdscore 25.1)

3.1.1 Bodyweight on PND 1

3.1.1.1 Dataset

Name: P1

Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
0	14	0	14
0	11	0	11
0	10	0	10
0	12	0	12
0	11	0	11
0	14	3	14
0	8	0	8
0	11	1	11
0	13	0	13
0	13	0	13
0	14	0	14
0	13	2	13
0	10	0	10
0	10	0	10
0	11	1	11
0	11	0	11
0	12	0	12
0	11	0	11
0	13	0	13
0	15	2	15
0	4	0	4
0	11	5	11
0	13	0	13
0	17	0	17
0	13	0	13
26.8	7	0	7
26.8	11	0	11
26.8	15	4	15
26.8	14	7	14
26.8	13	2	13

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Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
26.8	10	0	10
26.8	12	0	12
26.8	14	1	14
26.8	13	2	13
26.8	11	2	11
26.8	10	0	10
26.8	9	0	9
26.8	11	1	11
26.8	14	7	14
26.8	14	2	14
26.8	12	0	12
26.8	13	0	13
26.8	16	4	16
26.8	11	0	11
26.8	13	0	13
26.8	12	0	12
26.8	11	0	11
26.8	5	1	5
26.8	9	0	9
45.6	14	0	14
45.6	15	9	15
45.6	7	0	7
45.6	10	0	10
45.6	10	2	10
45.6	11	7	11
45.6	12	2	12
45.6	14	3	14
45.6	12	0	12
45.6	11	0	11
45.6	14	3	14
45.6	11	0	11
45.6	13	4	13
45.6	10	0	10
45.6	11	0	11
45.6	5	0	5
45.6	14	9	14
45.6	8	0	8
45.6	11	1	11
45.6	7	0	7
45.6	11	7	11
45.6	12	8	12
45.6	1	0	1
45.6	12	4	12
45.6	14	5	14

Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
91.7	3	0	3
91.7	10	1	10
91.7	13	10	13
91.7	10	1	10
91.7	9	0	9
91.7	11	0	11
91.7	13	1	13
91.7	16	11	16
91.7	11	1	11
91.7	12	1	12
91.7	12	0	12
91.7	15	13	15
91.7	11	0	11
91.7	9	2	9
91.7	15	15	15
91.7	16	13	16
91.7	16	10	16
91.7	13	6	13
91.7	12	3	12
91.7	8	0	8
91.7	13	1	13
91.7	11	0	11
91.7	9	1	9
91.7	11	7	11
91.7	13	5	13

3.1.1.2 Settings

Setting	Value
BMR	5% Extra Risk
Confidence Level (one sided)	0.95
Litter Specific Covariate	Overall Mean (11.485)
Intralitter Correlation	Estimate
Estimate Background	True
Bootstrap Runs	3
Bootstrap Seed	388
Bootstrap Iterations	1000

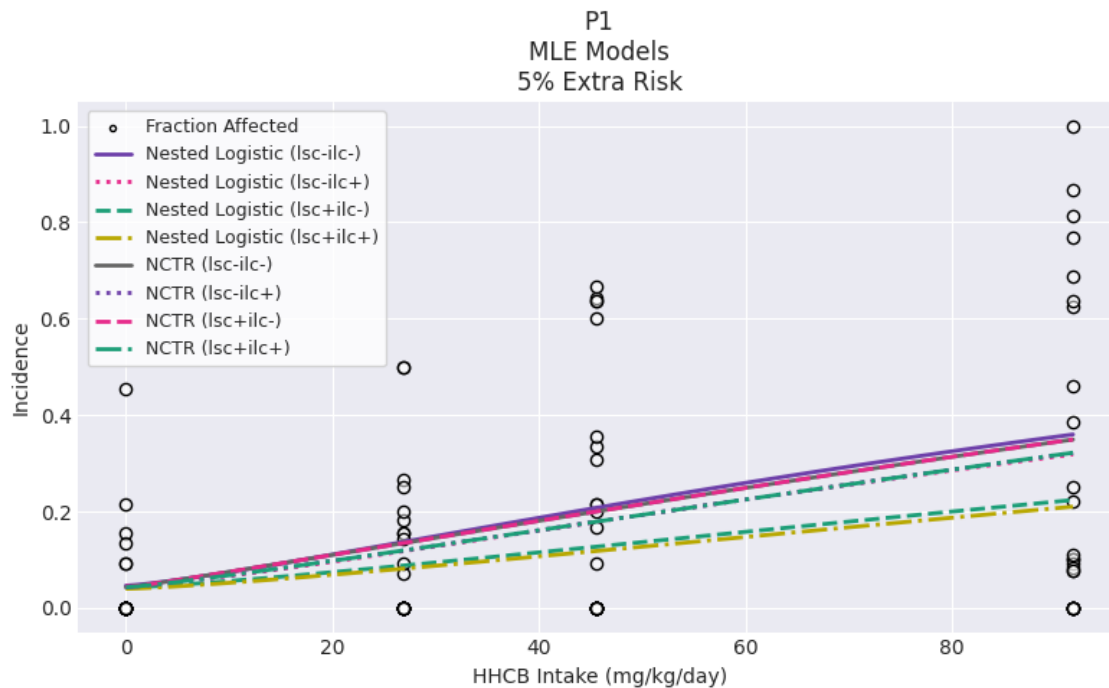
3.1.1.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Recommendation and Notes
Nested Logistic (lsc-ilc-)	9.608	15.469	15.469	0	1009.707	Questionable Goodness of fit p-value < 0.1

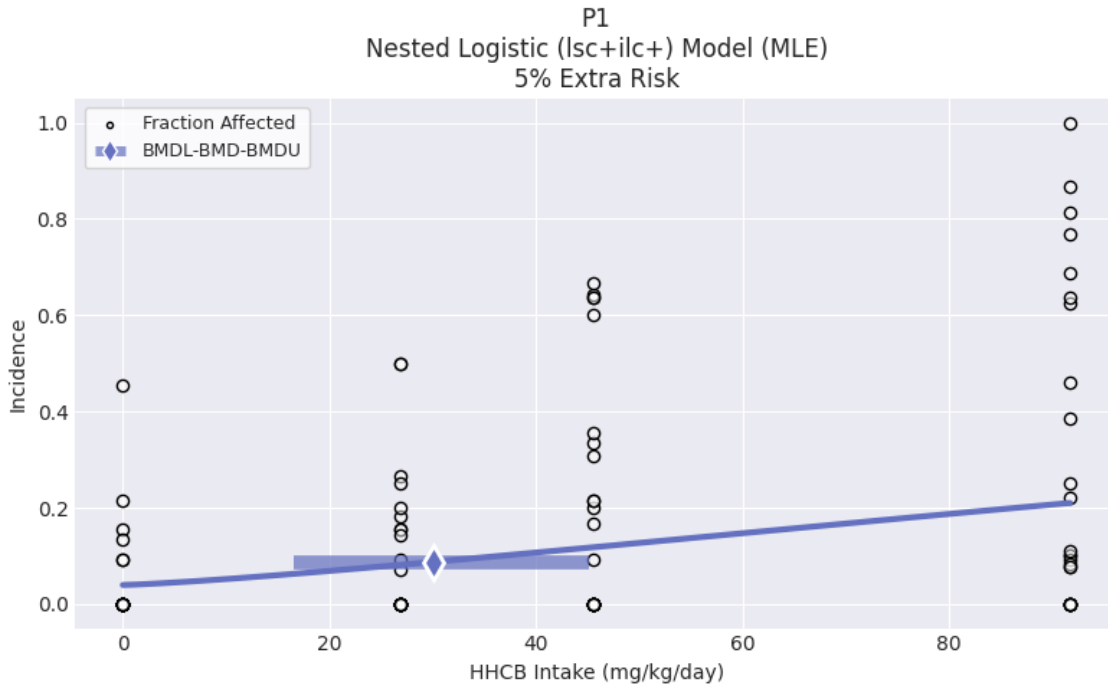
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Model	BMDL	BMD	BMDU	P-Value	AIC	Recommendation and Notes
Nested Logistic (lsc-ilc+)	9.631	18.958	18.958	0.479	819.39	Viable
Nested Logistic (lsc-ilc-)	19.014	27.901	27.901	0	877.199	Questionable Goodness of fit p-value < 0.1
Nested Logistic (lsc+ilc+) ^{a b}	16.515	30.11	30.11	0.399	785.13	Recommended - Lowest AIC
NCTR (lsc-ilc-)	7.259	14.518	14.518	0	954.807	Questionable lowest dose/BMDL ratio > 3.0 Goodness of fit p-value < 0.1
NCTR (lsc-ilc+)	8.826	17.652	17.652	0.589	805.632	Viable lowest dose/BMDL ratio > 3.0
NCTR (lsc+ilc-)	7.259	14.518	14.518	0	954.807	Questionable lowest dose/BMDL ratio > 3.0 Goodness of fit p-value < 0.1
NCTR (lsc+ilc+)	8.826	17.652	17.652	0.589	805.632	Viable lowest dose/BMDL ratio > 3.0

^a BMDS recommended best fitting model
^b User selected best fitting model



3.1.1.4 Selected Model: Nested Logistic (lsc+ilc+)



Nested Logistic (lsc+ilc+) Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	5% Extra Risk
Confidence Level (one sided)	0.95
Litter Specific Covariate	Overall Mean (11.485)
Intralitter Correlation	Estimate
Estimate Background	True
Bootstrap Runs	3
Bootstrap Iterations	1000
Bootstrap Seed	388

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	1
b	0	-18	18
theta1	0	0	1
theta2	0	-18	18
rho	1	1	18
phi1	0	0	1e+06
phi2	0	0	1e+06
phi3	0	0	1e+06
phi4	0	0	1e+06

Modeling Summary:

BMD	30.1097
BMDL	16.5153
BMDU	45.1646
AIC	785.13
P-Value	0.399

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d.f.	90
Chi ²	100.898
Log-Likelihood	-383.565

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	0.0177295	no	0.0408822
b	-14.1096	no	2.48748
theta1	0.00190102	no	0.031824
theta2	0.596571	no	0.127854
rho	1.26692	no	0.387256
phi1	0.16904	no	0.121736
phi2	0.129171	no	0.0904731
phi3	0.250979	no	0.105768
phi4	0.202283	no	0.0939057

Bootstrap Runs:

Run	P-Value	50th	90th	95th	99th
1	0.376	92.2445	138.145	155.515	178.755
2	0.399	93.1049	138.044	154.701	177.875
3	0.422	94.3085	138.529	152.309	190.694
Combined	0.399	93.1785	138.143	154.252	182.277

Scaled Residuals (for dose group nearest the BMD):

Minimum scaled residual	-0.602258
Minimum ABS(scaled residual)	0.177026
Average scaled residual	-0.134687
Average ABS(scaled residual)	0.588022
Maximum scaled residual	0.956311
Maximum ABS(scaled residual)	0.956311

Litter Data:

Dose	LSC	Est. Prob.	Litter N	Expected	Observed	Scaled Residual
0	4	0.0253336	4	0.101334	0	-0.262649
0	8	0.0329377	8	0.263501	0	-0.353272
0	10	0.0367397	10	0.367397	0	-0.388936
0	10	0.0367397	10	0.367397	0	-0.388936
0	10	0.0367397	10	0.367397	0	-0.388936
0	11	0.0386407	11	0.425048	0	-0.405385
0	11	0.0386407	11	0.425048	5	4.36331
0	11	0.0386407	11	0.425048	1	0.548354
0	11	0.0386407	11	0.425048	1	0.548354
0	11	0.0386407	11	0.425048	0	-0.405385
0	11	0.0386407	11	0.425048	0	-0.405385
0	11	0.0386407	11	0.425048	0	-0.405385
0	12	0.0405418	12	0.486501	0	-0.421103
0	12	0.0405418	12	0.486501	0	-0.421103
0	13	0.0424428	13	0.551756	0	-0.436193
0	13	0.0424428	13	0.551756	0	-0.436193
0	13	0.0424428	13	0.551756	0	-0.436193
0	13	0.0424428	13	0.551756	0	-0.436193
0	13	0.0424428	13	0.551756	2	1.14491
0	14	0.0443438	14	0.620813	0	-0.450736
0	14	0.0443438	14	0.620813	0	-0.450736
0	14	0.0443438	14	0.620813	3	1.72739
0	15	0.0462448	15	0.693672	2	0.875312
0	17	0.0500469	17	0.850797	0	-0.491687
26.8	5	0.0281564	5	0.140782	1	1.88619
26.8	7	0.0340577	7	0.238404	0	-0.372889
26.8	9	0.0446907	9	0.402217	0	-0.455041
26.8	9	0.0446907	9	0.402217	0	-0.455041

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3337	26.8	10	0.0544472	10	0.544472	0	-0.516016
3338	26.8	10	0.0544472	10	0.544472	0	-0.516016
3339	26.8	11	0.0702577	11	0.772835	2	0.956311
3340	26.8	11	0.0702577	11	0.772835	0	-0.602258
3341	26.8	11	0.0702577	11	0.772835	0	-0.602258
3342	26.8	11	0.0702577	11	0.772835	0	-0.602258
3343	26.8	11	0.0702577	11	0.772835	1	0.177026
3344	26.8	12	0.0963436	12	1.15612	0	-0.726966
3345	26.8	12	0.0963436	12	1.15612	0	-0.726966
3346	26.8	12	0.0963436	12	1.15612	0	-0.726966
3347	26.8	13	0.13899	13	1.80687	0	-0.907163
3348	26.8	13	0.13899	13	1.80687	2	0.0969623
3349	26.8	13	0.13899	13	1.80687	2	0.0969623
3350	26.8	13	0.13899	13	1.80687	0	-0.907163
3351	26.8	14	0.206015	14	2.88421	1	-0.760686
3352	26.8	14	0.206015	14	2.88421	2	-0.356969
3353	26.8	14	0.206015	14	2.88421	7	1.66161
3354	26.8	14	0.206015	14	2.88421	7	1.66161
3355	26.8	15	0.303701	15	4.55551	4	-0.186122
3356	26.8	16	0.430512	16	6.88819	4	-0.850819
3357	45.6	1	0.0197982	1	0.0197982	0	-0.14212
3358	45.6	5	0.0290404	5	0.145202	0	-0.273178
3359	45.6	7	0.0369428	7	0.2586	0	-0.327347
3360	45.6	7	0.0369428	7	0.2586	0	-0.327347
3361	45.6	8	0.0435885	8	0.348708	0	-0.363665
3362	45.6	10	0.0708587	10	0.708587	0	-0.483756
3363	45.6	10	0.0708587	10	0.708587	0	-0.483756
3364	45.6	10	0.0708587	10	0.708587	2	0.881654
3365	45.6	11	0.0987377	11	1.08612	1	-0.0464596
3366	45.6	11	0.0987377	11	1.08612	7	3.19057
3367	45.6	11	0.0987377	11	1.08612	7	3.19057
3368	45.6	11	0.0987377	11	1.08612	0	-0.585965
3369	45.6	11	0.0987377	11	1.08612	0	-0.585965
3370	45.6	11	0.0987377	11	1.08612	0	-0.585965
3371	45.6	12	0.14417	12	1.73004	0	-0.733155
3372	45.6	12	0.14417	12	1.73004	2	0.114405
3373	45.6	12	0.14417	12	1.73004	8	2.65709
3374	45.6	12	0.14417	12	1.73004	4	0.961965
3375	45.6	13	0.215037	13	2.79548	4	0.405971
3376	45.6	14	0.317031	14	4.43843	0	-1.23473
3377	45.6	14	0.317031	14	4.43843	9	1.26898
3378	45.6	14	0.317031	14	4.43843	5	0.156222
3379	45.6	14	0.317031	14	4.43843	3	-0.400157
3380	45.6	14	0.317031	14	4.43843	3	-0.400157
3381	45.6	15	0.447105	15	6.70658	9	0.56059
3382	91.7	3	0.0247655	3	0.0742964	0	-0.232894
3383	91.7	8	0.0583486	8	0.466789	0	-0.452969
3384	91.7	9	0.0799246	9	0.719321	0	-0.546441
3385	91.7	9	0.0799246	9	0.719321	2	0.972882
3386	91.7	9	0.0799246	9	0.719321	1	0.213221
3387	91.7	10	0.115449	10	1.15449	1	-0.0910298
3388	91.7	10	0.115449	10	1.15449	1	-0.0910298
3389	91.7	11	0.17237	11	1.89607	1	-0.411426
3390	91.7	11	0.17237	11	1.89607	0	-0.870568
3391	91.7	11	0.17237	11	1.89607	0	-0.870568
3392	91.7	11	0.17237	11	1.89607	0	-0.870568
3393	91.7	11	0.17237	11	1.89607	7	2.34343
3394	91.7	12	0.258196	12	3.09836	1	-0.77072
3395	91.7	12	0.258196	12	3.09836	0	-1.13802
3396	91.7	12	0.258196	12	3.09836	3	-0.0361265
3397	91.7	13	0.37529	13	4.87877	1	-1.2001
3398	91.7	13	0.37529	13	4.87877	10	1.58452
3399	91.7	13	0.37529	13	4.87877	6	0.346911
3400	91.7	13	0.37529	13	4.87877	5	0.0375088
3401	91.7	13	0.37529	13	4.87877	1	-1.2001
3402	91.7	15	0.654045	15	9.81067	13	0.88436
3403	91.7	15	0.654045	15	9.81067	15	1.43893
3404	91.7	16	0.772842	16	12.3655	10	-0.702697
3405	91.7	16	0.772842	16	12.3655	11	-0.405633
3406	91.7	16	0.772842	16	12.3655	13	0.188494
3407							
3408							

3.1.2 Bodyweight on PND 4 (Pre-Culling)

3.1.2.1 Dataset

Name: P4pr

Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
0	14	0	14
0	11	0	11
0	10	0	10
0	12	0	12
0	10	0	11
0	14	1	14
0	8	0	8
0	11	0	11
0	13	0	13
0	13	0	13
0	14	0	14
0	13	2	13
0	10	0	10
0	10	0	10
0	11	0	11
0	11	0	11
0	12	0	12
0	11	0	11
0	13	0	13
0	15	3	15
0	4	0	4
0	11	6	11
0	13	0	13
0	17	0	17
0	13	0	13
26.8	7	0	7
26.8	11	0	11
26.8	15	1	15
26.8	13	0	13
26.8	10	0	10
26.8	12	0	12
26.8	13	0	14
26.8	13	0	13
26.8	11	0	11
26.8	10	0	10
26.8	9	0	9
26.8	11	0	11
26.8	14	2	14
26.8	14	2	14
26.8	12	1	12
26.8	13	0	13

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Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
26.8	15	1	16
26.8	11	0	11
26.8	13	0	13
26.8	12	0	12
26.8	11	0	11
26.8	5	0	5
26.8	9	0	9
45.6	14	0	14
45.6	14	5	15
45.6	7	0	7
45.6	10	0	10
45.6	10	1	10
45.6	11	0	11
45.6	12	1	12
45.6	14	0	14
45.6	12	0	12
45.6	11	0	11
45.6	14	2	14
45.6	11	0	11
45.6	13	0	13
45.6	10	0	10
45.6	11	0	11
45.6	5	0	5
45.6	14	2	14
45.6	8	0	8
45.6	11	0	11
45.6	7	0	7
45.6	11	11	11
45.6	12	0	12
45.6	1	0	1
45.6	12	1	12
45.6	14	7	14
91.7	3	0	3
91.7	10	0	10
91.7	13	7	13
91.7	10	1	10
91.7	9	0	9
91.7	11	0	11
91.7	13	0	13
91.7	16	3	16
91.7	11	0	11
91.7	12	0	12
91.7	12	0	12
91.7	15	4	15

Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
91.7	11	0	11
91.7	9	0	9
91.7	15	13	15
91.7	16	4	16
91.7	16	4	16
91.7	13	5	13
91.7	12	0	12
91.7	8	0	8
91.7	13	1	13
91.7	11	0	11
91.7	9	0	9
91.7	11	0	11
91.7	13	1	13

3.1.2.2 Settings

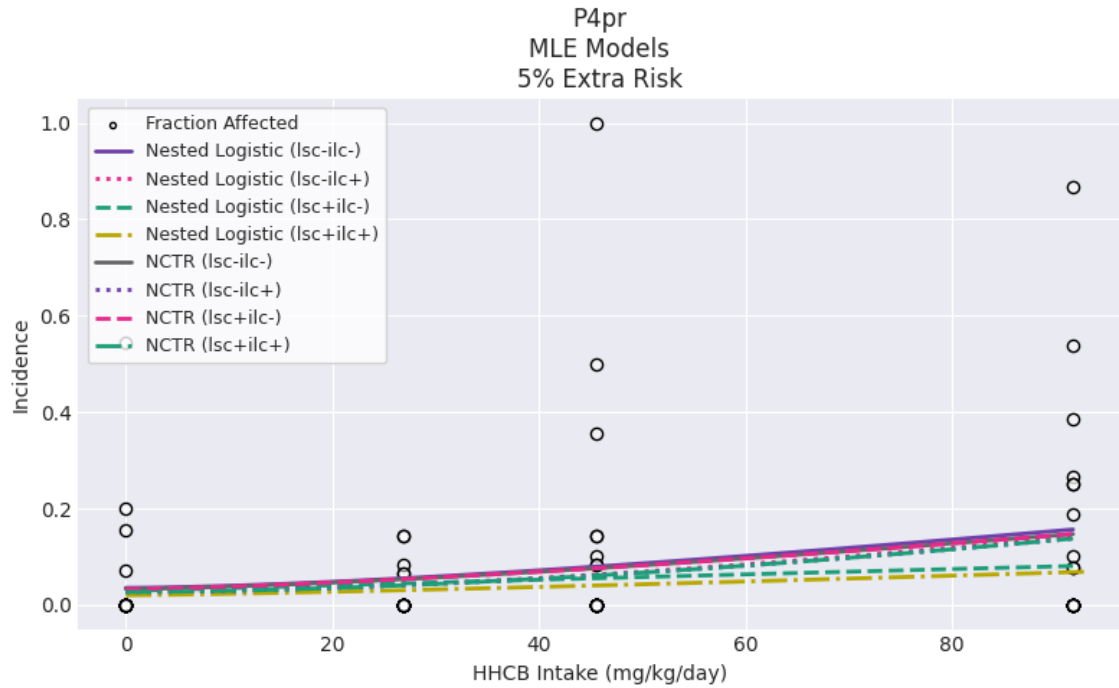
Setting	Value
BMR	5% Extra Risk
Confidence Level (one sided)	0.95
Litter Specific Covariate	Overall Mean (11.459)
Intralitter Correlation	Estimate
Estimate Background	True
Bootstrap Runs	3
Bootstrap Seed	388
Bootstrap Iterations	1000

3.1.2.3 Maximum Likelihood Approach

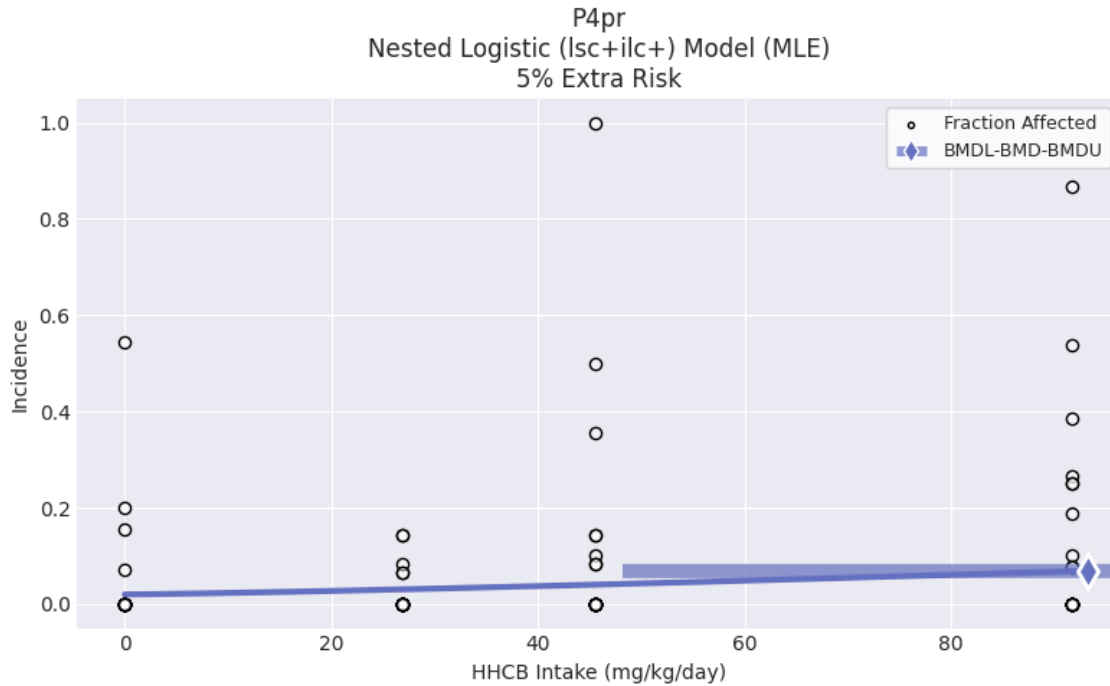
Model	BMDL	BMD	BMDU	P-Value	AIC	Recommendation and Notes
Nested Logistic (lsc-ilc-)	33.135	48.293	48.293	0	623.986	Questionable Residual near BMD > 2.0 Goodness of fit p-value < 0.1
Nested Logistic (lsc-ilc+)	29.204	55.044	55.044	0.233	477.563	Viable
Nested Logistic (lsc+ilc-)	53.194	85.711	85.711	0	575.063	Questionable Goodness of fit p-value < 0.1
Nested Logistic (lsc+ilc+) ^{a b}	48.248	93.262	93.262	0.1	454.784	Recommended - Lowest AIC BMD/highest dose ratio > 1.0
NCTR (lsc-ilc-)	24.744	49.489	49.489	0	601.097	Questionable Residual near BMD > 2.0 Goodness of fit p-value < 0.1

Model	BMDL	BMD	BMDU	P-Value	AIC	Recommendation and Notes
NCTR (lsc-ilc+)	27.962	55.923	55.923	0.27	468.129	Viable
NCTR (lsc+ilc-)	24.744	49.489	49.489	0	601.097	Questionable Residual near BMD > 2.0 Goodness of fit p-value < 0.1
NCTR (lsc+ilc+)	27.962	55.923	55.923	0.27	468.129	Viable

^a BMDs recommended best fitting model
^b User selected best fitting model



3.1.2.4 Selected Model: Nested Logistic (lsc+ilc+)



Nested Logistic (lsc+ilc+) Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	5% Extra Risk
Confidence Level (one sided)	0.95
Litter Specific Covariate	Overall Mean (11.459)
Intralitter Correlation	Estimate
Estimate Background	True
Bootstrap Runs	3
Bootstrap Iterations	1000
Bootstrap Seed	388

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	1
b	0	-18	18
theta1	0	0	1
theta2	0	-18	18
rho	1	1	18
phi1	0	0	1e+06
phi2	0	0	1e+06
phi3	0	0	1e+06
phi4	0	0	1e+06

Modeling Summary:

BMD	93.2623
BMDL	48.2485
BMDU	139.894
AIC	454.784
P-Value	0.100333
d.f.	89
Chi ²	156.051
Log-Likelihood	-218.392

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Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-0.00191237	no	0.0752279
b	-15.9084	no	3.55211
theta1	0.00191237	no	0.0290612
theta2	0.627169	no	0.197324
rho	1.27379	no	0.757045
phi1	0.232858	no	0.167745
phi2	0.0414056	no	0.15453
phi3	0.348634	no	0.182985
phi4	0.259037	no	0.138703

Bootstrap Runs:

Run	P-Value	50th	90th	95th	99th
1	0.093	82.6444	153.099	186.608	242.858
2	0.118	85.5718	164.497	196.928	266.68
3	0.09	84.3471	151.534	175.286	228.794
Combined	0.100333	83.9859	156.128	186.662	249.806

Scaled Residuals (for dose group nearest the BMD):

Minimum scaled residual	-0.424696
Minimum ABS(scaled residual)	0.424696
Average scaled residual	-0.424696
Average ABS(scaled residual)	0.424696
Maximum scaled residual	-0.424696
Maximum ABS(scaled residual)	0.424696

Litter Data:

Dose	LSC	Est. Prob.	Litter N	Expected	Observed	Scaled Residual
0	4	0.00573711	4	0.0229484	0	-0.116569
0	8	0.0133866	8	0.107093	0	-0.203155
0	10	0.0172113	10	0.172113	0	-0.237846
0	10	0.0172113	10	0.172113	0	-0.237846
0	10	0.0172113	10	0.172113	0	-0.237846
0	11	0.0191237	11	0.210361	0	-0.253832
0	11	0.0191237	11	0.210361	6	6.98607
0	11	0.0191237	10	0.191237	0	-0.250956
0	11	0.0191237	11	0.210361	0	-0.253832
0	11	0.0191237	11	0.210361	0	-0.253832
0	11	0.0191237	11	0.210361	0	-0.253832
0	11	0.0191237	11	0.210361	0	-0.253832
0	12	0.0210361	12	0.252433	0	-0.269077
0	12	0.0210361	12	0.252433	0	-0.269077
0	13	0.0229484	13	0.298329	0	-0.283677
0	13	0.0229484	13	0.298329	0	-0.283677
0	13	0.0229484	13	0.298329	0	-0.283677
0	13	0.0229484	13	0.298329	0	-0.283677
0	13	0.0229484	13	0.298329	2	1.61809
0	14	0.0248608	14	0.348051	0	-0.297707
0	14	0.0248608	14	0.348051	0	-0.297707
0	14	0.0248608	14	0.348051	1	0.557648
0	15	0.0267732	15	0.401597	3	2.01372
0	17	0.0305979	17	0.520164	0	-0.336965
26.8	5	0.00783511	5	0.0391755	0	-0.18405
26.8	7	0.0121221	7	0.084855	0	-0.262304
26.8	9	0.0175578	9	0.15802	0	-0.347595
26.8	9	0.0175578	9	0.15802	0	-0.347595
26.8	10	0.0214239	10	0.214239	0	-0.399367
26.8	10	0.0214239	10	0.214239	0	-0.399367
26.8	11	0.0269662	11	0.296628	0	-0.464311

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3537	26.8	11	0.0269662	11	0.296628	0	-0.464311
3538	26.8	11	0.0269662	11	0.296628	0	-0.464311
3539	26.8	11	0.0269662	11	0.296628	0	-0.464311
3540	26.8	11	0.0269662	11	0.296628	0	-0.464311
3541	26.8	12	0.0355895	12	0.427074	1	0.739973
3542	26.8	12	0.0355895	12	0.427074	0	-0.551595
3543	26.8	12	0.0355895	12	0.427074	0	-0.551595
3544	26.8	13	0.0497955	13	0.647341	0	-0.674631
3545	26.8	13	0.0497955	13	0.647341	0	-0.674631
3546	26.8	13	0.0497955	13	0.647341	0	-0.674631
3547	26.8	13	0.0497955	13	0.647341	0	-0.674631
3548	26.8	14	0.0738539	13	0.960101	0	-0.832199
3549	26.8	14	0.0738539	14	1.03396	2	0.795958
3550	26.8	14	0.0738539	14	1.03396	2	0.795958
3551	26.8	15	0.114479	15	1.71719	1	-0.462745
3552	26.8	16	0.180631	15	2.70946	1	-0.912839
3553	45.6	1	2.99629e-05	1	2.99629e-05	0	-0.00547392
3554	45.6	5	0.00801474	5	0.0400737	0	-0.129887
3555	45.6	7	0.0127485	7	0.0892397	0	-0.170986
3556	45.6	7	0.0127485	7	0.0892397	0	-0.170986
3557	45.6	8	0.0157652	8	0.126122	0	-0.192992
3558	45.6	10	0.0254675	10	0.254675	1	0.735488
3559	45.6	10	0.0254675	10	0.254675	0	-0.251313
3560	45.6	10	0.0254675	10	0.254675	0	-0.251313
3561	45.6	11	0.0344394	11	0.378833	11	8.29111
3562	45.6	11	0.0344394	11	0.378833	0	-0.295725
3563	45.6	11	0.0344394	11	0.378833	0	-0.295725
3564	45.6	11	0.0344394	11	0.378833	0	-0.295725
3565	45.6	11	0.0344394	11	0.378833	0	-0.295725
3566	45.6	11	0.0344394	11	0.378833	0	-0.295725
3567	45.6	12	0.0492712	12	0.591254	0	-0.358643
3568	45.6	12	0.0492712	12	0.591254	0	-0.358643
3569	45.6	12	0.0492712	12	0.591254	1	0.247937
3570	45.6	12	0.0492712	12	0.591254	1	0.247937
3571	45.6	13	0.074415	13	0.967395	0	-0.449033
3572	45.6	14	0.116808	14	1.63532	0	-0.578526
3573	45.6	14	0.116808	14	1.63532	2	0.129015
3574	45.6	14	0.116808	14	1.63532	2	0.129015
3575	45.6	14	0.116808	14	1.63532	7	1.89787
3576	45.6	14	0.116808	14	1.63532	0	-0.578526
3577	45.6	15	0.185531	14	2.59743	5	0.702288
3578	91.7	3	0.00407945	3	0.0122383	0	-0.089971
3579	91.7	8	0.0191582	8	0.153266	0	-0.235678
3580	91.7	9	0.0260295	9	0.234266	0	-0.279801
3581	91.7	9	0.0260295	9	0.234266	0	-0.279801
3582	91.7	9	0.0260295	9	0.234266	0	-0.279801
3583	91.7	10	0.0370744	10	0.370744	1	0.577012
3584	91.7	10	0.0370744	10	0.370744	0	-0.339963
3585	91.7	11	0.055598	11	0.611578	0	-0.424696
3586	91.7	11	0.055598	11	0.611578	0	-0.424696
3587	91.7	11	0.055598	11	0.611578	0	-0.424696
3588	91.7	11	0.055598	11	0.611578	0	-0.424696
3589	91.7	11	0.055598	11	0.611578	0	-0.424696
3590	91.7	12	0.0870525	12	1.04463	0	-0.545207
3591	91.7	12	0.0870525	12	1.04463	0	-0.545207
3592	91.7	12	0.0870525	12	1.04463	0	-0.545207
3593	91.7	13	0.139456	13	1.81293	7	2.04883
3594	91.7	13	0.139456	13	1.81293	5	1.25885
3595	91.7	13	0.139456	13	1.81293	0	-0.716086
3596	91.7	13	0.139456	13	1.81293	1	-0.321098
3597	91.7	13	0.139456	13	1.81293	1	-0.321098
3598	91.7	15	0.340009	15	5.10014	4	-0.27878
3599	91.7	15	0.340009	15	5.10014	13	2.00185
3600	91.7	16	0.485698	16	7.77117	3	-1.07973
3601	91.7	16	0.485698	16	7.77117	4	-0.853428
3602	91.7	16	0.485698	16	7.77117	4	-0.853428
3603							
3604							

3.1.3 Bodyweight on PND 4 (Post-Culling)

3.1.3.1 Dataset

Name: P4po

Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
0	8	0	14
0	8	0	11
0	8	0	10
0	8	0	12
0	8	0	11
0	8	1	14
0	8	0	8
0	8	0	11
0	8	0	13
0	8	0	13
0	8	0	14
0	8	1	13
0	8	0	10
0	8	0	10
0	8	0	11
0	8	0	11
0	8	0	12
0	8	0	11
0	8	0	13
0	8	2	15
0	4	0	4
0	8	5	11
0	8	0	13
0	8	0	17
0	8	0	13
26.8	7	0	7
26.8	8	0	11
26.8	8	0	15
26.8	9	0	13
26.8	8	0	10
26.8	8	0	12
26.8	8	0	14
26.8	8	0	13
26.8	8	0	11
26.8	8	0	10
26.8	8	0	9
26.8	8	0	11
26.8	8	1	14
26.8	8	1	14
26.8	8	1	12
26.8	8	0	13

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Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
26.8	8	0	16
26.8	8	0	11
26.8	8	0	13
26.8	8	0	12
26.8	8	0	11
26.8	5	0	5
26.8	8	0	9
45.6	8	0	14
45.6	8	3	15
45.6	7	0	7
45.6	8	0	10
45.6	8	1	10
45.6	8	0	11
45.6	8	0	12
45.6	8	0	14
45.6	8	0	12
45.6	8	0	11
45.6	8	0	14
45.6	8	0	11
45.6	8	0	13
45.6	8	0	10
45.6	8	0	11
45.6	5	0	5
45.6	8	2	14
45.6	8	0	8
45.6	8	0	11
45.6	7	0	7
45.6	8	8	11
45.6	8	0	12
45.6	1	0	1
45.6	8	1	12
45.6	8	3	14
91.7	3	0	3
91.7	8	0	10
91.7	8	4	13
91.7	8	0	10
91.7	8	0	9
91.7	8	0	11
91.7	8	0	13
91.7	8	1	16
91.7	8	0	11
91.7	8	0	12
91.7	8	0	12
91.7	8	2	15

Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
91.7	8	0	11
91.7	8	0	9
91.7	8	7	15
91.7	8	2	16
91.7	8	3	16
91.7	8	2	13
91.7	8	0	12
91.7	8	0	8
91.7	8	1	13
91.7	8	0	11
91.7	8	0	9
91.7	8	0	11
91.7	8	0	13

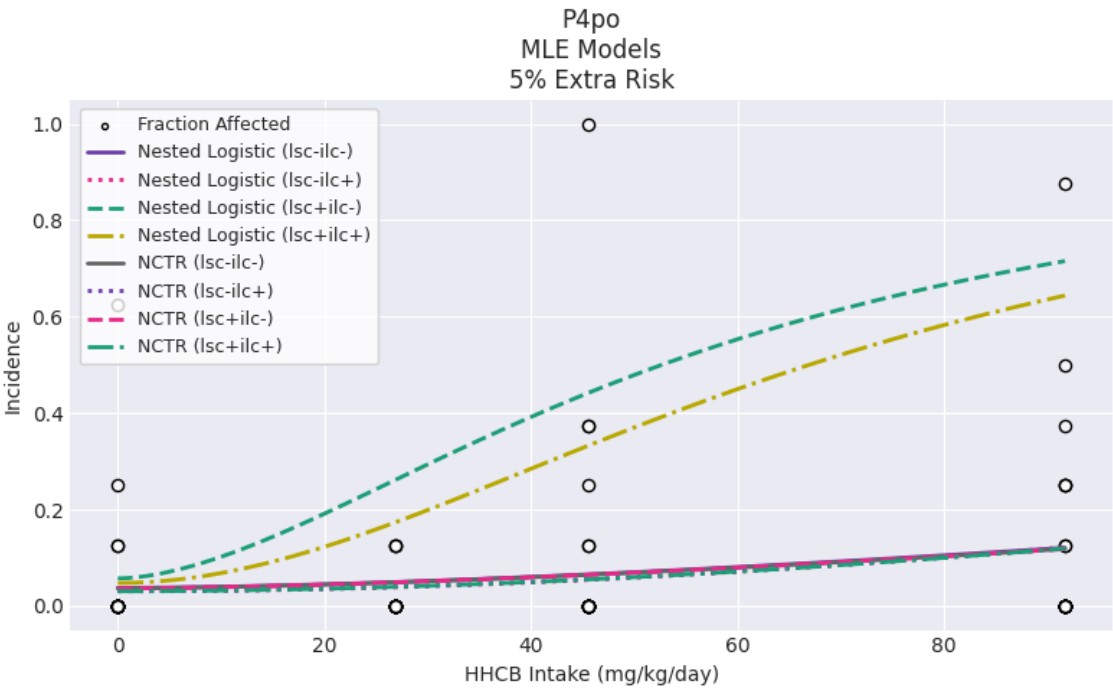
3.1.3.2 Settings

Setting	Value
BMR	5% Extra Risk
Confidence Level (one sided)	0.95
Litter Specific Covariate	Overall Mean (11.459)
Intralitter Correlation	Estimate
Estimate Background	True
Bootstrap Runs	3
Bootstrap Seed	388
Bootstrap Iterations	1000

3.1.3.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Recommendation and Notes
Nested Logistic (lsc-ilc-)	41.901	64.244	64.244	0	386.172	Questionable Residual near BMD > 2.0 Goodness of fit p-value < 0.1
Nested Logistic (lsc-ilc+)	31.425	65.67	65.67	0.234	299.345	Viable
Nested Logistic (lsc+ilc-)	0.05	10.291	10.291	0	384.037	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 Goodness of fit p-value < 0.1 BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0

Model	BMDL	BMD	BMDU	P-Value	AIC	Recommendation and Notes
Nested Logistic (lsc+ilc+)	0.002	15.598	15.598	<0.001	298.149	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 Goodness of fit p-value < 0.1 BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0
NCTR (lsc-ilc-)	32.308	64.613	64.613	0	371.109	Questionable Residual near BMD > 2.0 Goodness of fit p-value < 0.1
NCTR (lsc-ilc+) ^{ab}	32.929	65.826	65.826	0.289	291.676	Recommended - Lowest AIC
NCTR (lsc+ilc-)	32.308	64.613	64.613	0	371.109	Questionable Residual near BMD > 2.0 Goodness of fit p-value < 0.1
NCTR (lsc+ilc+)	32.929	65.826	65.826	0.289	291.676	Viable
^a BMDS recommended best fitting model						
^b User selected best fitting model						

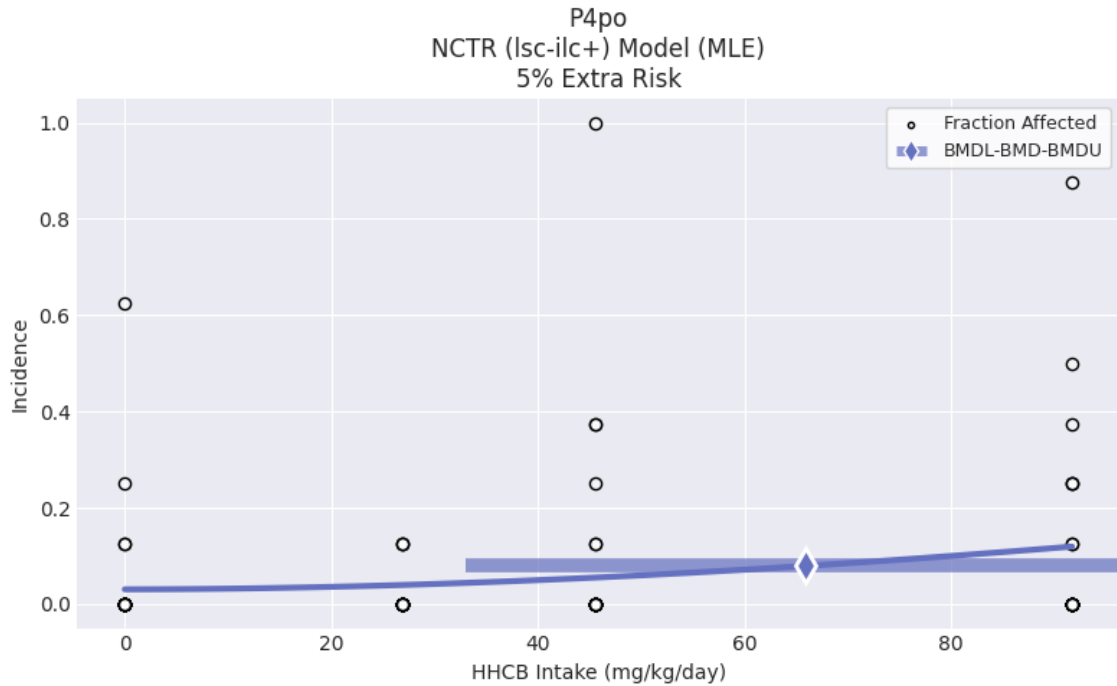


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3.1.3.4 Selected Model: NCTR (lsc-ilc+)



NCTR (lsc-ilc+) Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	5% Extra Risk
Confidence Level (one sided)	0.95
Litter Specific Covariate	Unused
Intralitter Correlation	Estimate
Estimate Background	True
Bootstrap Runs	3
Bootstrap Iterations	1000
Bootstrap Seed	388

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	18
b	0	0	18
theta1	-1	-1	-0.111111
theta2	-1	-1	-0.111111
rho	1	1	18
phi1	0	0	1e+08
phi2	0	0	1e+08
phi3	0	0	1e+08
phi4	0	0	1e+08

Modeling Summary:

BMD	65.8255
BMDL	32.9288
BMDU	98.7383
AIC	291.676
P-Value	0.288667
d.f.	89
Chi ²	112.088

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Log-Likelihood	-136.838
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Model Parameters:

Variable	Estimate	On Bound	Std Error
a	0.0309837	no	0.109412
b	1.83979e-05	no	Not Reported
theta1	0.00296234	no	0.138109
theta2	1.75902e-06	no	0.115977
rho	1.89469	no	Not Reported
phi1	0.258085	no	0.500419
phi2	0.0735299	no	6.48254
phi3	0.418951	no	0.455055
phi4	0.351939	no	0.337022

Bootstrap Runs:

Run	P-Value	50th	90th	95th	99th
1	0.289	90.8864	148.084	168.365	209.908
2	0.302	89.7281	147.816	173.349	220.842
3	0.275	89.2344	145.557	168.037	228.683
Combined	0.288667	89.7966	146.563	169.178	222.13

Scaled Residuals (for dose group nearest the BMD):

Minimum scaled residual	-0.336234
Minimum ABS(scaled residual)	0.336234
Average scaled residual	0.728155
Average ABS(scaled residual)	1.28854
Maximum scaled residual	6.0501
Maximum ABS(scaled residual)	6.0501

Litter Data:

Dose	LSC	Est. Prob.	Litter N	Expected	Observed	Scaled Residual
0	4	0.00884766	4	0.0353906	0	-0.141862
0	8	0.0205229	8	0.164183	0	-0.244386
0	10	0.0263088	8	0.210471	0	-0.277521
0	10	0.0263088	8	0.210471	0	-0.277521
0	10	0.0263088	8	0.210471	0	-0.277521
0	11	0.029189	8	0.233512	5	5.97567
0	11	0.029189	8	0.233512	0	-0.29275
0	11	0.029189	8	0.233512	0	-0.29275
0	11	0.029189	8	0.233512	0	-0.29275
0	11	0.029189	8	0.233512	0	-0.29275
0	11	0.029189	8	0.233512	0	-0.29275
0	11	0.029189	8	0.233512	0	-0.29275
0	11	0.029189	8	0.233512	0	-0.29275
0	12	0.0320606	8	0.256485	0	-0.307268
0	12	0.0320606	8	0.256485	0	-0.307268
0	13	0.0349237	8	0.27939	0	-0.32117
0	13	0.0349237	8	0.27939	1	0.82837
0	13	0.0349237	8	0.27939	0	-0.32117
0	13	0.0349237	8	0.27939	0	-0.32117
0	13	0.0349237	8	0.27939	0	-0.32117
0	13	0.0349237	8	0.27939	0	-0.32117
0	14	0.0377784	8	0.302227	0	-0.334533
0	14	0.0377784	8	0.302227	0	-0.334533
0	14	0.0377784	8	0.302227	1	0.77236
0	15	0.0406246	8	0.324997	2	1.79057
0	17	0.0462918	8	0.370334	0	-0.371963
26.8	5	0.0153054	5	0.0765272	0	-0.245059
26.8	7	0.0228701	7	0.160091	0	-0.337169
26.8	9	0.0303766	8	0.243013	0	-0.40677
26.8	9	0.0303766	8	0.243013	0	-0.40677
26.8	10	0.0341082	8	0.272866	0	-0.431863
26.8	10	0.0341082	8	0.272866	0	-0.431863

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3736	26.8	11	0.0378255	8	0.302604	0	-0.455665
3737	26.8	11	0.0378255	8	0.302604	0	-0.455665
3738	26.8	11	0.0378255	8	0.302604	0	-0.455665
3739	26.8	11	0.0378255	8	0.302604	0	-0.455665
3740	26.8	11	0.0378255	8	0.302604	0	-0.455665
3741	26.8	12	0.0415284	8	0.332227	1	0.961516
3742	26.8	12	0.0415284	8	0.332227	0	-0.478369
3743	26.8	12	0.0415284	8	0.332227	0	-0.478369
3744	26.8	13	0.0452171	8	0.361737	0	-0.500126
3745	26.8	13	0.0452171	8	0.361737	0	-0.500126
3746	26.8	13	0.0452171	9	0.406954	0	-0.518039
3747	26.8	13	0.0452171	8	0.361737	0	-0.500126
3748	26.8	14	0.0488916	8	0.391133	0	-0.521054
3749	26.8	14	0.0488916	8	0.391133	1	0.811112
3750	26.8	14	0.0488916	8	0.391133	1	0.811112
3751	26.8	15	0.052552	8	0.420416	0	-0.541249
3752	26.8	16	0.0561983	8	0.449586	0	-0.560791
3753	45.6	1	0	1	0	0	0
3754	45.6	5	0.0214019	5	0.107009	0	-0.202154
3755	45.6	7	0.0319304	7	0.223513	0	-0.256339
3756	45.6	7	0.0319304	7	0.223513	0	-0.256339
3757	45.6	8	0.0371522	8	0.297217	0	-0.280166
3758	45.6	10	0.0475113	8	0.38009	1	0.519532
3759	45.6	10	0.0475113	8	0.38009	0	-0.318544
3760	45.6	10	0.0475113	8	0.38009	0	-0.318544
3761	45.6	11	0.0526489	8	0.421191	0	-0.336234
3762	45.6	11	0.0526489	8	0.421191	8	6.0501
3763	45.6	11	0.0526489	8	0.421191	0	-0.336234
3764	45.6	11	0.0526489	8	0.421191	0	-0.336234
3765	45.6	11	0.0526489	8	0.421191	0	-0.336234
3766	45.6	11	0.0526489	8	0.421191	0	-0.336234
3767	45.6	12	0.0577589	8	0.462071	0	-0.353126
3768	45.6	12	0.0577589	8	0.462071	0	-0.353126
3769	45.6	12	0.0577589	8	0.462071	1	0.411099
3770	45.6	12	0.0577589	8	0.462071	0	-0.353126
3771	45.6	13	0.0628413	8	0.50273	0	-0.369333
3772	45.6	14	0.0678963	8	0.54317	0	-0.38494
3773	45.6	14	0.0678963	8	0.54317	0	-0.38494
3774	45.6	14	0.0678963	8	0.54317	0	-0.38494
3775	45.6	14	0.0678963	8	0.54317	2	1.03244
3776	45.6	14	0.0678963	8	0.54317	3	1.74113
3777	45.6	15	0.072924	8	0.583392	3	1.65701
3778	91.7	3	0.0240132	3	0.0720395	0	-0.208135
3779	91.7	8	0.0815535	8	0.652428	0	-0.452874
3780	91.7	9	0.092648	8	0.741184	0	-0.485638
3781	91.7	9	0.092648	8	0.741184	0	-0.485638
3782	91.7	9	0.092648	8	0.741184	0	-0.485638
3783	91.7	10	0.103608	8	0.828867	0	-0.516692
3784	91.7	10	0.103608	8	0.828867	0	-0.516692
3785	91.7	11	0.114436	8	0.915491	0	-0.54633
3786	91.7	11	0.114436	8	0.915491	0	-0.54633
3787	91.7	11	0.114436	8	0.915491	0	-0.54633
3788	91.7	11	0.114436	8	0.915491	0	-0.54633
3789	91.7	11	0.114436	8	0.915491	0	-0.54633
3790	91.7	12	0.125134	8	1.00107	0	-0.574776
3791	91.7	12	0.125134	8	1.00107	0	-0.574776
3792	91.7	12	0.125134	8	1.00107	0	-0.574776
3793	91.7	13	0.135702	8	1.08561	0	-0.602204
3794	91.7	13	0.135702	8	1.08561	4	1.61665
3795	91.7	13	0.135702	8	1.08561	2	0.507223
3796	91.7	13	0.135702	8	1.08561	1	-0.0474904
3797	91.7	13	0.135702	8	1.08561	0	-0.602204
3798	91.7	15	0.156456	8	1.25165	2	0.391334
3799	91.7	15	0.156456	8	1.25165	7	3.00598
3800	91.7	16	0.166646	8	1.33317	2	0.339937
3801	91.7	16	0.166646	8	1.33317	1	-0.169841
3802	91.7	16	0.166646	8	1.33317	3	0.849715

3.1.4 Bodyweight on PND 7

3.1.4.1 Dataset

Name: P7

Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
0	8	0	14
0	8	0	11
0	8	0	10
0	8	0	12
0	8	0	11
0	8	1	14
0	8	0	8
0	8	1	11
0	8	0	13
0	8	0	13
0	8	0	14
0	8	0	13
0	8	0	10
0	8	0	10
0	8	0	11
0	8	1	11
0	8	0	12
0	8	0	11
0	8	0	13
0	8	2	15
0	4	0	4
0	8	5	11
0	8	0	13
0	8	0	17
0	8	0	13
26.8	7	0	7
26.8	8	0	11
26.8	8	0	15
26.8	8	0	13
26.8	8	0	10
26.8	8	0	12
26.8	8	0	14
26.8	8	0	13
26.8	8	1	11
26.8	8	0	10
26.8	8	0	9
26.8	8	0	11
26.8	8	2	14
26.8	8	1	14

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Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
26.8	8	0	12
26.8	8	0	13
26.8	8	0	16
26.8	8	0	11
26.8	8	0	13
26.8	8	0	12
26.8	8	0	11
26.8	5	1	5
26.8	8	0	9
45.6	8	0	14
45.6	8	3	15
45.6	7	0	7
45.6	8	0	10
45.6	8	1	10
45.6	8	0	11
45.6	8	0	12
45.6	8	1	14
45.6	8	0	12
45.6	8	1	11
45.6	8	0	14
45.6	8	0	11
45.6	8	2	13
45.6	8	0	10
45.6	8	0	11
45.6	5	0	5
45.6	8	2	14
45.6	8	0	8
45.6	8	0	11
45.6	7	0	7
45.6	8	8	11
45.6	8	0	12
45.6	8	1	12
45.6	8	4	14
91.7	3	0	3
91.7	8	1	10
91.7	8	7	13
91.7	8	1	10
91.7	8	0	9
91.7	8	0	11
91.7	8	2	13
91.7	8	6	16
91.7	8	0	11
91.7	8	0	12
91.7	8	0	12

Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
91.7	8	3	15
91.7	8	0	11
91.7	8	3	9
91.7	8	5	15
91.7	8	2	16
91.7	8	5	16
91.7	8	4	13
91.7	8	3	12
91.7	8	0	8
91.7	8	1	13
91.7	8	0	11
91.7	8	1	9
91.7	8	0	11
91.7	8	1	13

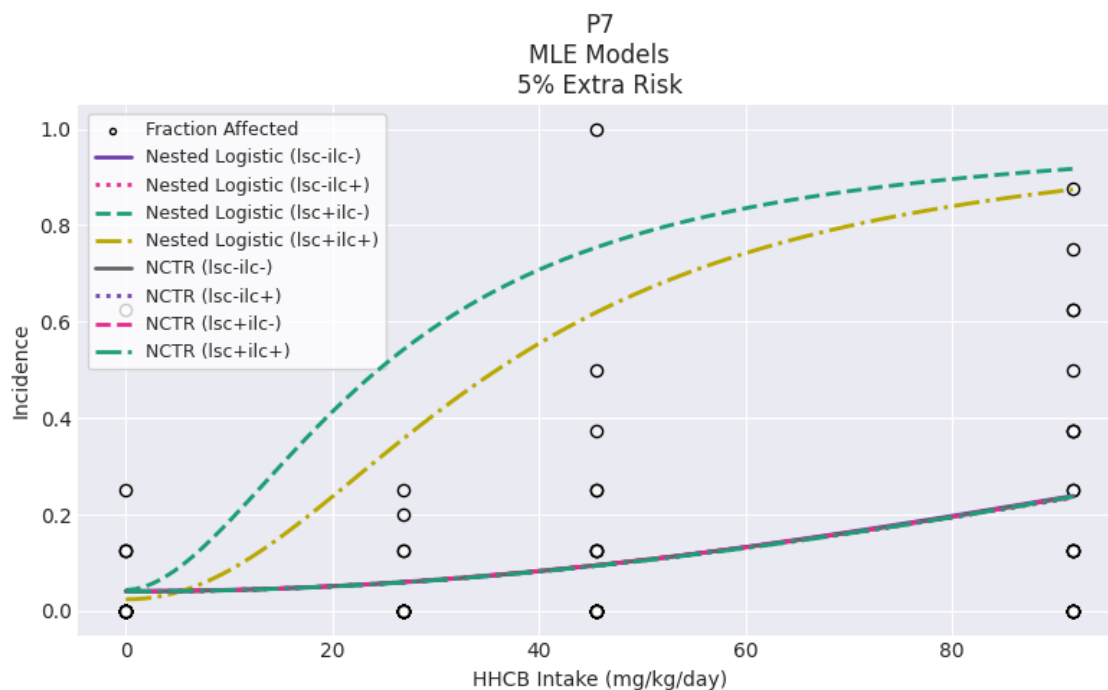
3.1.4.2 Settings

Setting	Value
BMR	5% Extra Risk
Confidence Level (one sided)	0.95
Litter Specific Covariate	Overall Mean (11.567)
Intralitter Correlation	Estimate
Estimate Background	True
Bootstrap Runs	3
Bootstrap Seed	388
Bootstrap Iterations	1000

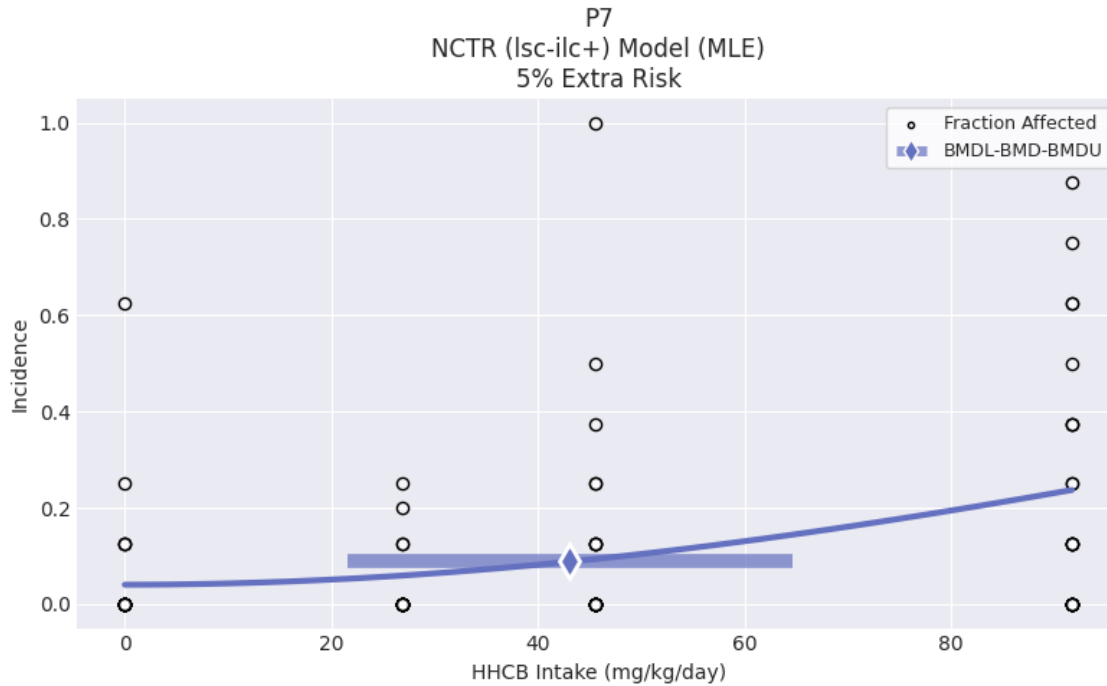
3.1.4.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Recommendation and Notes
Nested Logistic (lsc-ilc-)	30.786	43.32	43.32	0	498.876	Questionable Goodness of fit p-value < 0.1
Nested Logistic (lsc-ilc+)	19.299	43.081	43.081	0.363	421.981	Viable
Nested Logistic (lsc+ilc-)	<0.001	5.223	5.223	0	496.474	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 lowest dose/BMD ratio > 3.0 Goodness of fit p-value < 0.1 BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0

Model	BMDL	BMD	BMDU	P-Value	AIC	Recommendation and Notes
Nested Logistic (lsc+ilc+)	<0.001	9.01	9.01	0	420.634	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 Goodness of fit p-value < 0.1 BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0
NCTR (lsc-ilc-)	21.266	42.532	42.532	0	478.435	Questionable Goodness of fit p-value < 0.1
NCTR (lsc-ilc+) ^{a b}	21.55	43.1	43.1	0.386	414.188	Recommended - Lowest AIC
NCTR (lsc+ilc-)	21.266	42.532	42.532	0	478.435	Questionable Goodness of fit p-value < 0.1
NCTR (lsc+ilc+)	21.55	43.1	43.1	0.386	414.188	Viable
^a BMDS recommended best fitting model						
^b User selected best fitting model						



3.1.4.4 Selected Model: NCTR (lsc-ilc+)



NCTR (lsc-ilc+) Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	5% Extra Risk
Confidence Level (one sided)	0.95
Litter Specific Covariate	Unused
Intralitter Correlation	Estimate
Estimate Background	True
Bootstrap Runs	3
Bootstrap Iterations	1000
Bootstrap Seed	388

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	18
b	0	0	18
theta1	-0.333333	-0.333333	-0.125
theta2	-0.333333	-0.333333	-0.125
rho	1	1	18
phi1	0	0	1e+08
phi2	0	0	1e+08
phi3	0	0	1e+08
phi4	0	0	1e+08

Modeling Summary:

BMD	43.1002
BMDL	21.5502
BMDU	64.6503
AIC	414.188
P-Value	0.385667

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d.f.	88
Chi ²	102.011
Log-Likelihood	-198.094

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	0.0409257	no	0.00786572
b	2.92267e-05	no	Not Reported
theta1	0.00353273	no	0.0678714
theta2	3.41154e-06	no	Not Reported
rho	1.9849	no	Not Reported
phi1	0.219399	no	0.160304
phi2	0.18386	no	0.353911
phi3	0.318647	no	0.177661
phi4	0.254025	no	0.0834426

Bootstrap Runs:

Run	P-Value	50th	90th	95th	99th
1	0.376	92.0283	141.77	162.335	200.261
2	0.392	91.7499	139.457	156.636	196.026
3	0.389	93.4554	139.607	154.228	196.459
Combined	0.385667	92.4423	140.078	156.7	196.381

Scaled Residuals (for dose group nearest the BMD):

Minimum scaled residual	-0.517592
Minimum ABS(scaled residual)	0.145158
Average scaled residual	-0.351905
Average ABS(scaled residual)	0.424484
Maximum scaled residual	0.145158
Maximum ABS(scaled residual)	0.517592

Litter Data:

Dose	LSC	Est. Prob.	Litter N	Expected	Observed	Scaled Residual
0	4	0.0140932	4	0.0563729	0	-0.185695
0	8	0.027927	8	0.223416	0	-0.301059
0	10	0.034771	8	0.278168	0	-0.337118
0	10	0.034771	8	0.278168	0	-0.337118
0	10	0.034771	8	0.278168	0	-0.337118
0	11	0.0381749	8	0.305399	5	5.43952
0	11	0.0381749	8	0.305399	1	0.804817
0	11	0.0381749	8	0.305399	1	0.804817
0	11	0.0381749	8	0.305399	0	-0.353858
0	11	0.0381749	8	0.305399	0	-0.353858
0	11	0.0381749	8	0.305399	0	-0.353858
0	11	0.0381749	8	0.305399	0	-0.353858
0	12	0.0415667	8	0.332534	0	-0.369897
0	12	0.0415667	8	0.332534	0	-0.369897
0	13	0.0449467	8	0.359573	0	-0.385322
0	13	0.0449467	8	0.359573	0	-0.385322
0	13	0.0449467	8	0.359573	0	-0.385322
0	13	0.0449467	8	0.359573	0	-0.385322
0	13	0.0449467	8	0.359573	0	-0.385322
0	14	0.0483147	8	0.386517	0	-0.400204
0	14	0.0483147	8	0.386517	0	-0.400204
0	14	0.0483147	8	0.386517	1	0.635206
0	15	0.0516708	8	0.413366	2	1.59138
0	17	0.0583476	8	0.46678	0	-0.442134
26.8	5	0.0221407	5	0.110703	1	2.05174
26.8	7	0.0335427	7	0.234799	0	-0.339876
26.8	9	0.0448118	8	0.358494	0	-0.405099
26.8	9	0.0448118	8	0.358494	0	-0.405099

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3936	26.8	10	0.050397	8	0.403176	0	-0.430865
3937	26.8	10	0.050397	8	0.403176	0	-0.430865
3938	26.8	11	0.0559495	8	0.447596	0	-0.455313
3939	26.8	11	0.0559495	8	0.447596	1	0.561929
3940	26.8	11	0.0559495	8	0.447596	0	-0.455313
3941	26.8	11	0.0559495	8	0.447596	0	-0.455313
3942	26.8	11	0.0559495	8	0.447596	0	-0.455313
3943	26.8	12	0.0614695	8	0.491756	0	-0.478647
3944	26.8	12	0.0614695	8	0.491756	0	-0.478647
3945	26.8	12	0.0614695	8	0.491756	0	-0.478647
3946	26.8	13	0.0669573	8	0.535658	0	-0.501023
3947	26.8	13	0.0669573	8	0.535658	0	-0.501023
3948	26.8	13	0.0669573	8	0.535658	0	-0.501023
3949	26.8	13	0.0669573	8	0.535658	0	-0.501023
3950	26.8	14	0.072413	8	0.579304	0	-0.522565
3951	26.8	14	0.072413	8	0.579304	1	0.379492
3952	26.8	14	0.072413	8	0.579304	2	1.28155
3953	26.8	15	0.0778367	8	0.622694	0	-0.543373
3954	26.8	16	0.0832288	8	0.66583	0	-0.563529
3955	45.6	5	0.0306395	5	0.153198	0	-0.263592
3956	45.6	7	0.0502692	7	0.351885	0	-0.356708
3957	45.6	7	0.0502692	7	0.351885	0	-0.356708
3958	45.6	8	0.0599345	8	0.479476	0	-0.397345
3959	45.6	10	0.078971	8	0.631768	1	0.268577
3960	45.6	10	0.078971	8	0.631768	0	-0.460793
3961	45.6	10	0.078971	8	0.631768	0	-0.460793
3962	45.6	11	0.0883442	8	0.706753	8	5.05516
3963	45.6	11	0.0883442	8	0.706753	1	0.203258
3964	45.6	11	0.0883442	8	0.706753	0	-0.489871
3965	45.6	11	0.0883442	8	0.706753	0	-0.489871
3966	45.6	11	0.0883442	8	0.706753	0	-0.489871
3967	45.6	11	0.0883442	8	0.706753	0	-0.489871
3968	45.6	12	0.097622	8	0.780976	0	-0.517592
3969	45.6	12	0.097622	8	0.780976	0	-0.517592
3970	45.6	12	0.097622	8	0.780976	1	0.145158
3971	45.6	12	0.097622	8	0.780976	0	-0.517592
3972	45.6	13	0.106805	8	0.854443	2	0.729568
3973	45.6	14	0.115895	8	0.927162	0	-0.569757
3974	45.6	14	0.115895	8	0.927162	0	-0.569757
3975	45.6	14	0.115895	8	0.927162	1	0.04476
3976	45.6	14	0.115895	8	0.927162	2	0.659277
3977	45.6	14	0.115895	8	0.927162	4	1.88831
3978	45.6	15	0.124893	8	0.999142	3	1.19052
3979	91.7	3	0.0106041	3	0.0318124	0	-0.146018
3980	91.7	8	0.149815	8	1.19852	0	-0.712339
3981	91.7	9	0.175213	8	1.4017	0	-0.782126
3982	91.7	9	0.175213	8	1.4017	3	0.891824
3983	91.7	9	0.175213	8	1.4017	1	-0.224143
3984	91.7	10	0.199852	8	1.59881	1	-0.317634
3985	91.7	10	0.199852	8	1.59881	1	-0.317634
3986	91.7	11	0.223754	8	1.79003	0	-0.911069
3987	91.7	11	0.223754	8	1.79003	0	-0.911069
3988	91.7	11	0.223754	8	1.79003	0	-0.911069
3989	91.7	11	0.223754	8	1.79003	0	-0.911069
3990	91.7	11	0.223754	8	1.79003	0	-0.911069
3991	91.7	12	0.246943	8	1.97554	0	-0.971739
3992	91.7	12	0.246943	8	1.97554	0	-0.971739
3993	91.7	12	0.246943	8	1.97554	3	0.503914
3994	91.7	13	0.269439	8	2.15551	7	2.31614
3995	91.7	13	0.269439	8	2.15551	4	0.881846
3996	91.7	13	0.269439	8	2.15551	2	-0.0743497
3997	91.7	13	0.269439	8	2.15551	1	-0.552447
3998	91.7	13	0.269439	8	2.15551	1	-0.552447
3999	91.7	15	0.312435	8	2.49948	3	0.229066
4000	91.7	15	0.312435	8	2.49948	5	1.14438
4001	91.7	16	0.332974	8	2.6638	2	-0.298767
4002	91.7	16	0.332974	8	2.6638	5	1.0515
4003	91.7	16	0.332974	8	2.6638	6	1.50159
4004							
4005							

3.1.5 Bodyweight on PND 14

3.1.5.1 Dataset

Name: P14

Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
0	8	0	14
0	8	0	11
0	8	0	10
0	8	0	12
0	8	0	11
0	8	1	14
0	8	0	8
0	8	1	11
0	8	0	13
0	8	0	13
0	8	0	14
0	8	0	13
0	8	0	10
0	8	0	10
0	8	0	11
0	8	0	11
0	8	0	12
0	8	0	11
0	8	0	13
0	8	3	15
0	4	0	4
0	8	5	11
0	8	0	13
0	8	0	17
0	8	0	13
26.8	7	0	7
26.8	8	0	11
26.8	8	0	15
26.8	8	0	13
26.8	8	1	10
26.8	8	0	12
26.8	8	0	14
26.8	8	0	13
26.8	8	0	11
26.8	8	0	10
26.8	8	0	9
26.8	8	3	11
26.8	8	5	14
26.8	8	1	14
26.8	8	1	12
26.8	8	0	13

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Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
26.8	8	0	16
26.8	8	0	11
26.8	8	0	13
26.8	8	0	12
26.8	8	1	11
26.8	5	0	5
26.8	8	0	9
45.6	8	0	14
45.6	8	1	15
45.6	7	0	7
45.6	8	1	10
45.6	8	1	10
45.6	8	2	11
45.6	8	0	12
45.6	8	0	14
45.6	8	0	12
45.6	8	0	11
45.6	8	0	14
45.6	8	0	11
45.6	8	4	13
45.6	8	0	10
45.6	8	0	11
45.6	5	0	5
45.6	8	1	14
45.6	8	1	8
45.6	8	0	11
45.6	7	0	7
45.6	8	8	11
45.6	8	1	12
45.6	8	5	12
45.6	8	2	14
91.7	3	0	3
91.7	8	5	10
91.7	8	8	13
91.7	8	5	10
91.7	8	0	9
91.7	8	0	11
91.7	8	6	13
91.7	8	1	16
91.7	8	1	11
91.7	8	2	12
91.7	8	0	12
91.7	8	2	15
91.7	8	0	11

Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
91.7	8	8	9
91.7	8	5	15
91.7	8	3	16
91.7	8	3	16
91.7	8	2	13
91.7	8	7	12
91.7	8	1	8
91.7	8	1	13
91.7	8	0	11
91.7	8	6	9
91.7	8	0	11
91.7	8	1	13

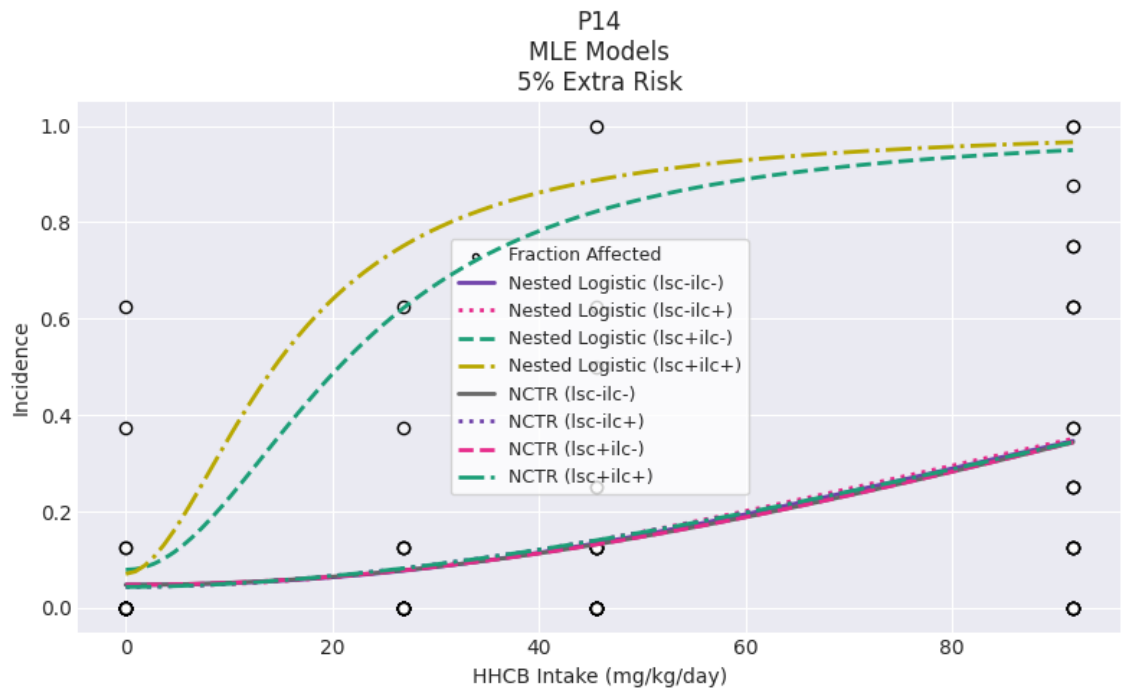
3.1.5.2 Settings

Setting	Value
BMR	5% Extra Risk
Confidence Level (one sided)	0.95
Litter Specific Covariate	Overall Mean (11.567)
Intralitter Correlation	Estimate
Estimate Background	True
Bootstrap Runs	3
Bootstrap Seed	388
Bootstrap Iterations	1000

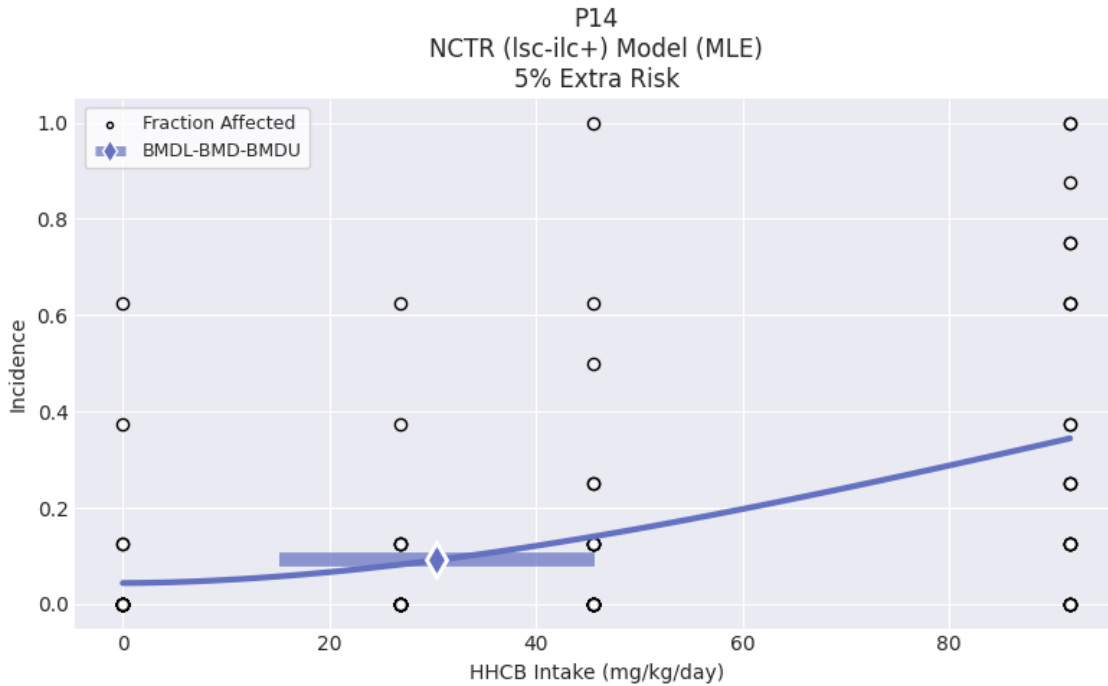
3.1.5.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Recommendation and Notes
Nested Logistic (lsc-ilc-)	23.866	33.922	33.922	0	590.975	Questionable Goodness of fit p-value < 0.1
Nested Logistic (lsc-ilc+)	14.787	31.961	31.961	0.391	475.959	Viable
Nested Logistic (lsc+ilc-)	<0.001	5.265	5.265	0	583.759	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 lowest dose/BMD ratio > 3.0 Goodness of fit p-value < 0.1 BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0
Nested Logistic (lsc+ilc+)	<0.001	3.182	3.182	0	471.561	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio >

Model	BMDL	BMD	BMDU	P-Value	AIC	Recommendation and Notes
						10.0 lowest dose/BMD ratio > 3.0 Goodness of fit p-value < 0.1 BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0
NCTR (lsc-ilc-)	16.977	33.955	33.955	0	587.471	Questionable Goodness of fit p-value < 0.1
NCTR (lsc-ilc+) ^{a b}	15.204	30.409	30.409	0.384	472.657	Recommended - Lowest AIC
NCTR (lsc+ilc-)	16.977	33.955	33.955	0	587.471	Questionable Goodness of fit p-value < 0.1
NCTR (lsc+ilc+)	15.204	30.409	30.409	0.384	472.657	Viable
^a BMDS recommended best fitting model ^b User selected best fitting model						



3.1.5.4 Selected Model: NCTR (lsc-ilc+)



NCTR (lsc-ilc+) Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	5% Extra Risk
Confidence Level (one sided)	0.95
Litter Specific Covariate	Unused
Intralitter Correlation	Estimate
Estimate Background	True
Bootstrap Runs	3
Bootstrap Iterations	1000
Bootstrap Seed	388

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	18
b	0	0	18
theta1	-0.333333	-0.333333	-0.125
theta2	-0.333333	-0.333333	-0.125
rho	1	1	18
phi1	0	0	1e+08
phi2	0	0	1e+08
phi3	0	0	1e+08
phi4	0	0	1e+08

Modeling Summary:

BMD	30.4085
BMDL	15.2044
BMDU	45.6128

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AIC	472.657
P-Value	0.384333
d.f.	88
Chi ²	99.802
Log-Likelihood	-227.328

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	0.0445619	no	0.00730836
b	0.000106938	no	Not Reported
theta1	0.00520157	no	0.0709857
theta2	1.24825e-05	no	Not Reported
rho	1.80778	no	Not Reported
phi1	0.33028	no	0.239058
phi2	0.263242	no	0.227115
phi3	0.321295	no	0.182415
phi4	0.410648	no	0.128336

Bootstrap Runs:

Run	P-Value	50th	90th	95th	99th
1	0.39	90.8078	137.364	151.292	181.93
2	0.375	90.1483	136.621	149.959	187.088
3	0.388	89.8493	137.496	152.151	190.523
Combined	0.384333	90.388	136.802	151.266	186.431

Scaled Residuals (for dose group nearest the BMD):

Minimum scaled residual	-0.513906
Minimum ABS(scaled residual)	0.234852
Average scaled residual	-0.26432
Average ABS(scaled residual)	0.420888
Maximum scaled residual	0.234852
Maximum ABS(scaled residual)	0.513906

Litter Data:

Dose	LSC	Est. Prob.	Litter N	Expected	Observed	Scaled Residual
0	4	0.00518806	4	0.0207523	0	-0.102363
0	8	0.0256725	8	0.20538	0	-0.252281
0	10	0.0357561	8	0.286049	0	-0.299284
0	10	0.0357561	8	0.286049	0	-0.299284
0	10	0.0357561	8	0.286049	0	-0.299284
0	11	0.0407586	8	0.326069	5	4.5922
0	11	0.0407586	8	0.326069	1	0.662146
0	11	0.0407586	8	0.326069	0	-0.320367
0	11	0.0407586	8	0.326069	0	-0.320367
0	11	0.0407586	8	0.326069	0	-0.320367
0	11	0.0407586	8	0.326069	0	-0.320367
0	11	0.0407586	8	0.326069	0	-0.320367
0	12	0.0457352	8	0.365882	0	-0.340246
0	12	0.0457352	8	0.365882	0	-0.340246
0	13	0.050686	8	0.405488	0	-0.359122
0	13	0.050686	8	0.405488	0	-0.359122
0	13	0.050686	8	0.405488	0	-0.359122
0	13	0.050686	8	0.405488	0	-0.359122
0	13	0.050686	8	0.405488	0	-0.359122
0	13	0.050686	8	0.405488	0	-0.359122
0	14	0.0556111	8	0.444889	0	-0.377144
0	14	0.0556111	8	0.444889	0	-0.377144
0	14	0.0556111	8	0.444889	1	0.470583
0	15	0.0605107	8	0.484085	3	2.04996
0	17	0.0702336	8	0.561869	0	-0.427157
26.8	5	0.0197356	5	0.0986781	0	-0.221436
26.8	7	0.0390817	7	0.273572	0	-0.332223

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4134	26.8	9	0.0580461	8	0.464369	0	-0.416439
4135	26.8	9	0.0580461	8	0.464369	0	-0.416439
4136	26.8	10	0.0673874	8	0.539099	1	0.385529
4137	26.8	10	0.0673874	8	0.539099	0	-0.45094
4138	26.8	11	0.0766361	8	0.613089	0	-0.483293
4139	26.8	11	0.0766361	8	0.613089	1	0.304999
4140	26.8	11	0.0766361	8	0.613089	3	1.88158
4141	26.8	11	0.0766361	8	0.613089	0	-0.483293
4142	26.8	11	0.0766361	8	0.613089	0	-0.483293
4143	26.8	12	0.0857931	8	0.686345	0	-0.513906
4144	26.8	12	0.0857931	8	0.686345	0	-0.513906
4145	26.8	12	0.0857931	8	0.686345	1	0.234852
4146	26.8	13	0.0948593	8	0.758874	0	-0.543078
4147	26.8	13	0.0948593	8	0.758874	0	-0.543078
4148	26.8	13	0.0948593	8	0.758874	0	-0.543078
4149	26.8	13	0.0948593	8	0.758874	0	-0.543078
4150	26.8	14	0.103836	8	0.830684	5	2.86608
4151	26.8	14	0.103836	8	0.830684	1	0.116391
4152	26.8	14	0.103836	8	0.830684	0	-0.57103
4153	26.8	15	0.112723	8	0.901782	0	-0.597938
4154	26.8	16	0.121522	8	0.972175	0	-0.623939
4155	45.6	5	0.034697	5	0.173485	0	-0.280439
4156	45.6	7	0.0681901	7	0.477331	0	-0.41829
4157	45.6	7	0.0681901	7	0.477331	0	-0.41829
4158	45.6	8	0.0844983	8	0.675986	1	0.2285
4159	45.6	10	0.116263	8	0.930108	0	-0.569149
4160	45.6	10	0.116263	8	0.930108	1	0.0427684
4161	45.6	10	0.116263	8	0.930108	1	0.0427684
4162	45.6	11	0.13173	8	1.05384	8	4.02856
4163	45.6	11	0.13173	8	1.05384	2	0.548743
4164	45.6	11	0.13173	8	1.05384	0	-0.611197
4165	45.6	11	0.13173	8	1.05384	0	-0.611197
4166	45.6	11	0.13173	8	1.05384	0	-0.611197
4167	45.6	11	0.13173	8	1.05384	0	-0.611197
4168	45.6	12	0.146926	8	1.17541	0	-0.651212
4169	45.6	12	0.146926	8	1.17541	0	-0.651212
4170	45.6	12	0.146926	8	1.17541	1	-0.0971831
4171	45.6	12	0.146926	8	1.17541	5	2.11893
4172	45.6	13	0.161857	8	1.29485	4	1.4406
4173	45.6	14	0.176526	8	1.4122	0	-0.726515
4174	45.6	14	0.176526	8	1.4122	0	-0.726515
4175	45.6	14	0.176526	8	1.4122	1	-0.21206
4176	45.6	14	0.176526	8	1.4122	0	-0.726515
4177	45.6	14	0.176526	8	1.4122	2	0.302394
4178	45.6	15	0.190938	8	1.5275	1	-0.263247
4179	91.7	3	0	3	0	0	0
4180	91.7	8	0.218235	8	1.74588	1	-0.32435
4181	91.7	9	0.255797	8	2.04637	0	-0.842436
4182	91.7	9	0.255797	8	2.04637	6	1.6276
4183	91.7	9	0.255797	8	2.04637	8	2.45094
4184	91.7	10	0.291554	8	2.33243	5	1.05426
4185	91.7	10	0.291554	8	2.33243	5	1.05426
4186	91.7	11	0.325593	8	2.60474	0	-0.998416
4187	91.7	11	0.325593	8	2.60474	0	-0.998416
4188	91.7	11	0.325593	8	2.60474	1	-0.615109
4189	91.7	11	0.325593	8	2.60474	0	-0.998416
4190	91.7	11	0.325593	8	2.60474	0	-0.998416
4191	91.7	12	0.357997	8	2.86397	0	-1.07302
4192	91.7	12	0.357997	8	2.86397	7	1.5496
4193	91.7	12	0.357997	8	2.86397	2	-0.323696
4194	91.7	13	0.388843	8	3.11075	6	1.06455
4195	91.7	13	0.388843	8	3.11075	8	1.80146
4196	91.7	13	0.388843	8	3.11075	2	-0.409257
4197	91.7	13	0.388843	8	3.11075	1	-0.77771
4198	91.7	13	0.388843	8	3.11075	1	-0.77771
4199	91.7	15	0.446162	8	3.56929	5	0.516961
4200	91.7	15	0.446162	8	3.56929	2	-0.567037
4201	91.7	16	0.472772	8	3.78218	3	-0.281401
4202	91.7	16	0.472772	8	3.78218	3	-0.281401
4203	91.7	16	0.472772	8	3.78218	1	-1.00093
4204							
4205							

3.1.6 Bodyweight on PND 21**3.1.6.1 Dataset**

Name: P21

Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
0	8	0	14
0	8	0	11
0	8	0	10
0	8	0	12
0	8	0	11
0	8	0	14
0	8	0	8
0	8	2	11
0	8	2	13
0	8	0	13
0	8	0	14
0	8	0	13
0	8	0	10
0	8	0	10
0	8	0	11
0	8	0	11
0	8	0	12
0	8	0	11
0	8	0	13
0	8	1	15
0	4	0	4
0	8	5	11
0	8	0	13
0	8	0	17
0	8	0	13
26.8	7	0	7
26.8	8	1	11
26.8	8	0	15
26.8	8	1	13
26.8	8	1	10
26.8	8	0	12
26.8	8	0	14
26.8	8	0	13
26.8	8	0	11
26.8	8	0	10
26.8	8	0	9
26.8	8	3	11
26.8	8	2	14
26.8	8	0	14
26.8	8	1	12
26.8	8	0	13

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Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
26.8	8	0	16
26.8	8	1	11
26.8	8	0	13
26.8	8	0	12
26.8	8	0	11
26.8	5	0	5
26.8	8	0	9
45.6	8	0	14
45.6	8	1	15
45.6	7	0	7
45.6	8	2	10
45.6	8	1	10
45.6	8	4	11
45.6	8	0	12
45.6	8	0	14
45.6	8	0	12
45.6	8	0	11
45.6	8	2	14
45.6	8	0	11
45.6	8	2	13
45.6	8	0	10
45.6	8	0	11
45.6	5	0	5
45.6	8	1	14
45.6	8	1	8
45.6	8	0	11
45.6	7	0	7
45.6	8	8	11
45.6	8	3	12
45.6	8	7	12
45.6	8	3	14
91.7	3	0	3
91.7	8	7	10
91.7	8	7	13
91.7	8	8	10
91.7	8	0	9
91.7	8	0	11
91.7	8	5	13
91.7	8	3	16
91.7	8	1	11
91.7	8	4	12
91.7	8	0	12
91.7	8	4	15
91.7	8	0	11

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Dose (mg/kg/day)	Litter N	Incidence	Litter Covariates
91.7	8	4	9
91.7	8	7	15
91.7	8	2	16
91.7	8	2	16
91.7	8	5	13
91.7	8	8	12
91.7	8	3	8
91.7	8	1	13
91.7	8	0	11
91.7	8	8	9
91.7	8	3	11
91.7	8	1	13

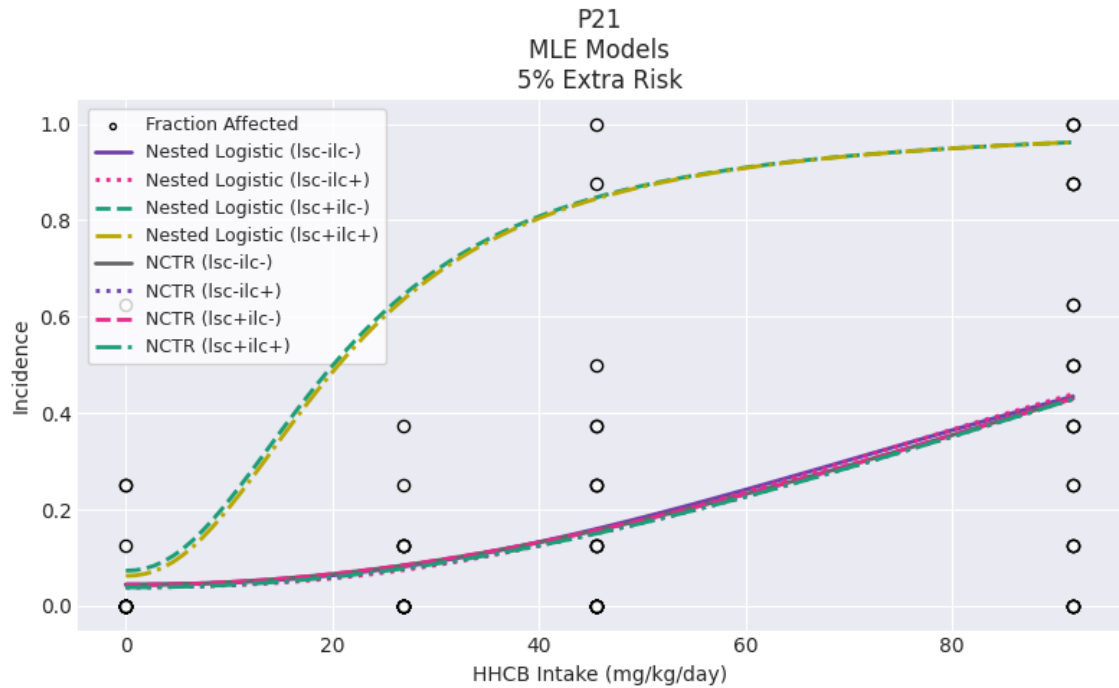
3.1.6.2 Settings

Setting	Value
BMR	5% Extra Risk
Confidence Level (one sided)	0.95
Litter Specific Covariate	Overall Mean (11.567)
Intralitter Correlation	Estimate
Estimate Background	True
Bootstrap Runs	3
Bootstrap Seed	388
Bootstrap Iterations	1000

3.1.6.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Recommendation and Notes
Nested Logistic (lsc-ilc-)	22.753	30.111	30.111	0	623.575	Questionable Goodness of fit p-value < 0.1
Nested Logistic (lsc-ilc+)	19.098	30.885	30.885	0.352	507.427	Viable
Nested Logistic (lsc+ilc-)	<0.001	5.58	5.58	0	614.608	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 lowest dose/BMD ratio > 3.0 Goodness of fit p-value < 0.1 BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0
Nested Logistic (lsc+ilc+)	<0.001	5.755	5.755	0	502.391	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio >

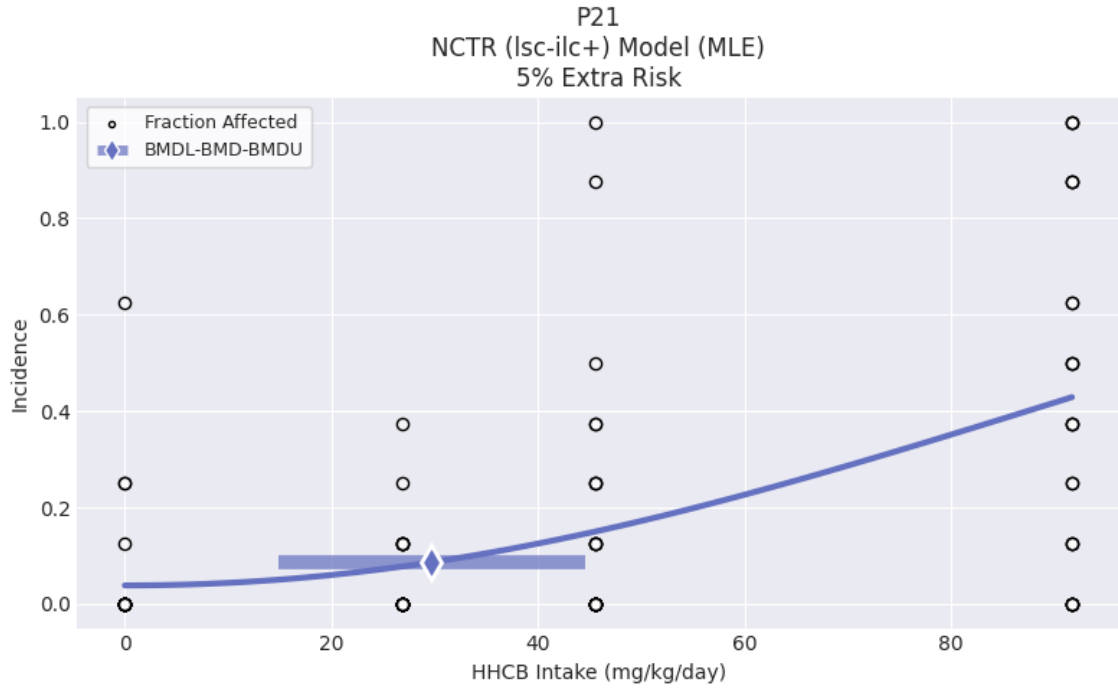
Model	BMDL	BMD	BMDU	P-Value	AIC	Recommendation and Notes
						10.0 lowest dose/BMD ratio > 3.0 Goodness of fit p-value < 0.1 BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0
NCTR (lsc-ilc-)	14.634	29.269	29.269	0	622.978	Questionable Goodness of fit p-value < 0.1
NCTR (lsc-ilc+) ^{a b}	14.85	29.699	29.699	0.318	505.155	Recommended - Lowest AIC
NCTR (lsc+ilc-)	14.634	29.269	29.269	0	622.978	Questionable Goodness of fit p-value < 0.1
NCTR (lsc+ilc+)	14.85	29.699	29.699	0.318	505.155	Viable
^a BMDS recommended best fitting model ^b User selected best fitting model						



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3.1.6.4 Selected Model: NCTR (lsc-ilc+)



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NCTR (lsc-ilc+) Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	5% Extra Risk
Confidence Level (one sided)	0.95
Litter Specific Covariate	Unused
Intralitter Correlation	Estimate
Estimate Background	True
Bootstrap Runs	3
Bootstrap Iterations	1000
Bootstrap Seed	388

Parameter Settings:

Parameter	Initial	Min	Max
a	0	0	18
b	0	0	18
theta1	-0.333333	-0.333333	-0.125
theta2	-0.333333	-0.333333	-0.125
rho	1	1	18
phi1	0	0	1e+08
phi2	0	0	1e+08
phi3	0	0	1e+08
phi4	0	0	1e+08

Modeling Summary:

BMD	29.6993
BMDL	14.8496

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BMDU	44.5489
AIC	505.155
P-Value	0.317667
d.f.	88
Chi ²	106.014
Log-Likelihood	-243.578

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	0.0390654	no	0.00609698
b	4.8006e-05	no	Not Reported
theta1	0.00455998	no	0.0710639
theta2	5.17147e-06	no	Not Reported
rho	2.05654	no	Not Reported
phi1	0.309123	no	0.227607
phi2	0.099292	no	0.116768
phi3	0.349675	no	0.158695
phi4	0.442634	no	0.115276

Bootstrap Runs:

Run	P-Value	50th	90th	95th	99th
1	0.334	92.6076	136.36	152.585	187.964
2	0.306	91.3006	133.852	155.553	200.776
3	0.313	91.8895	135.933	146.316	184.163
Combined	0.317667	91.8935	135.668	149.475	191.628

Scaled Residuals (for dose group nearest the BMD):

Minimum scaled residual	-0.645102
Minimum ABS(scaled residual)	0.35005
Average scaled residual	-0.313385
Average ABS(scaled residual)	0.546751
Maximum scaled residual	0.35005
Maximum ABS(scaled residual)	0.645102

Litter Data:

Dose	LSC	Est. Prob.	Litter N	Expected	Observed	Scaled Residual
0	4	0.0045496	4	0.0181984	0	-0.0973922
0	8	0.0225419	8	0.180336	0	-0.241481
0	10	0.0314158	8	0.251326	0	-0.286379
0	10	0.0314158	8	0.251326	0	-0.286379
0	10	0.0314158	8	0.251326	0	-0.286379
0	11	0.0358225	8	0.28658	0	-0.306504
0	11	0.0358225	8	0.28658	0	-0.306504
0	11	0.0358225	8	0.28658	0	-0.306504
0	11	0.0358225	8	0.28658	0	-0.306504
0	11	0.0358225	8	0.28658	0	-0.306504
0	11	0.0358225	8	0.28658	2	1.83254
0	11	0.0358225	8	0.28658	5	5.04111
0	12	0.0402091	8	0.321673	0	-0.325469
0	12	0.0402091	8	0.321673	0	-0.325469
0	13	0.0445758	8	0.356606	0	-0.343469
0	13	0.0445758	8	0.356606	0	-0.343469
0	13	0.0445758	8	0.356606	2	1.58285
0	13	0.0445758	8	0.356606	0	-0.343469
0	13	0.0445758	8	0.356606	0	-0.343469
0	13	0.0445758	8	0.356606	0	-0.343469
0	13	0.0445758	8	0.356606	0	-0.343469
0	14	0.0489225	8	0.39138	0	-0.360648
0	14	0.0489225	8	0.39138	0	-0.360648
0	14	0.0489225	8	0.39138	0	-0.360648
0	15	0.0532496	8	0.425997	1	0.508142
0	17	0.0618446	8	0.494757	0	-0.408272
26.8	5	0.0210444	5	0.105222	0	-0.277362

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4330	26.8	7	0.0385721	7	0.270004	0	-0.419512
4331	26.8	9	0.0557859	8	0.446287	0	-0.528058
4332	26.8	9	0.0557859	8	0.446287	0	-0.528058
4333	26.8	10	0.0642769	8	0.514215	1	0.537907
4334	26.8	10	0.0642769	8	0.514215	0	-0.569388
4335	26.8	11	0.0726916	8	0.581533	0	-0.608253
4336	26.8	11	0.0726916	8	0.581533	3	2.52959
4337	26.8	11	0.0726916	8	0.581533	1	0.437695
4338	26.8	11	0.0726916	8	0.581533	1	0.437695
4339	26.8	11	0.0726916	8	0.581533	0	-0.608253
4340	26.8	12	0.0810306	8	0.648244	0	-0.645102
4341	26.8	12	0.0810306	8	0.648244	0	-0.645102
4342	26.8	12	0.0810306	8	0.648244	1	0.35005
4343	26.8	13	0.0892945	8	0.714356	0	-0.680265
4344	26.8	13	0.0892945	8	0.714356	0	-0.680265
4345	26.8	13	0.0892945	8	0.714356	0	-0.680265
4346	26.8	13	0.0892945	8	0.714356	1	0.272012
4347	26.8	14	0.0974842	8	0.779874	0	-0.713994
4348	26.8	14	0.0974842	8	0.779874	0	-0.713994
4349	26.8	14	0.0974842	8	0.779874	2	1.11706
4350	26.8	15	0.1056	8	0.844802	0	-0.746485
4351	26.8	16	0.113643	8	0.909146	0	-0.777897
4352	45.6	5	0.0443517	5	0.221759	0	-0.311031
4353	45.6	7	0.0779696	7	0.545787	0	-0.437114
4354	45.6	7	0.0779696	7	0.545787	0	-0.437114
4355	45.6	8	0.0943324	8	0.754659	1	0.159825
4356	45.6	10	0.126192	8	1.00954	2	0.567942
4357	45.6	10	0.126192	8	1.00954	1	-0.00546788
4358	45.6	10	0.126192	8	1.00954	0	-0.578878
4359	45.6	11	0.141699	8	1.13359	0	-0.618931
4360	45.6	11	0.141699	8	1.13359	8	3.749
4361	45.6	11	0.141699	8	1.13359	4	1.56503
4362	45.6	11	0.141699	8	1.13359	0	-0.618931
4363	45.6	11	0.141699	8	1.13359	0	-0.618931
4364	45.6	11	0.141699	8	1.13359	0	-0.618931
4365	45.6	12	0.156931	8	1.25545	0	-0.657206
4366	45.6	12	0.156931	8	1.25545	3	0.913245
4367	45.6	12	0.156931	8	1.25545	0	-0.657206
4368	45.6	12	0.156931	8	1.25545	7	3.00718
4369	45.6	13	0.171892	8	1.37514	2	0.315356
4370	45.6	14	0.186588	8	1.49271	0	-0.729568
4371	45.6	14	0.186588	8	1.49271	1	-0.240813
4372	45.6	14	0.186588	8	1.49271	2	0.247942
4373	45.6	14	0.186588	8	1.49271	0	-0.729568
4374	45.6	14	0.186588	8	1.49271	3	0.736698
4375	45.6	15	0.201024	8	1.60819	1	-0.288959
4376	91.7	3	0.0393945	3	0.118184	0	-0.255458
4377	91.7	8	0.29087	8	2.32696	3	0.258806
4378	91.7	9	0.332637	8	2.6611	0	-0.986371
4379	91.7	9	0.332637	8	2.6611	8	1.97893
4380	91.7	9	0.332637	8	2.6611	4	0.496282
4381	91.7	10	0.371944	8	2.97555	8	1.8155
4382	91.7	10	0.371944	8	2.97555	7	1.45417
4383	91.7	11	0.408936	8	3.27149	0	-1.16211
4384	91.7	11	0.408936	8	3.27149	3	-0.0964394
4385	91.7	11	0.408936	8	3.27149	1	-0.806885
4386	91.7	11	0.408936	8	3.27149	0	-1.16211
4387	91.7	11	0.408936	8	3.27149	0	-1.16211
4388	91.7	12	0.443749	8	3.55	4	0.158183
4389	91.7	12	0.443749	8	3.55	0	-1.24787
4390	91.7	12	0.443749	8	3.55	8	1.56424
4391	91.7	13	0.476512	8	3.8121	1	-0.983299
4392	91.7	13	0.476512	8	3.8121	1	-0.983299
4393	91.7	13	0.476512	8	3.8121	5	0.415371
4394	91.7	13	0.476512	8	3.8121	5	0.415371
4395	91.7	13	0.476512	8	3.8121	7	1.11471
4396	91.7	15	0.536362	8	4.2909	4	-0.101875
4397	91.7	15	0.536362	8	4.2909	7	0.948753
4398	91.7	16	0.56367	8	4.50936	2	-0.883667
4399	91.7	16	0.56367	8	4.50936	2	-0.883667
4400	91.7	16	0.56367	8	4.50936	3	-0.531519
4401							
4402							

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