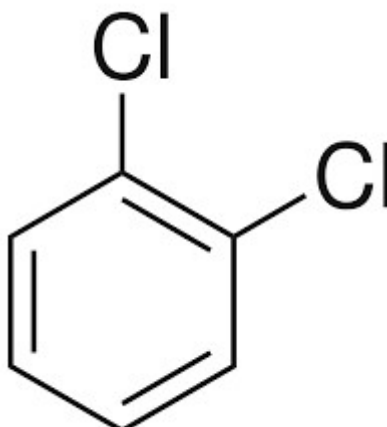




## Draft Benchmark Dose Modeling Results for *o*- Dichlorobenzene

CASRN: 95-50-1



*April 2026*

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# 1 BMDS-GENERATED REPORTS FOR *o*-DICHLOROBENZENE

This document presents the BMDS-generated Microsoft Word output reports for each dataset modeled for *p*-dichlorobenzene. For each relevant BMR that was applied, output reports from the selected model are included. For continuous datasets, if a constant variance model was deemed appropriate based on the statistical test provided in BMDS (i.e., Test 2; p-value > 0.05), the final BMD results were estimated from a constant variance model; in this instance, only modeling results from the constant variance model are shown. If the test for constant variance failed (p-value < 0.05), the dataset was run again applying the nonconstant variance model. If a nonconstant variance model was deemed appropriate based on the statistical test provided in BMDS (i.e., Test 3; p-value > 0.05), the final BMD results were estimated from a nonconstant variance model; in this instance, only modeling results from the nonconstant variance model are shown. If neither constant nor nonconstant variance models provided an adequate fit to the data using a normal distribution, the dataset was run again applying the lognormal distribution option, unless another measurement with successful modeling was determined to be adequate (i.e., absolute vs. relative liver weight). If a lognormal distribution model was viable, only modeling results from the lognormal distribution model are shown. If none of the variance or distribution models provided an adequate fit to the data, all of the model runs are shown to document that the dataset was unsuitable for BMD modeling.

## 2 INDIVIDUAL STUDY RESULTS

### 2.1 { Cho, 2023, 13037009@@author-year }

13-week inhalation study in mice

Report Generated: 2026-Jan-20 15:01 UTC

Analysis URL: [View](#)

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

#### 2.1.1 Eosinophilic Globules (Nasal Cavity) (Score 2,3,4), Male Mice; BMR: 10% ER

##### Dataset

Name: Eosinophilic globules in males (score 2,3,4)

Dose (ppm)	N	Incidence
0	10	0
2.025	10	3
4.05	10	8
8.1	10	8

##### Settings

Setting	Value
BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Maximum Multistage Degree	3

##### Maximum Likelihood Approach

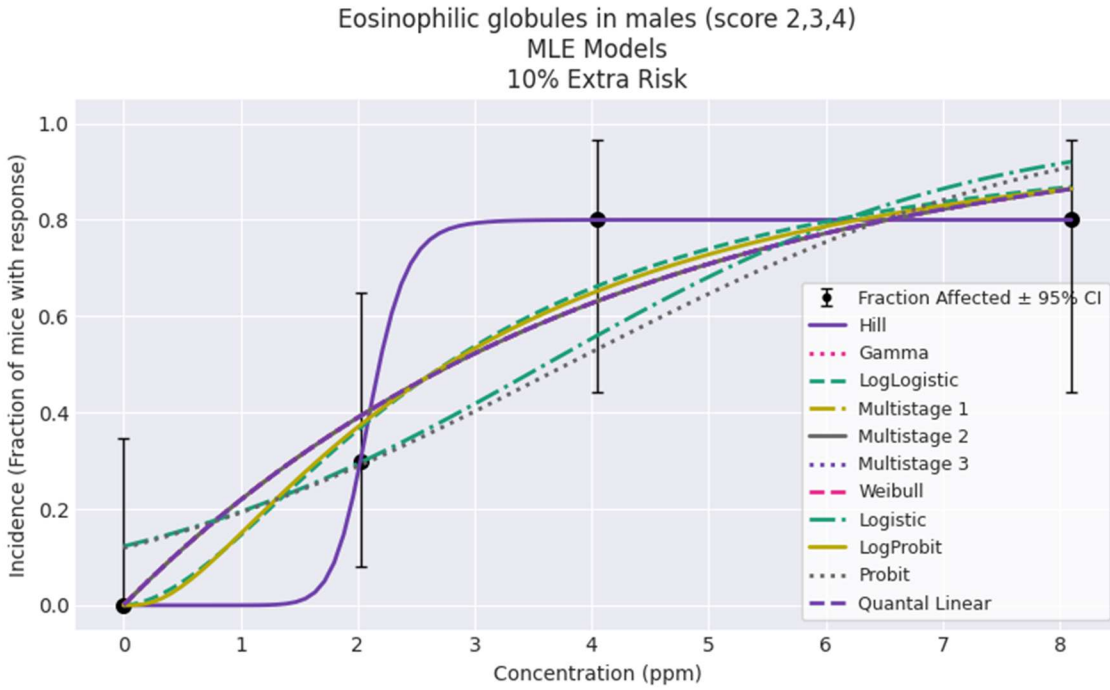
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
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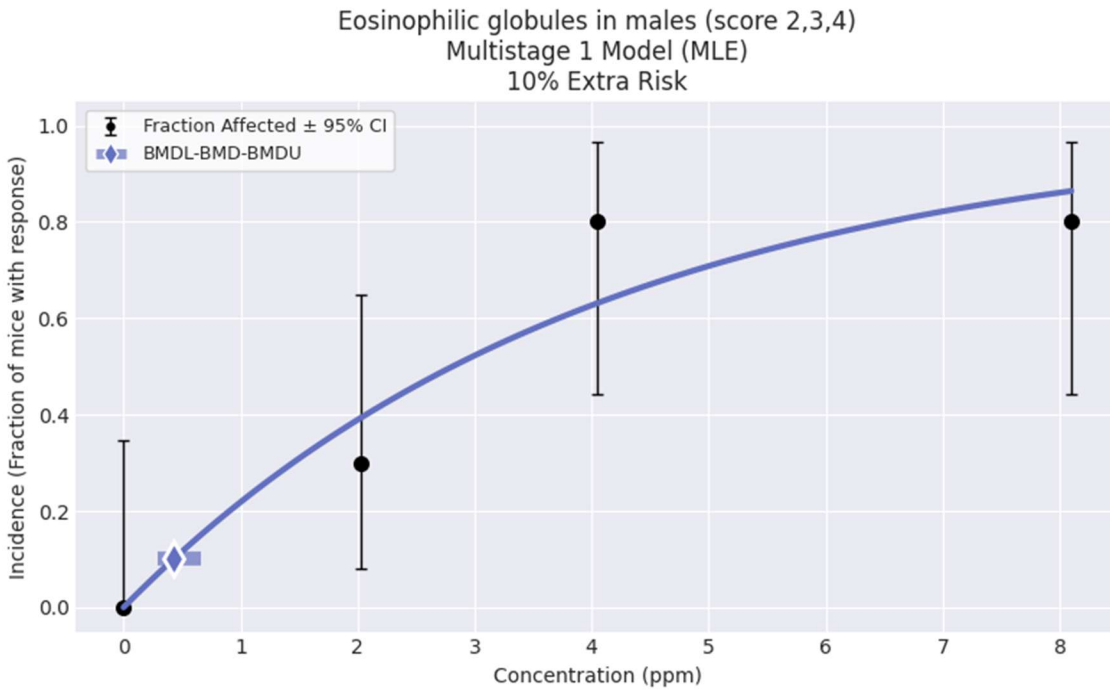
Hill	0.204	1.819	2.012	0.999	38.233	-3.90e-4	-2.22e-7	<b>Viable</b> lowest dose/BMDL ratio > 3.0 BMD/BMDL ratio > 3.0
Gamma	0.289	0.427	1.453	0.586	36.262	-3.90e-4	-3.90e-4	<b>Viable</b> lowest dose/BMDL ratio > 3.0 lowest dose/BMD ratio > 3.0
LogLogistic	0.147	0.785	1.642	0.482	37.728	-3.90e-4	-3.90e-4	<b>Questionable</b> lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 BMD/BMDL ratio > 3.0
Multistage 1 <sup>ab</sup>	0.289	0.427	0.658	0.586	36.262	-3.90e-4	-3.90e-4	<b>Recommended - Lowest AIC</b> lowest dose/BMDL ratio > 3.0 lowest dose/BMD ratio > 3.0
Multistage 2	0.289	0.427	1.063	0.586	36.262	-3.90e-4	-3.90e-4	<b>Viable</b> lowest dose/BMDL ratio > 3.0 lowest dose/BMD ratio > 3.0
Multistage 3	0.289	0.427	1.063	0.586	36.262	-3.90e-4	-3.90e-4	<b>Viable</b> lowest dose/BMDL ratio > 3.0 lowest dose/BMD ratio > 3.0
Weibull	0.289	0.427	1.248	0.586	36.262	-3.90e-4	-3.90e-4	<b>Viable</b> lowest dose/BMDL ratio > 3.0 lowest dose/BMD ratio > 3.0
Logistic	0.777	1.183	1.809	0.057	42.851	-1.181	0.024	<b>Questionable</b> Goodness of fit p-value < 0.1
LogProbit	0.018	0.793	1.652	0.458	37.854	-3.90e-4	-3.90e-4	<b>Questionable</b> lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0
Probit	0.802	1.169	1.762	0.057	43.03	-1.161	0.063	<b>Questionable</b> Goodness of fit p-value < 0.1
Quantal Linear	0.289	0.427	0.658	0.586	36.262	-3.90e-4	-3.90e-4	<b>Viable</b> lowest dose/BMDL ratio > 3.0 lowest dose/BMD ratio > 3.0

<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> Selected based on lowest AIC



### Selected Model: Multistage 1



Multistage 1 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Modeling approach	frequentist restricted
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-18	18
b1	0	0	10000

Modeling Summary:

BMD	0.427443
BMDL	0.288859
BMDU	0.657699
AIC	36.2619
Log-Likelihood	-17.1309
P-Value	0.586301
Overall d.f.	3
Chi <sup>2</sup>	1.93361

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
b1	0.24649	no	0.497517

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	Size	Observed	Expected	Est Prob	Scaled Residual
0	10	0	1.523e-07	1.523e-08	-0.000390256
2.025	10	3	3.92949	0.392949	-0.601816
4.05	10	8	6.31489	0.631489	1.10464
8.1	10	8	8.642	0.8642	-0.592619

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-16.1167	4	-	-	-
Fitted model	-17.1309	1	2.0285	3	0.566512
Reduced model	-27.6759	1	23.1183	3	3.81529e-05

## 2.2 { Hayes, 1985, 503@@author-year}

Inhalation exposure on GD 6-15 in rats

Report Generated: 2026-Jan-26 01:01 UTC

Analysis URL: [View](#)

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

## 2.2.1 Maternal Absolute Body Weight on GD16, Rats; BMR: 10% RD; Normal Distribution + Constant Variance

### Dataset

Name: Rat maternal absolute body weight GD16

Dose (ppm)	N	Mean (g)	Std. Dev. (g)
0	27	229	9
25	27	223	9
50	28	220	10
100	28	214	10

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.8927

Test 3 Variance Model Selection: 0.8927

### Settings

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

### Maximum Likelihood Approach

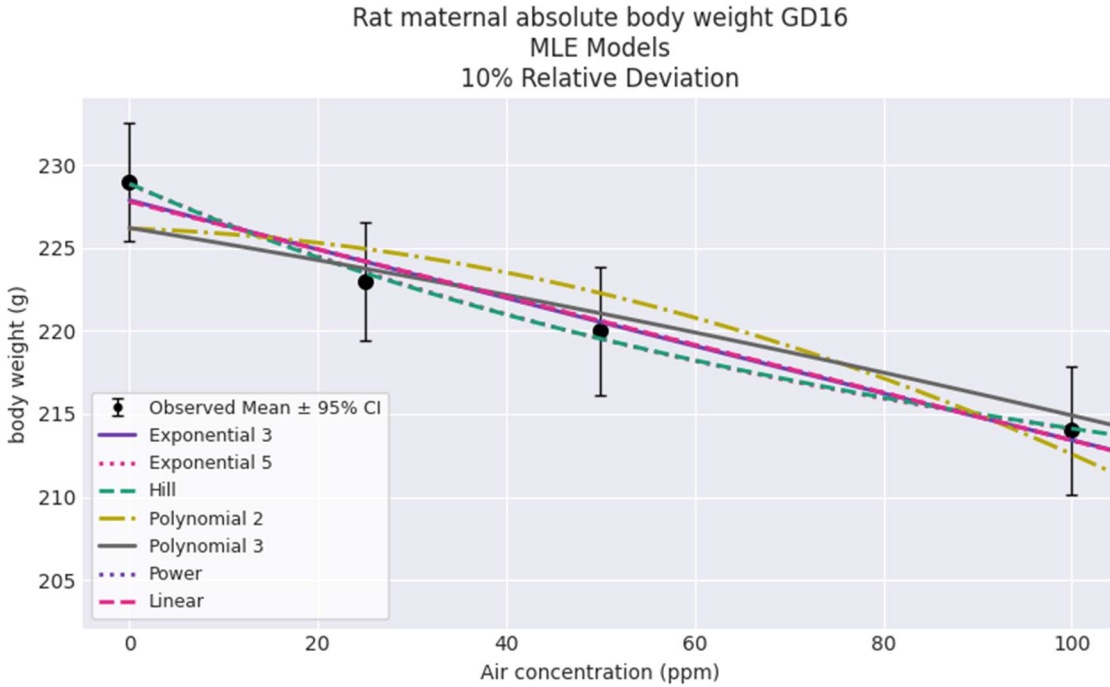
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 <sup>ab</sup>	125.678	160.931	223.233	0.799	810.906	0.625	0.322	<b>Recommended - Lowest AIC</b> BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Exponential 5	-	-	-	0.672	812.077	0.095	-	<b>Unusable</b> Did not successfully execute.
Hill	139.017	259.097	-	0.696	812.05	0.072	-0.071	<b>Viable</b> BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Polynomial 2	120.736	131.361	137.661	0.016	817.685	1.533	0.781	<b>Questionable</b> Goodness of fit p-value < 0.1 BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Polynomial 3	115.683	176.547	180.202	0.072	815.128	1.51	-0.503	<b>Questionable</b> Goodness of fit p-value < 0.1 BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0

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Power	124.797	158.407	217.828	0.573	811.013	0.669	0.332	<b>Viable</b> BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Linear	124.797	158.407	217.828	0.573	811.013	0.669	0.332	<b>Viable</b> BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0

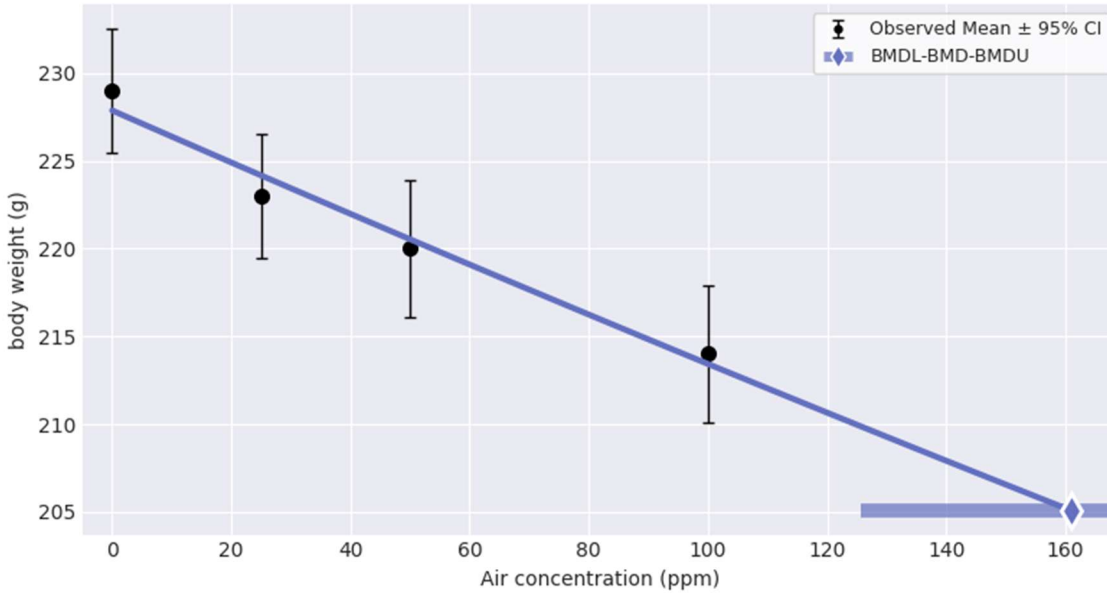
<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model



### Selected Model: Exponential 3

Rat maternal absolute body weight GD16  
Exponential 3 Model (MLE)  
10% Relative Deviation



#### Exponential 3 Model

Version: pybmds 25.1 (bmdscore 25.1)

#### 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	1	1	18
log-alpha	0	-18	18

#### Modeling Summary:

BMD	160.931
BMDL	125.678
BMDU	223.233
AIC	810.906
Log-Likelihood	-402.453
P-Value	0.799248
Model d.f.	3

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Model Parameters:

Variable	Estimate	On Bound	Std Error
a	227.87	no	1.41284
b	0.000654694	no	0.000110504
d	1	yes	Not Reported
log-alpha	4.47945	no	0.13484

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	27	229	227.87	0.625387
25	27	223	224.17	-0.647668
50	28	220	220.531	-0.299369
100	28	214	213.429	0.321667

Dose	N	Sample SD	Model Fitted SD
0	27	9	9.39076
25	27	9	9.39076
50	28	10	9.39076
100	28	10	9.39076

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-401.949	5	813.898
A2	-401.641	8	819.282
A3	-401.949	5	813.898
fitted	-402.453	2	808.906
reduced	-417.826	2	839.653

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	32.3709	6	1.38519e-05
Test 2	0.616376	3	0.892673
Test 3	0.616376	3	0.892673
Test 4	1.00828	3	0.799248

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 Maternal Absolute Body Weight on GD16, Rats; BMR: 1 SD; Normal Distribution + Constant Variance

### Dataset

**Name:** Rat maternal absolute body weight GD16

Dose (ppm)	N	Mean (g)	Std. Dev. (g)
0	27	229	9
25	27	223	9
50	28	220	10
100	28	214	10

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.8927

Test 3 Variance Model Selection: 0.8927

### Settings

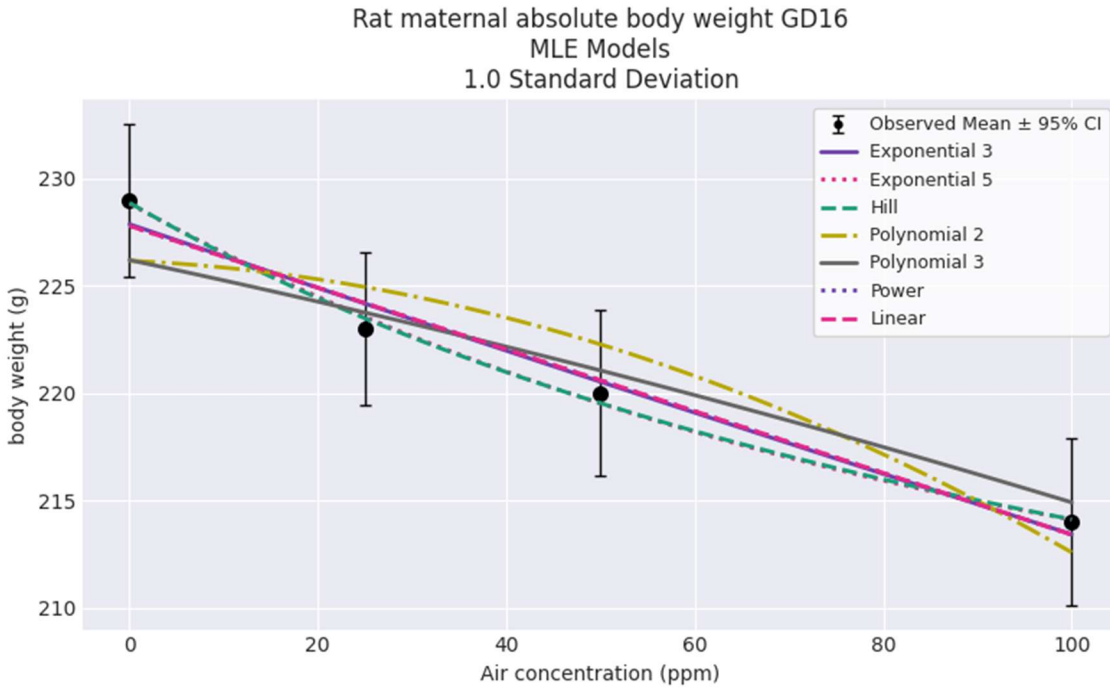
Setting	Value
<b>BMR</b>	1.0 Standard Deviation
<b>Distribution</b>	Normal + Constant variance
<b>Adverse Direction</b>	Down (↓)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

### Maximum Likelihood Approach

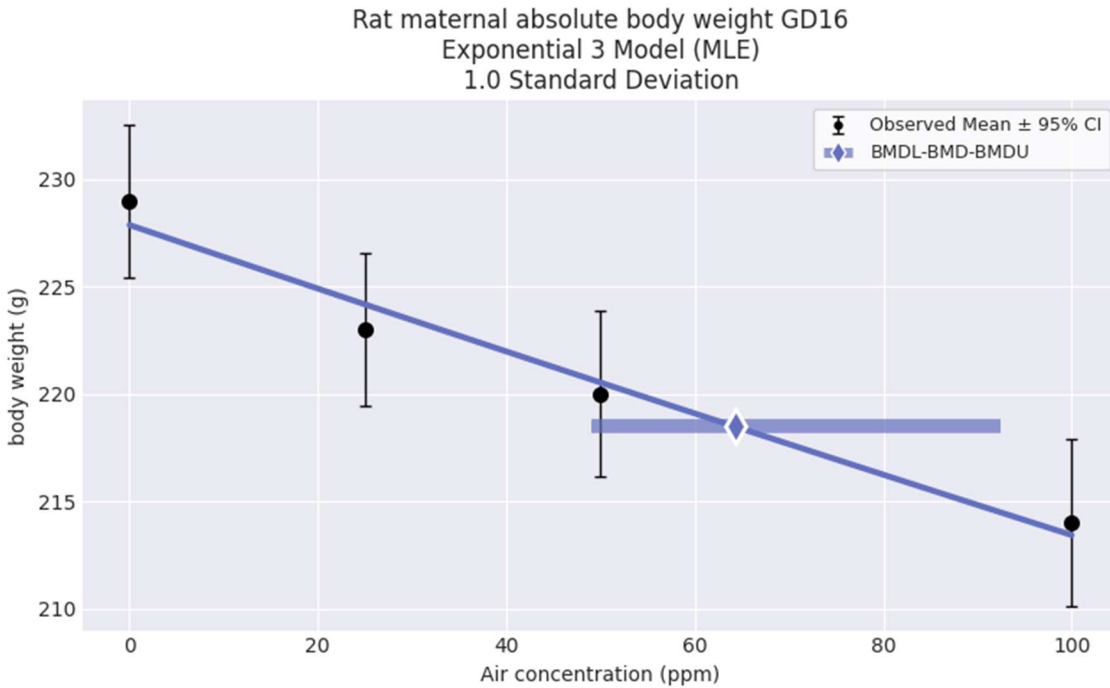
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 <sup>ab</sup>	49.044	64.281	92.386	0.604	810.906	0.625	-0.299	<b>Recommended - Lowest AIC</b>
Exponential 5	27.58	50.346	86.261	0.672	812.077	0.095	0.27	<b>Viable</b>
Hill	26.155	50.131	86.097	0.696	812.05	0.072	0.264	<b>Viable</b>
Polynomial 2	-	82.805	-	0.016	817.685	1.533	0.781	<b>Unusable</b> Did not successfully execute.
Polynomial 3	46.675	87.317	108.417	0.072	815.128	1.51	-0.503	<b>Questionable</b> Goodness of fit p-value < 0.1
Power	50.302	65.335	93.072	0.573	811.013	0.669	-0.339	<b>Viable</b>
Linear	50.302	65.335	93.072	0.573	811.013	0.669	-0.339	<b>Viable</b>

<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model



**Selected Model: Exponential 3**



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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	64.281
BMDL	49.0445
BMDU	92.3859
AIC	810.906
Log-Likelihood	-402.453
P-Value	0.604024
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	227.87	no	1.41284
b	0.000654694	no	0.000110504
d	1	yes	Not Reported
log-alpha	4.47945	no	0.13484

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	27	229	227.87	0.625387
25	27	223	224.17	-0.647668
50	28	220	220.531	-0.299369
100	28	214	213.429	0.321667

Dose	N	Sample SD	Model Fitted SD
0	27	9	9.39076
25	27	9	9.39076
50	28	10	9.39076
100	28	10	9.39076

Likelihoods:

Model	Log-Likelihood	# Params	AIC

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A1	-401.949	5	813.898
A2	-401.641	8	819.282
A3	-401.949	5	813.898
fitted	-402.453	3	810.906
reduced	-417.826	2	839.653

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	32.3709	6	1.38519e-05
Test 2	0.616376	3	0.892673
Test 3	0.616376	3	0.892673
Test 4	1.00828	2	0.604024

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 Maternal Body Weight Gain During GD 6-20, Rats; BMR: 10% RD; Normal Distribution + Constant Variance

#### Dataset

Name: Rat maternal body weight gain GD6-20

Dose (ppm)	N	Mean (g)	Std. Dev. (g)
0	27	71	13
25	27	59	14
50	28	60	14
100	28	56	16

Test 1 Dose Response: 0.0068

Test 2 Homogeneity of Variance: 0.7338

Test 3 Variance Model Selection: 0.7338

#### Settings

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

#### Maximum Likelihood Approach

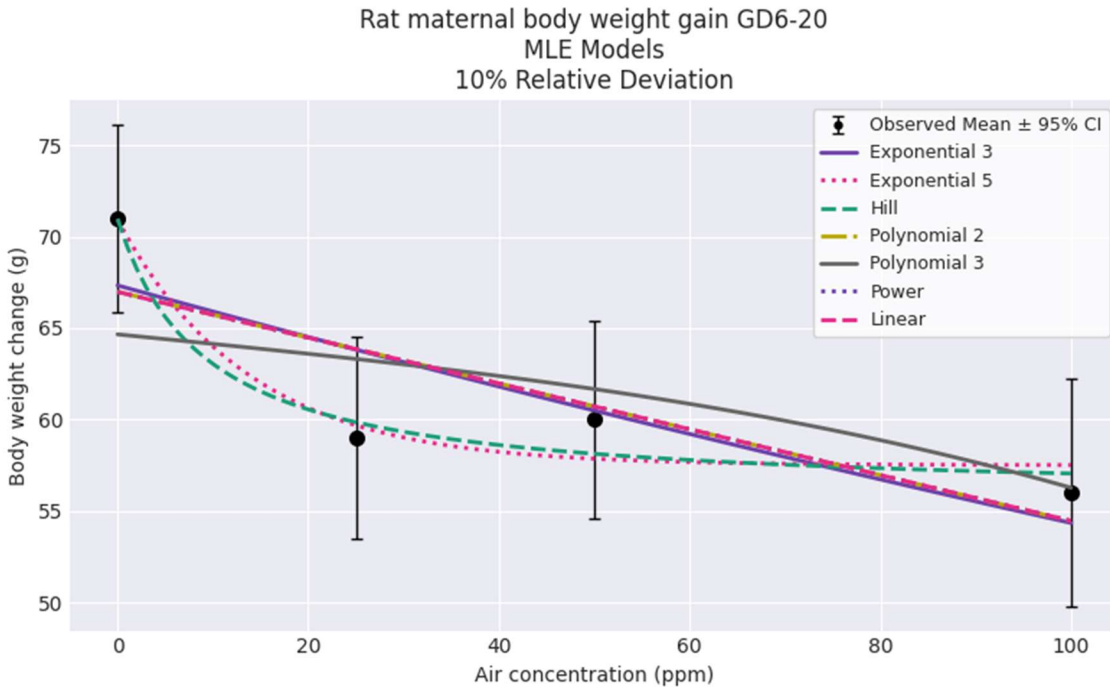
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3 <sup>ab</sup>	32.827	49.2	95.859	0.15	904.756	1.323	-0.184	Recommended - Lowest AIC

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Exponential 5	0.824	10.325	41.765	0.309	902.477	0.02	0.02	<b>Questionable</b> lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 BMD/BMDL ratio > 3.0
Hill	0.03	8.039	39.971	0.386	902.191	0.009	0.009	<b>Questionable</b> lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 lowest dose/BMD ratio > 3.0 BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0
Polynomial 2	37.286	53.456	100.877	0.058	905.134	1.446	-0.266	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 3	33.518	85.806	87.582	0.004	909.592	2.257	-0.101	<b>Questionable</b> Residual at control > 2.0 Goodness of fit p-value < 0.1
Power	37.284	53.518	100.877	0.058	905.134	1.448	-0.266	<b>Questionable</b> Goodness of fit p-value < 0.1
Linear	37.284	53.518	100.877	0.058	905.134	1.448	-0.266	<b>Questionable</b> Goodness of fit p-value < 0.1

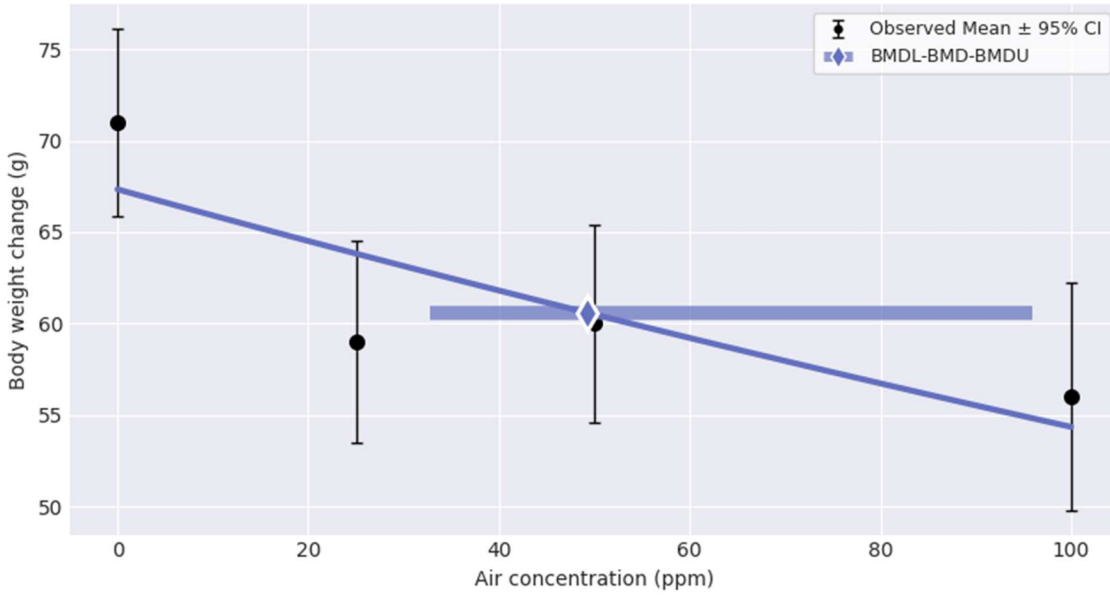
<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model



**Selected Model: Exponential 3**

Rat maternal body weight gain GD6-20  
Exponential 3 Model (MLE)  
10% Relative Deviation



Exponential 3 Model

Version: pybmds 25.1 (bmdscore 25.1)

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	1	1	18
log-alpha	0	-18	18

Modeling Summary:

BMD	49.2004
BMDL	32.8275
BMDU	95.8586
AIC	904.756
Log-Likelihood	-449.378
P-Value	0.150134
Model d.f.	3

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Model Parameters:

Variable	Estimate	On Bound	Std Error
a	67.3364	no	2.23487
b	0.00214146	no	0.000636876
d	1	yes	Not Reported
log-alpha	5.33263	no	0.13484

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	27	71	67.3364	1.32318
25	27	59	63.8263	-1.74313
50	28	60	60.4991	-0.183576
100	28	56	54.356	0.604648

Dose	N	Sample SD	Model Fitted SD
0	27	13	14.3868
25	27	14	14.3868
50	28	14	14.3868
100	28	16	14.3868

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-446.72	5	903.441
A2	-446.08	8	908.16
A3	-446.72	5	903.441
fitted	-449.378	2	902.756
reduced	-454.98	2	913.959

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	17.7986	6	0.00675566
Test 2	1.2802	3	0.733841
Test 3	1.2802	3	0.733841
Test 4	5.31497	3	0.150134

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 Maternal Body Weight Gain During GD 6-20, Rats; BMR: 1 SD; Normal Distribution + Constant Variance

### Dataset

Name: Rat maternal body weight gain GD6-20

Dose (ppm)	N	Mean (g)	Std. Dev. (g)
0	27	71	13
25	27	59	14
50	28	60	14
100	28	56	16

Test 1 Dose Response: 0.0068

Test 2 Homogeneity of Variance: 0.7338

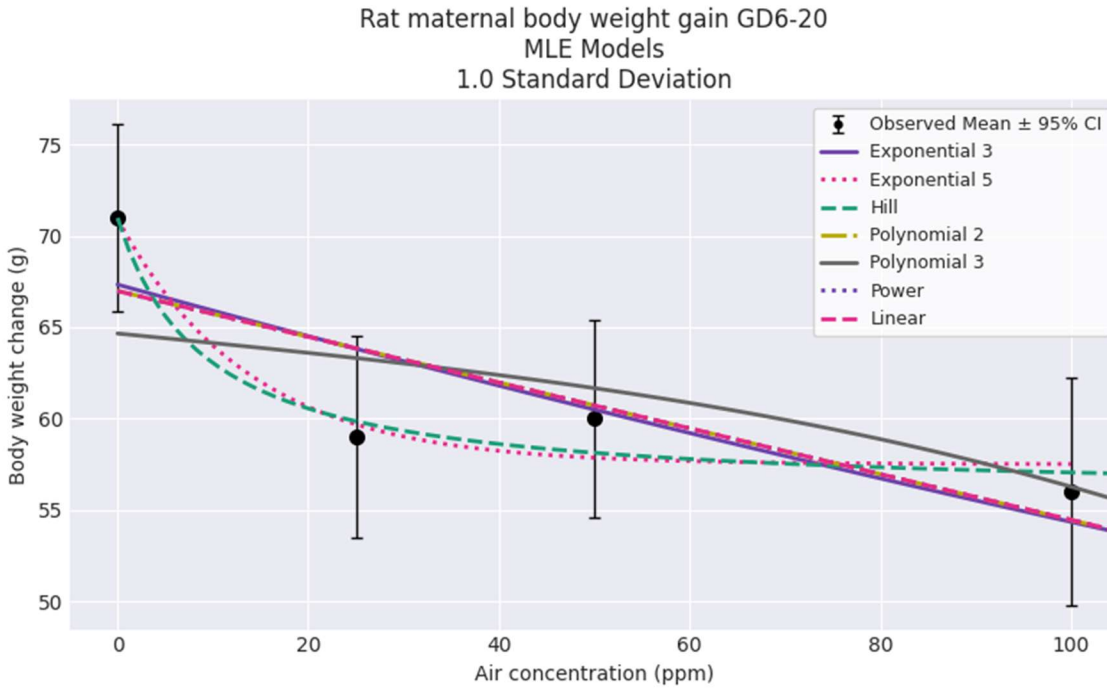
Test 3 Variance Model Selection: 0.7338

### 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

### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	71.029	112.242	234.724	0.07	904.756	1.323	0.605	<b>Questionable</b> Goodness of fit p-value < 0.1 BMD/highest dose ratio > 1.0
Exponential 5	-	-	-	0.309	902.477	0.02	-	<b>Unusable</b> Did not successfully execute.
Hill	0	117.002	-	0.386	902.191	0.009	-0.397	<b>Unusable</b> BMDL does not exist BMD/highest dose ratio > 1.0
Polynomial 2	76.751	114.998	230.313	0.058	905.134	1.446	0.566	<b>Questionable</b> Goodness of fit p-value < 0.1 BMD/highest dose ratio > 1.0
Polynomial 3	68.038	133.765	136.534	0.004	909.592	2.257	-0.101	<b>Questionable</b> Residual at control > 2.0 Goodness of fit p-value < 0.1 BMD/highest dose ratio > 1.0
Power	76.75	115.144	230.303	0.058	905.134	1.448	0.563	<b>Questionable</b> Goodness of fit p-value < 0.1 BMD/highest dose ratio > 1.0
Linear	76.75	115.144	230.303	0.058	905.134	1.448	0.563	<b>Questionable</b> Goodness of fit p-value < 0.1 BMD/highest dose ratio > 1.0



### Selected Model

No model was selected as a best-fitting model.

### 2.2.5 Maternal Body Weight Gain (Transformed with + 10 g) During GD 6-8, Rats; BMR: 1 SD; Normal Distribution + Nonconstant Variance

#### Dataset

**Name:** Rat maternal bw gain GD6-8 (transformed with +10)

Dose (ppm)	N	Mean (g)	Std. Dev. (g)
0	27	15	5
25	27	8	6
50	28	7	4
100	28	2	3

Test 1 Dose Response: 0

Test 2 Homogeneity of Variance: 0.0032

Test 3 Variance Model Selection: 0.0816

#### Settings

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

#### Maximum Likelihood Approach

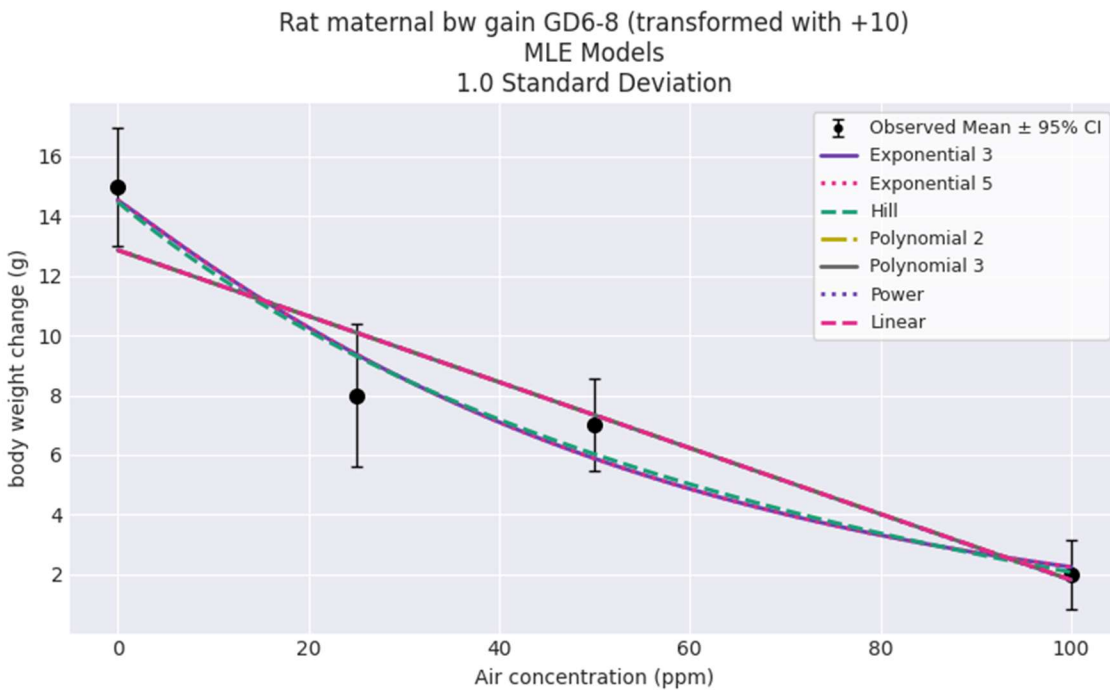
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes

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Exponential 3	19.596	29.28	47.551	0.098	648.666	0.414	-1.421	<b>Questionable</b> Goodness of fit p-value < 0.1
Exponential 5	19.596	29.28	47.551	-	650.666	0.414	-1.421	<b>Questionable</b> Zero degrees of freedom; saturated model
Hill <sup>ab</sup>	17.804	29.187	29.791	0.158	647.912	0.471	-1.367	<b>Recommended - Lowest AIC</b>
Polynomial 2	41.582	51.969	62.855	0.032	650.786	1.937	-0.378	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 3	41.579	51.895	66.872	0.032	650.787	1.939	-0.375	<b>Questionable</b> Goodness of fit p-value < 0.1
Power	41.572	51.641	67.152	0.032	650.79	1.931	-0.375	<b>Questionable</b> Goodness of fit p-value < 0.1
Linear	41.583	51.967	67.128	0.032	650.786	1.937	-0.378	<b>Questionable</b> Goodness of fit p-value < 0.1

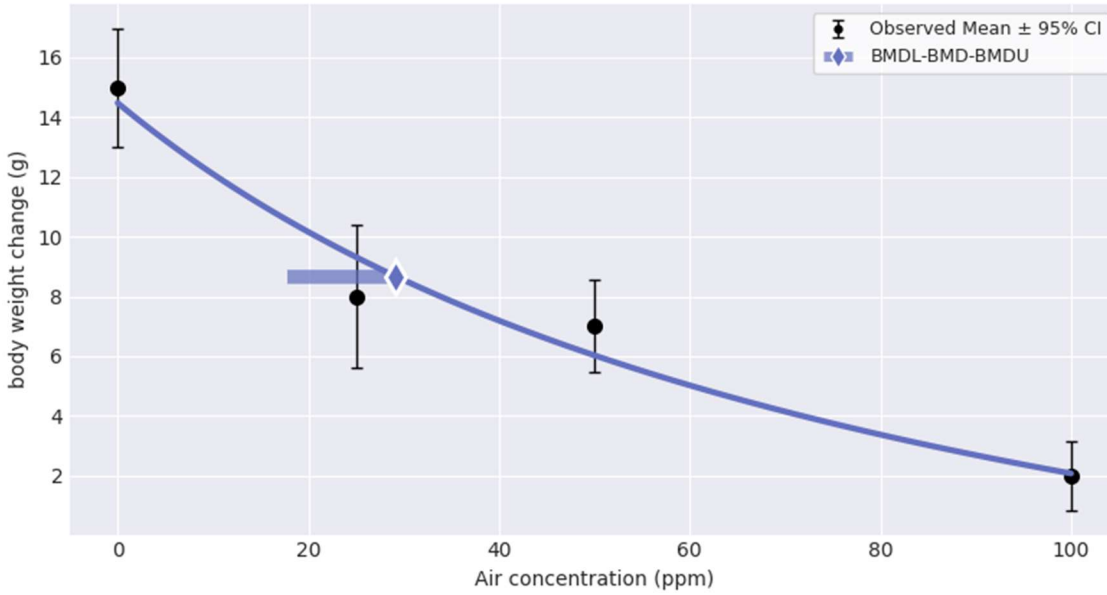
<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model



**Selected Model: Hill**

Rat maternal bw gain GD6-8 (transformed with +10)  
Hill Model (MLE)  
1.0 Standard Deviation



Hill Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant 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
rho	0	-18	18
alpha	0	-18	18

Modeling Summary:

BMD	29.1871
BMDL	17.8044
BMDU	29.7912
AIC	647.912
Log-Likelihood	-318.956
P-Value	0.158463
Model d.f.	1

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Model Parameters:

Variable	Estimate	On Bound	Std Error
g	14.4737	no	1.07995
v	-23.3146	no	5.45824
k	88.0079	no	46.6409
n	1	yes	Not Reported
rho	0.675904	no	0.218133
alpha	5.53835	no	13.6942

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	27	15	14.4737	0.47099
25	27	8	9.31595	-1.36672
50	28	7	6.02684	1.19245
100	28	2	2.07281	-0.127966

Dose	N	Sample SD	Model Fitted SD
0	27	5	5.80644
25	27	6	5.00313
50	28	4	4.3184
100	28	3	3.01073

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-322.353	5	654.706
A2	-315.456	8	646.911
A3	-317.961	6	647.923
fitted	-318.956	5	647.912
reduced	-361.65	2	727.3

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	92.3882	6	0
Test 2	13.7942	3	0.00319915
Test 3	5.01158	2	0.0816111
Test 4	1.98883	1	0.158463

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 {Umemura, 1996, 4912371@@author-year}

Acute oral toxicity study in mice

Report Generated: 2026-Jan-26 02:01 UTC

Analysis URL: [View](#)

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

### 2.3.1 Serum Alanine Aminotransferase (ALT), Male Mice; BMR: 1 SD; Normal Distribution + Nonconstant Variance

#### Dataset

Name: ALT activity in mice

Dose (mg/kg-day)	N	Mean (mU/mL)	Std. Dev. (mU/mL)
0	5	20	11
15.6	5	43	28
26	5	280	237
39	5	2677	1654

Test 1 Dose Response: 0

Test 2 Homogeneity of Variance: 0

Test 3 Variance Model Selection: 0.7746

#### Settings

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant variance
Adverse Direction	Up (↑)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

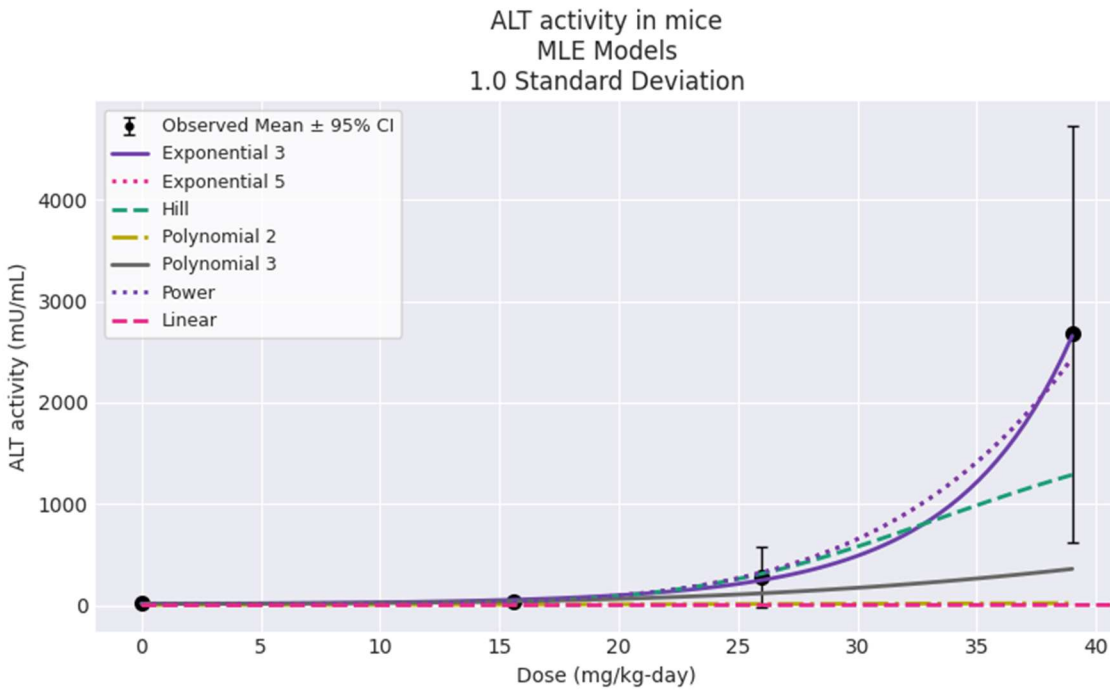
#### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	5.678	8.619	12.528	0.208	252.037	0.52	-0.935	<b>Viable</b>
Exponential 5	11.694	13.44	15.091	-	250.976	0.124	0.069	<b>Questionable</b> Zero degrees of freedom; saturated model
Hill	11.429	13.977	18.694	-	255.115	-0.227	0.316	<b>Questionable</b> Zero degrees of freedom; saturated model
Polynomial 2	-	36.89	-	<0.001	267.745	1.689	1.966	<b>Unusable</b> Did not successfully execute.
Polynomial 3	7.357	11.33	16.786	0.01	256.171	-0.328	-0.003	<b>Questionable</b> Goodness of fit p-value < 0.1
Power <sup>ab</sup>	11.006	13.44	16.613	0.778	248.976	0.124	0.069	<b>Recommended - Lowest AIC</b>

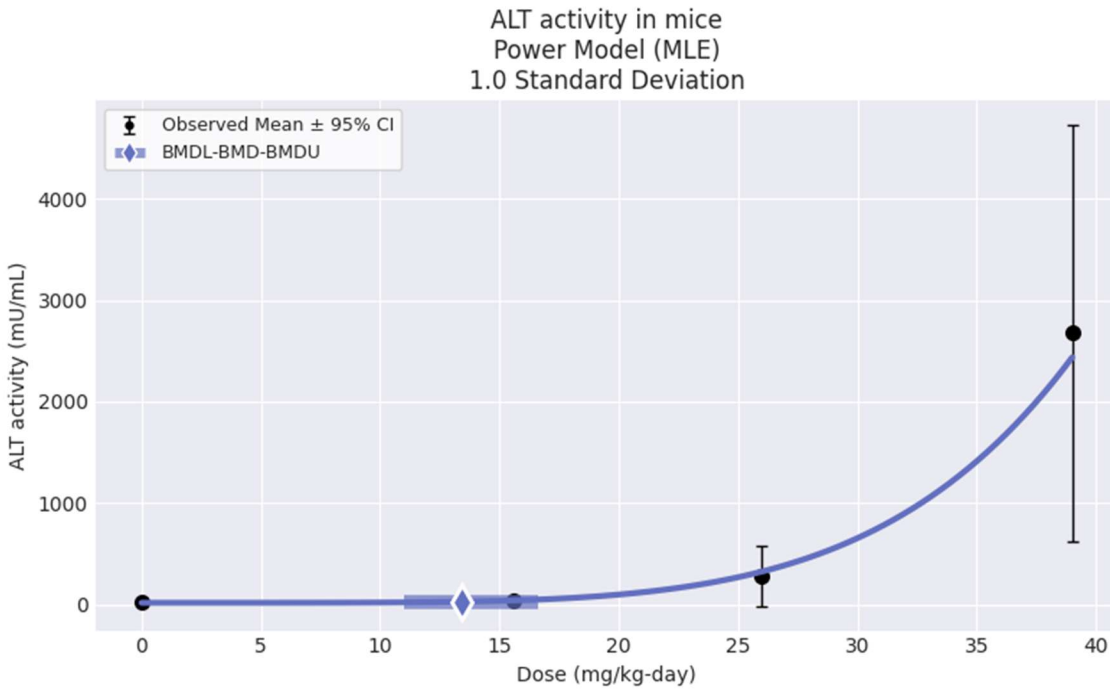
Linear	-	222.027	-	<0.001	282.506	2.37	2.74	<b>Unusable</b> Did not successfully execute.
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<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model



**Selected Model: Power**



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April 2026

Power Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR Distribution	1.0 Standard Deviation
Modeling Direction	Normal + Nonconstant variance
Confidence Level (one sided)	Up (↑)
Modeling Approach	0.95
	MLE

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-100	100
v	0	-10000	10000
n	1	1	18
rho	0	0	18
alpha	0	-18	18

Modeling Summary:

BMD	13.4401
BMDL	11.0055
BMDU	16.6131
AIC	248.976
Log-Likelihood	-119.488
P-Value	0.77808
Model d.f.	1

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	19.4046	no	4.29427
v	1.94714e-05	no	5.21852e-06
n	5.08716	no	0.522969
rho	2.07167	no	0.252529
alpha	0.246274	no	0.0800743

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	5	20	19.4046	0.124318
15.6	5	43	42.2615	0.0688468
26	5	280	326.731	-0.523708
39	5	2677	2437.12	0.335371

Dose	N	Sample SD	Model Fitted SD
0	5	11	10.7095
15.6	5	28	23.984
26	5	237	199.525
39	5	1654	1599.4

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-160.71	5	331.42

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A2	-119.193	8	254.386
A3	-119.448	6	250.897
fitted	-119.488	5	248.976
reduced	-172.413	2	348.827

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	106.441	6	0
Test 2	83.034	3	0
Test 3	0.510774	2	0.774617
Test 4	0.0794237	1	0.77808

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.

## 2.4 {Robinson, 1991, 5099073@@author-year}

90-day oral toxicity study in rats

Report Generated: 2026-Jan-26 03:01 UTC

Analysis URL: [View](#)

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

### 2.4.1 Liver Weight

#### 2.4.1.1 Absolute Liver Weight, Male Rats; BMR: 10% RD; Normal Distribution + Constant Variance

#### Dataset

Name: Absolute liver weight in males

Dose (mg/kg-day)	N	Mean (g)	Std. Dev. (g)
0	10	13.7	2.1
6	10	14.4	1.7
24	10	15.9	1.6
96	10	17.6	2.3

Test 1 Dose Response: 0.0012

Test 2 Homogeneity of Variance: 0.624

Test 3 Variance Model Selection: 0.624

#### Settings

Setting	Value
BMR	10% Relative Deviation
Distribution	Normal + Constant variance
Adverse Direction	Up (↑)

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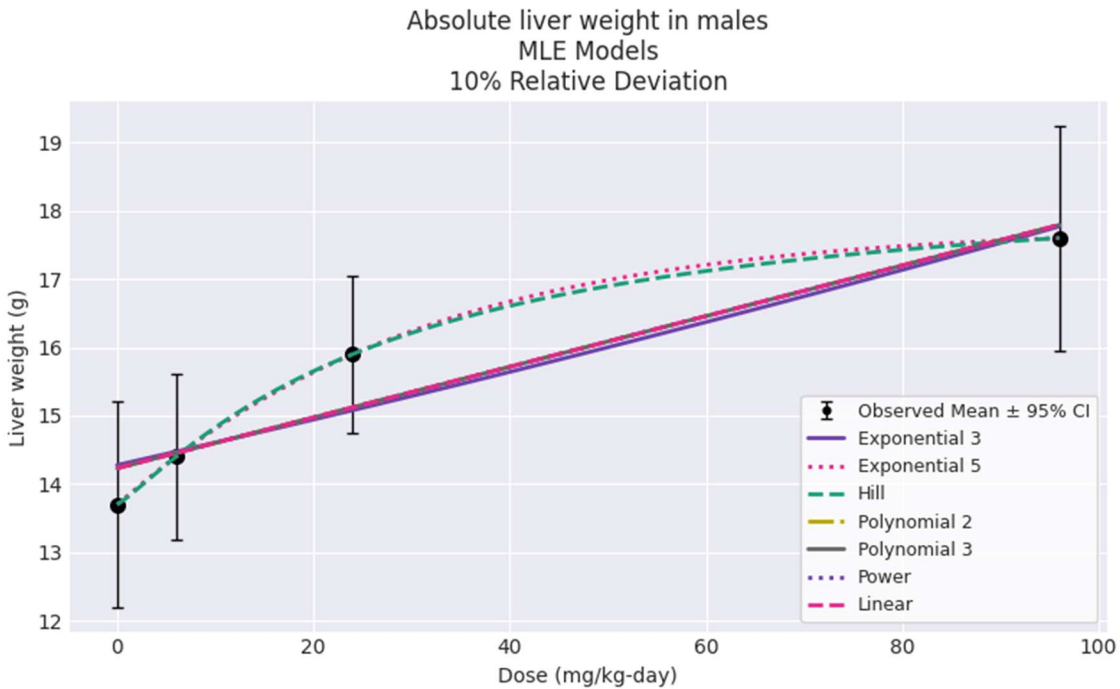
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

**Maximum Likelihood Approach**

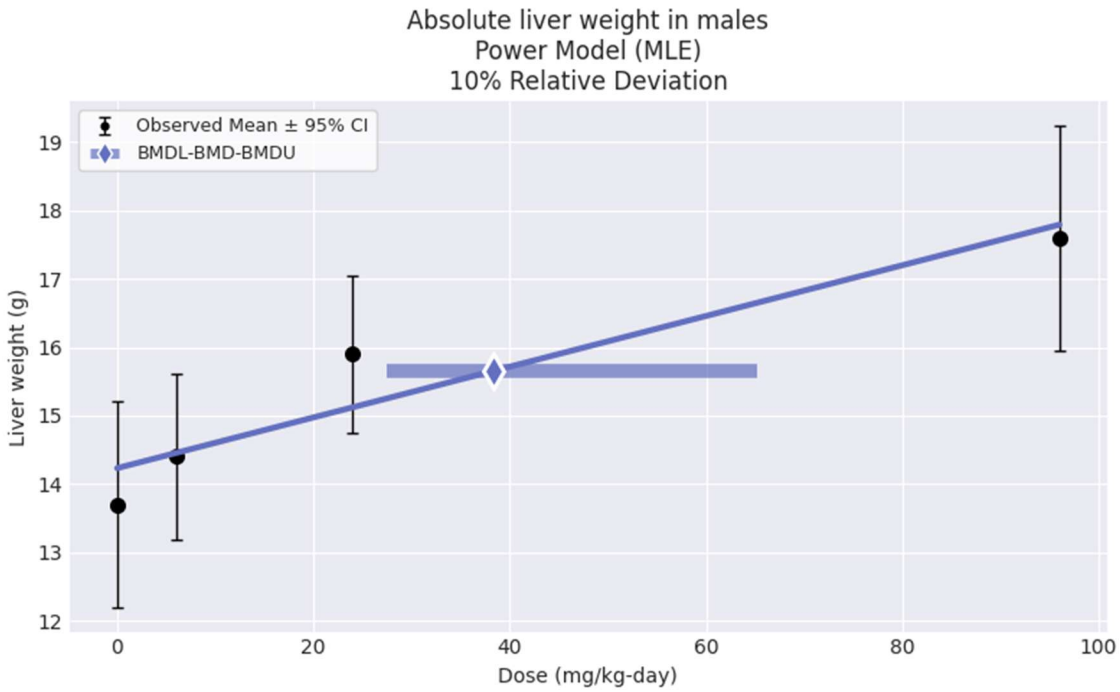
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	31.087	41.82	68.577	0.23	171.508	-0.954	1.353	<b>Viable</b>
Exponential 5	5.082	12.834	41.36	-	172.569	<0.001	-0.	<b>Questionable</b> Zero degrees of freedom; saturated model
Hill	3.712	12.544	40.697	-	172.569	-0.	<0.001	<b>Questionable</b> Zero degrees of freedom; saturated model BMD/BMDL ratio > 3.0
Polynomial 2	27.423	38.382	66.934	0.268	171.203	-0.882	1.29	<b>Viable</b>
Polynomial 3	27.422	38.394	70.655	0.268	171.203	-0.882	1.289	<b>Viable</b>
Power <sup>ab</sup>	27.422	38.392	65.269	0.268	171.203	-0.882	1.289	<b>Recommended - Lowest AIC</b>
Linear	27.422	38.392	61.395	0.268	171.203	-0.882	1.289	<b>Viable</b>

<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model



**Selected Model: Power**



Power Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

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

Modeling Summary:

BMD	38.3917
BMDL	27.4222
BMDU	65.2689
AIC	171.203
Log-Likelihood	-82.6015
P-Value	0.267918
Model d.f.	2

Model Parameters:

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Variable	Estimate	On Bound	Std Error
g	14.2323	no	0.390735
v	0.0370712	no	0.00788265
n	1	yes	Not Reported
alpha	3.64079	no	2.96389

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	10	13.7	14.2323	-0.882114
6	10	14.4	14.4547	-0.0906299
24	10	15.9	15.122	1.28944
96	10	17.6	17.7911	-0.316696

Dose	N	Sample SD	Model Fitted SD
0	10	2.1	1.90808
6	10	1.7	1.90808
24	10	1.6	1.90808
96	10	2.3	1.90808

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-81.2845	5	172.569
A2	-80.4051	8	176.81
A3	-81.2845	5	172.569
fitted	-82.6015	3	171.203
reduced	-91.4039	2	186.808

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	21.9976	6	0.00121208
Test 2	1.75868	3	0.623968
Test 3	1.75868	3	0.623968
Test 4	2.63415	2	0.267918

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.

### 2.4.1.2 Absolute Liver Weight, Male Rats; BMR: 1 SD; Normal Distribution + Constant Variance

#### Dataset

**Name:** Absolute liver weight in males

Dose (mg/kg-day)	N	Mean (g)	Std. Dev. (g)
0	10	13.7	2.1
6	10	14.4	1.7
24	10	15.9	1.6
96	10	17.6	2.3

Test 1 Dose Response: 0.0012

Test 2 Homogeneity of Variance: 0.624

Test 3 Variance Model Selection: 0.624

#### Settings

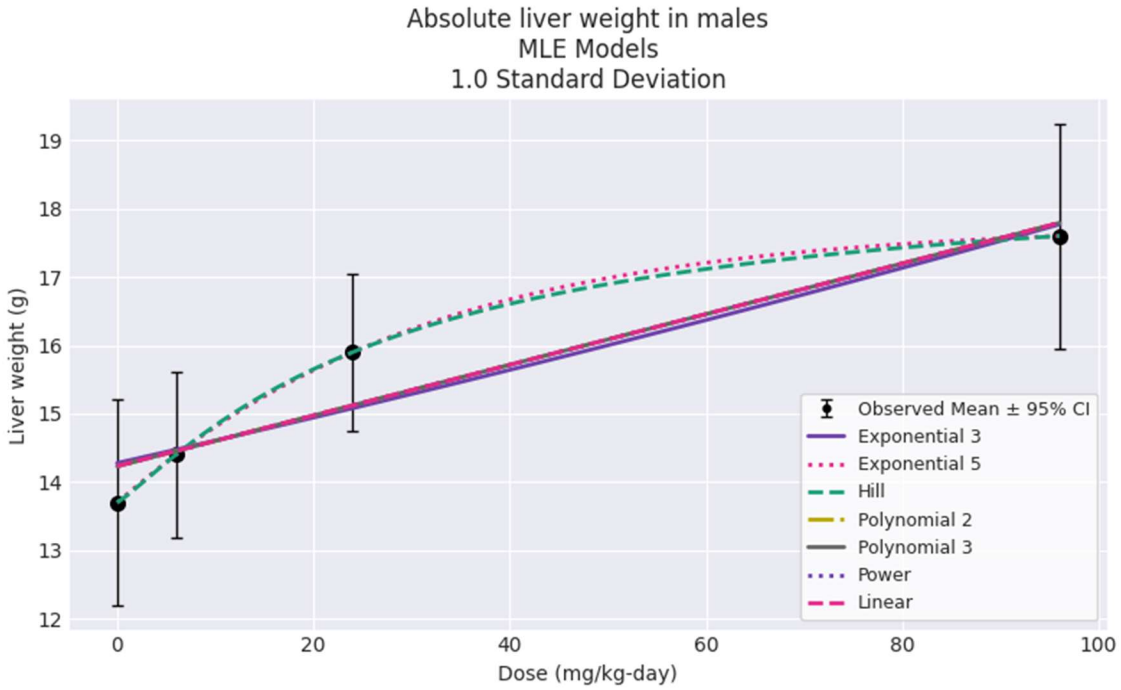
Setting	Value
<b>BMR</b>	1.0 Standard Deviation
<b>Distribution</b>	Normal + Constant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

#### Maximum Likelihood Approach

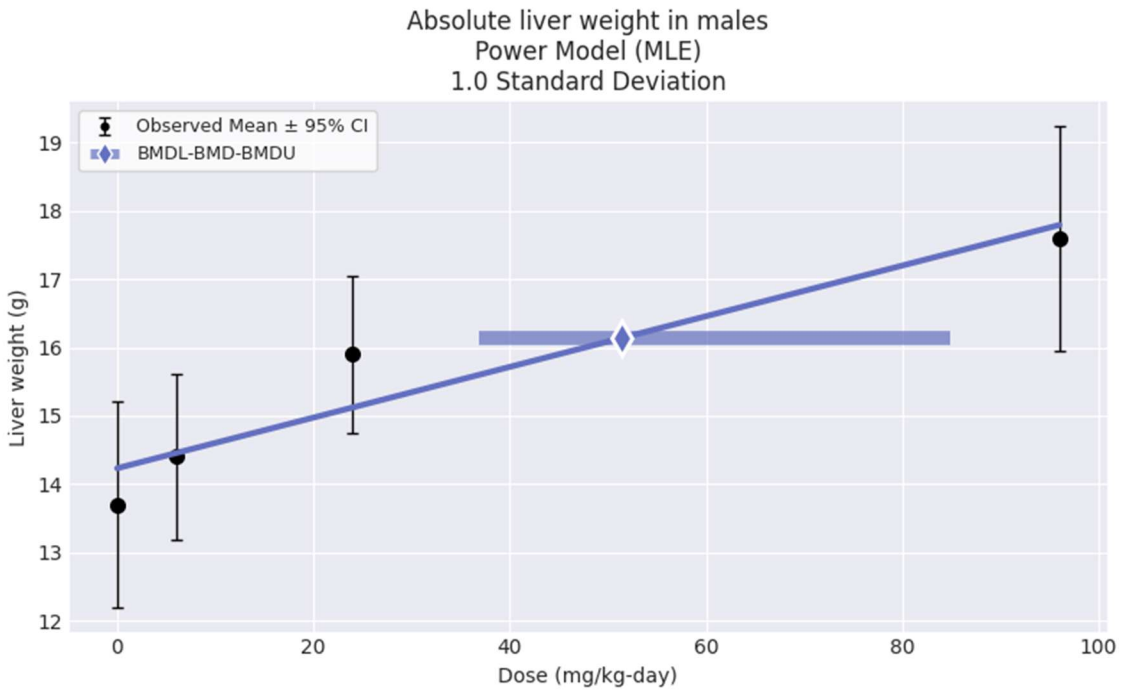
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	40.903	55.234	87.78	0.23	171.508	-0.954	1.353	<b>Viable</b>
Exponential 5	7.949	18.751	56.979	-	172.569	<0.001	<0.001	<b>Questionable</b> Zero degrees of freedom; saturated model
Hill	6.325	18.481	57.069	-	172.569	-0.	-0.	<b>Questionable</b> Zero degrees of freedom; saturated model
Polynomial 2	36.856	51.459	84.939	0.268	171.203	-0.882	1.29	<b>Viable</b>
Polynomial 3	36.855	51.473	85.198	0.268	171.203	-0.882	1.289	<b>Viable</b>
Power <sup>ab</sup>	36.855	51.471	84.937	0.268	171.203	-0.882	1.289	<b>Recommended - Lowest AIC</b>
Linear	36.855	51.471	84.94	0.268	171.203	-0.882	1.289	<b>Viable</b>

<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model



**Selected Model: Power**



Power Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

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

Modeling Summary:

BMD	51.4708
BMDL	36.8555
BMDU	84.9374
AIC	171.203
Log-Likelihood	-82.6015
P-Value	0.267918
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	14.2323	no	0.390735
v	0.0370712	no	0.00788265
n	1	yes	Not Reported
alpha	3.64079	no	2.96389

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	10	13.7	14.2323	-0.882114
6	10	14.4	14.4547	-0.0906299
24	10	15.9	15.122	1.28944
96	10	17.6	17.7911	-0.316696

Dose	N	Sample SD	Model Fitted SD
0	10	2.1	1.90808
6	10	1.7	1.90808
24	10	1.6	1.90808
96	10	2.3	1.90808

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-81.2845	5	172.569
A2	-80.4051	8	176.81
A3	-81.2845	5	172.569
fitted	-82.6015	3	171.203
reduced	-91.4039	2	186.808

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Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	21.9976	6	0.00121208
Test 2	1.75868	3	0.623968
Test 3	1.75868	3	0.623968
Test 4	2.63415	2	0.267918

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.

### 2.4.1.3 Relative Liver Weight, Male Rats; BMR: 10% RD; Normal Distribution + Constant Variance

#### Dataset

**Name:** Relative liver weight in males

Dose (mg/kg-d)	N	Mean (percent of bw)	Std. Dev. (percent of bw)
0	10	2.44	0.19
6	10	2.61	0.15
24	10	2.81	0.18
96	10	3.61	0.3

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.1266

Test 3 Variance Model Selection: 0.1266

#### Settings

Setting	Value
<b>BMR</b>	10% Relative Deviation
<b>Distribution</b>	Normal + Constant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

#### Maximum Likelihood Approach

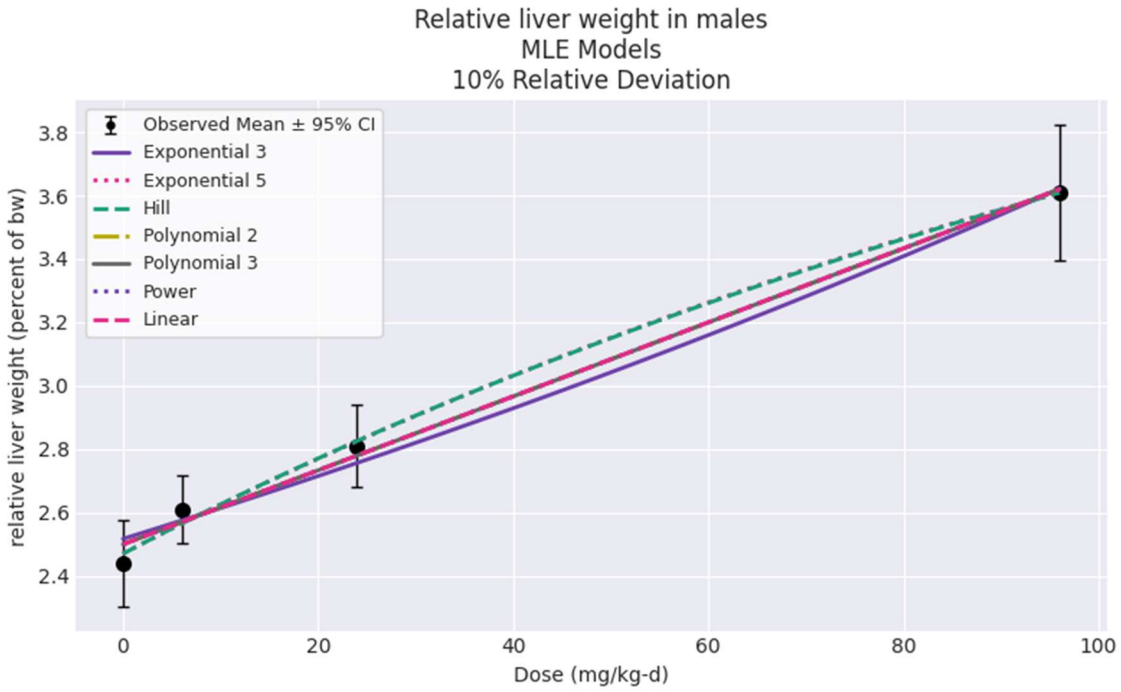
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	22.474	25.151	33.983	0.299	-6.106	-1.173	0.808	<b>Viable</b>
Exponential 5	10.145	16.331	28.528	0.375	-5.735	-0.48	-0.237	<b>Viable</b>
Hill	9.717	16.213	28.051	0.379	-5.746	-0.469	-0.248	<b>Viable</b>
Polynomial 2	18.706	21.434	31.616	0.474	-7.027	-0.924	0.461	<b>Viable</b>

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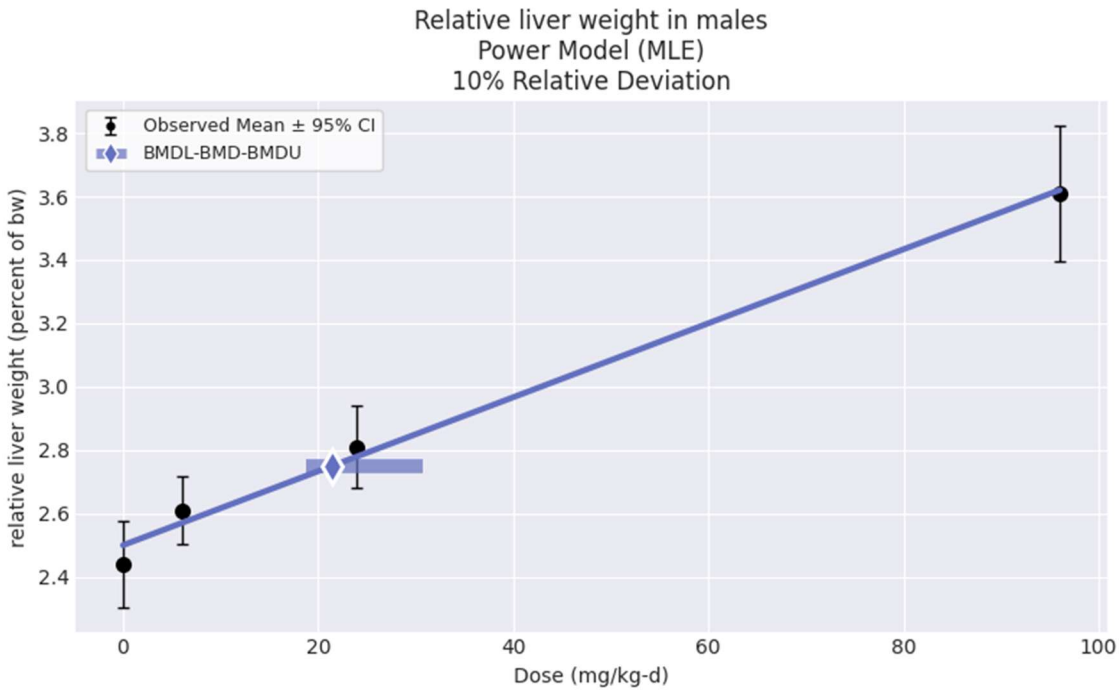
Polynomial 3	18.706	21.438	32.439	0.474	-7.027	-0.925	0.461	<b>Viable</b>
Power <sup>ab</sup>	18.706	21.429	30.688	0.474	-7.027	-0.923	0.461	<b>Recommended - Lowest AIC</b>
Linear	18.706	21.429	24.876	0.474	-7.027	-0.923	0.461	<b>Viable</b>

<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model



**Selected Model: Power**



Power Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

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

Modeling Summary:

BMD	21.4286
BMDL	18.7063
BMDU	30.688
AIC	-7.02729
Log-Likelihood	6.51365
P-Value	0.47375
Model d.f.	2

Model Parameters:

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Variable	Estimate	On Bound	Std Error
g	2.5	no	0.0421049
v	0.0116667	no	0.000849434
n	1	yes	Not Reported
alpha	0.042275	no	0.000399624

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	10	2.44	2.5	-0.922804
6	10	2.61	2.57	0.615203
24	10	2.81	2.78	0.461402
96	10	3.61	3.62	-0.153801

Dose	N	Sample SD	Model Fitted SD
0	10	0.19	0.205609
6	10	0.15	0.205609
24	10	0.18	0.205609
96	10	0.3	0.205609

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	7.26072	5	-4.52144
A2	10.1159	8	-4.23179
A3	7.26072	5	-4.52144
fitted	6.51365	3	-7.02729
reduced	-28.3517	2	60.7035

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	76.9352	6	1.53211e-14
Test 2	5.71034	3	0.126585
Test 3	5.71034	3	0.126585
Test 4	1.49415	2	0.47375

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.

### 2.4.1.4 Relative Liver Weight, Male Rats; BMR: 1 SD; Normal Distribution + Constant Variance

#### Dataset

**Name:** Relative liver weight in males

Dose (mg/kg-d)	N	Mean (percent of bw)	Std. Dev. (percent of bw)
0	10	2.44	0.19
6	10	2.61	0.15
24	10	2.81	0.18
96	10	3.61	0.3

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.1266

Test 3 Variance Model Selection: 0.1266

#### Settings

Setting	Value
<b>BMR</b>	1.0 Standard Deviation
<b>Distribution</b>	Normal + Constant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

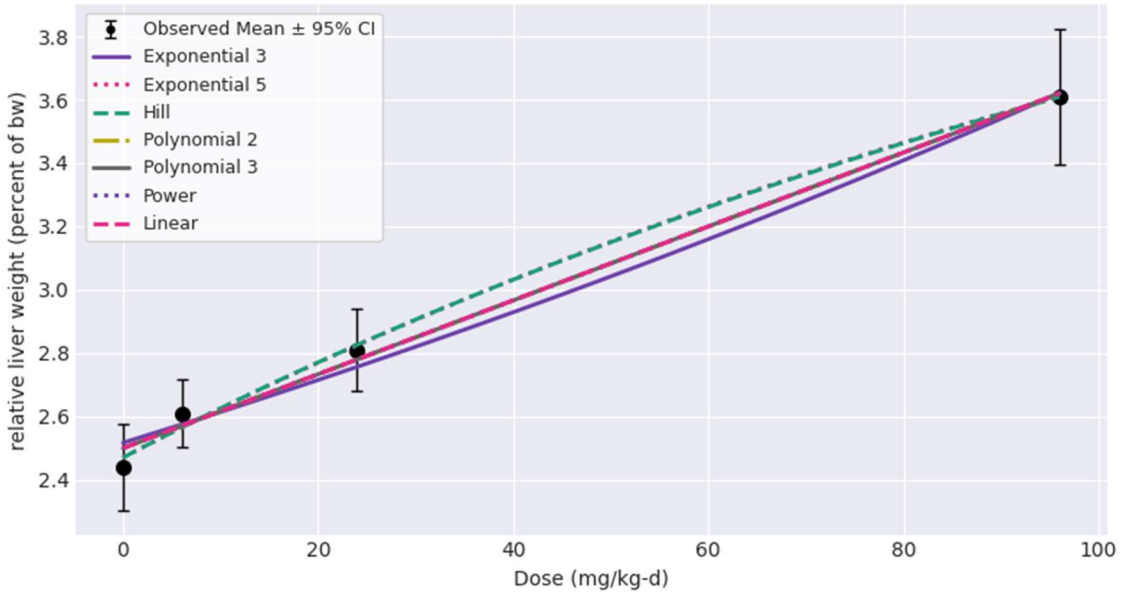
#### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	17.362	20.95	30.268	0.299	-6.106	-1.173	0.808	<b>Viable</b>
Exponential 5	8.374	13.341	24.701	0.375	-5.735	-0.48	0.701	<b>Viable</b>
Hill	8.032	13.232	24.609	0.379	-5.746	-0.469	0.697	<b>Viable</b>
Polynomial 2	14.407	17.631	27.645	0.474	-7.027	-0.924	0.461	<b>Viable</b>
Polynomial 3	14.407	17.63	28.077	0.474	-7.027	-0.925	0.461	<b>Viable</b>
Power <sup>ab</sup>	14.408	17.624	27.033	0.474	-7.027	-0.923	0.461	<b>Recommended - Lowest AIC</b>
Linear	14.408	17.624	22.46	0.474	-7.027	-0.923	0.461	<b>Viable</b>

<sup>a</sup> BMDS recommended best fitting model

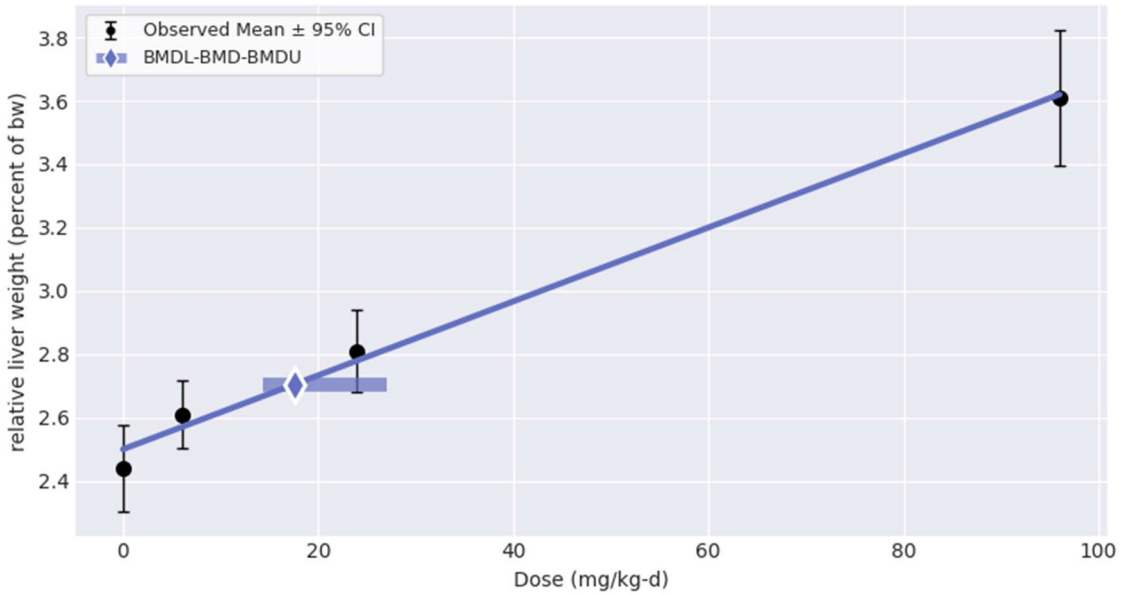
<sup>b</sup> User selected best fitting model

Relative liver weight in males  
MLE Models  
1.0 Standard Deviation



### Selected Model: Power

Relative liver weight in males  
Power Model (MLE)  
1.0 Standard Deviation



Power Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

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

Modeling Summary:

BMD	17.6236
BMDL	14.4076
BMDU	27.0327
AIC	-7.02729
Log-Likelihood	6.51365
P-Value	0.47375
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	2.5	no	0.0421049
v	0.0116667	no	0.000849434
n	1	yes	Not Reported
alpha	0.042275	no	0.000399624

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	10	2.44	2.5	-0.922804
6	10	2.61	2.57	0.615203
24	10	2.81	2.78	0.461402
96	10	3.61	3.62	-0.153801

Dose	N	Sample SD	Model Fitted SD
0	10	0.19	0.205609
6	10	0.15	0.205609
24	10	0.18	0.205609
96	10	0.3	0.205609

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	7.26072	5	-4.52144
A2	10.1159	8	-4.23179
A3	7.26072	5	-4.52144
fitted	6.51365	3	-7.02729
reduced	-28.3517	2	60.7035

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Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	76.9352	6	1.53211e-14
Test 2	5.71034	3	0.126585
Test 3	5.71034	3	0.126585
Test 4	1.49415	2	0.47375

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.

### 2.4.1.5 Absolute Liver Weight, Female Rats; BMR: 10% RD; Normal Distribution + Constant Variance

#### Dataset

**Name:** Absolute liver weight in females

Dose (mg/kg-day)	N	Mean (g)	Std. Dev. (g)
0	10	7	0.4
6	10	7.3	0.6
24	10	8.2	0.7
96	10	11.3	0.9

Test 1 Dose Response: 0

Test 2 Homogeneity of Variance: 0.0986

Test 3 Variance Model Selection: 0.0986

#### Settings

Setting	Value
<b>BMR</b>	10% Relative Deviation
<b>Distribution</b>	Normal + Constant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

#### Maximum Likelihood Approach

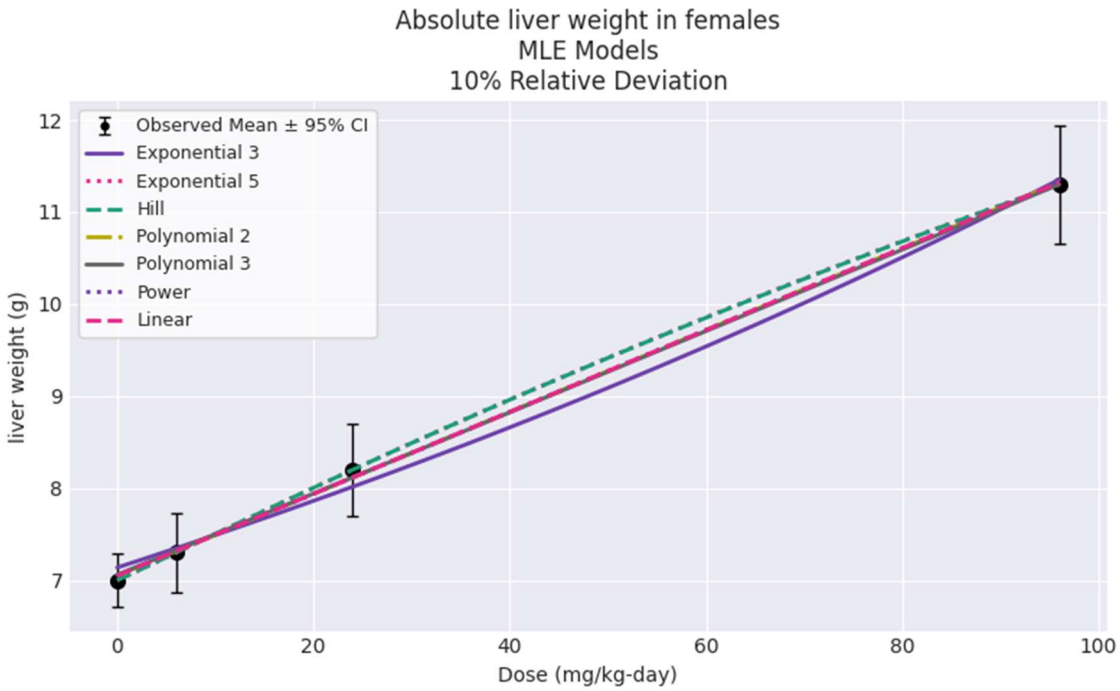
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	17.962	19.717	27.283	0.497	85.199	-0.663	0.887	<b>Viable</b> Control stdev. fit > 1.5
Exponential 5	8.888	13.914	24.069	-	87.802	-0.	<0.001	<b>Questionable</b> Zero degrees of freedom; saturated model Control stdev. fit > 1.5

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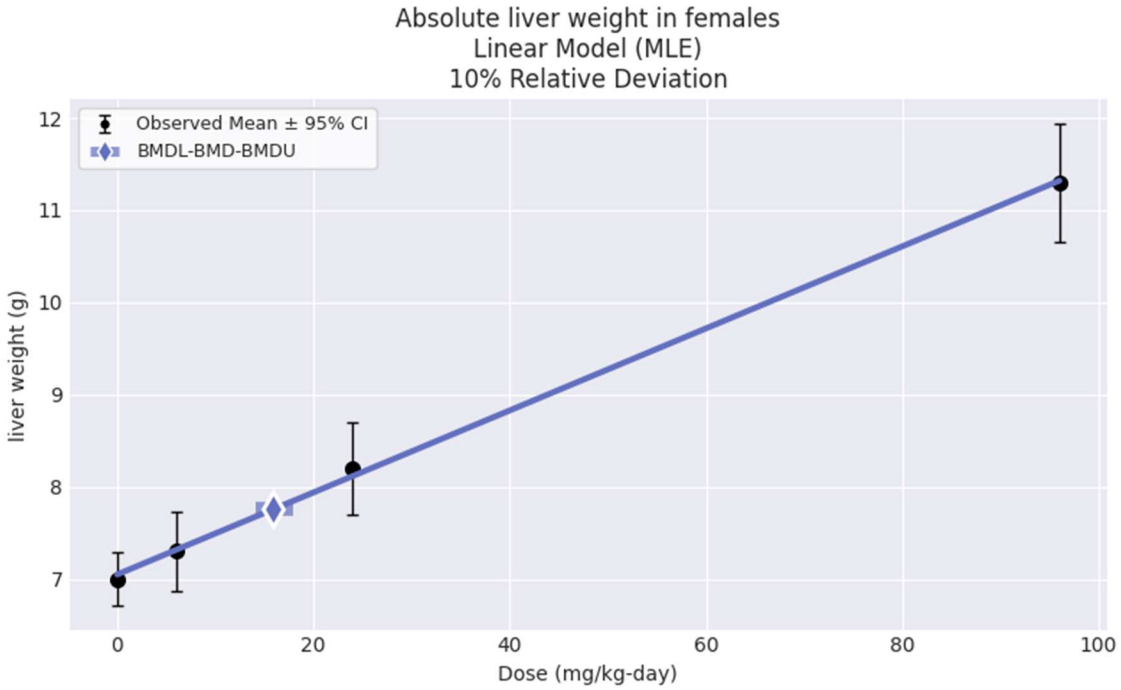
Hill	8.72	13.908	23.941	-	87.802	<0.001	-0.	<b>Questionable</b> Zero degrees of freedom; saturated model Control stdev. fit > 1.5
Polynomial 2	14.063	15.853	24.231	0.886	84.046	-0.243	0.411	<b>Viable</b> Control stdev. fit > 1.5
Polynomial 3	14.071	16.003	24.282	0.877	84.066	-0.29	0.406	<b>Viable</b> Control stdev. fit > 1.5
Power	14.062	15.841	24.462	0.886	84.045	-0.238	0.412	<b>Viable</b> Control stdev. fit > 1.5
Linear <sup>ab</sup>	14.062	15.841	17.989	0.886	84.045	-0.238	0.412	<b>Recommended - Lowest AIC</b> Control stdev. fit > 1.5

<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model



**Selected Model: Linear**



Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	10% Relative Deviation
Distribution	Normal + Constant variance
Modeling Direction	Up (↑)
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	15.8406
BMDL	14.0622
BMDU	17.9895
AIC	84.0454
Log-Likelihood	-39.0227
P-Value	0.885553
Model d.f.	2

Model Parameters:

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Variable	Estimate	On Bound	Std Error
g	7.04839	no	0.131443
b1	0.0444956	no	0.00265176
alpha	0.411996	no	0.0379555

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	10	7	7.04839	-0.238387
6	10	7.3	7.31536	-0.0756785
24	10	8.2	8.11628	0.412448
96	10	11.3	11.32	-0.0983821

Dose	N	Sample SD	Model Fitted SD
0	10	0.4	0.641869
6	10	0.6	0.641869
24	10	0.7	0.641869
96	10	0.9	0.641869

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-38.9012	5	87.8023
A2	-35.7588	8	87.5176
A3	-38.9012	5	87.8023
fitted	-39.0227	3	84.0454
reduced	-80.7086	2	165.417

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	89.8995	6	0
Test 2	6.28472	3	0.0985503
Test 3	6.28472	3	0.0985503
Test 4	0.243085	2	0.885553

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.

### 2.4.1.6 Absolute Liver Weight, Female Rats; BMR: 1 SD; Normal Distribution + Constant Variance

#### Dataset

**Name:** Absolute liver weight in females

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Dose (mg/kg-day)	N	Mean (g)	Std. Dev. (g)
0	10	7	0.4
6	10	7.3	0.6
24	10	8.2	0.7
96	10	11.3	0.9

Test 1 Dose Response: 0

Test 2 Homogeneity of Variance: 0.0986

Test 3 Variance Model Selection: 0.0986

### Settings

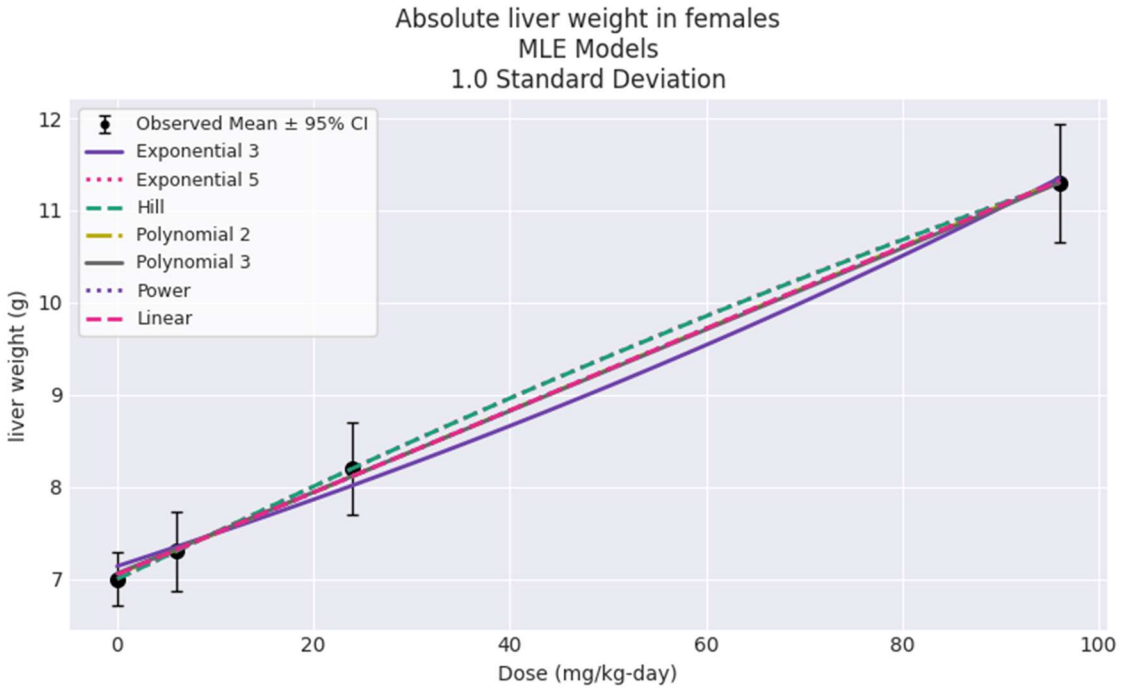
Setting	Value
<b>BMR</b>	1.0 Standard Deviation
<b>Distribution</b>	Normal + Constant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

### Maximum Likelihood Approach

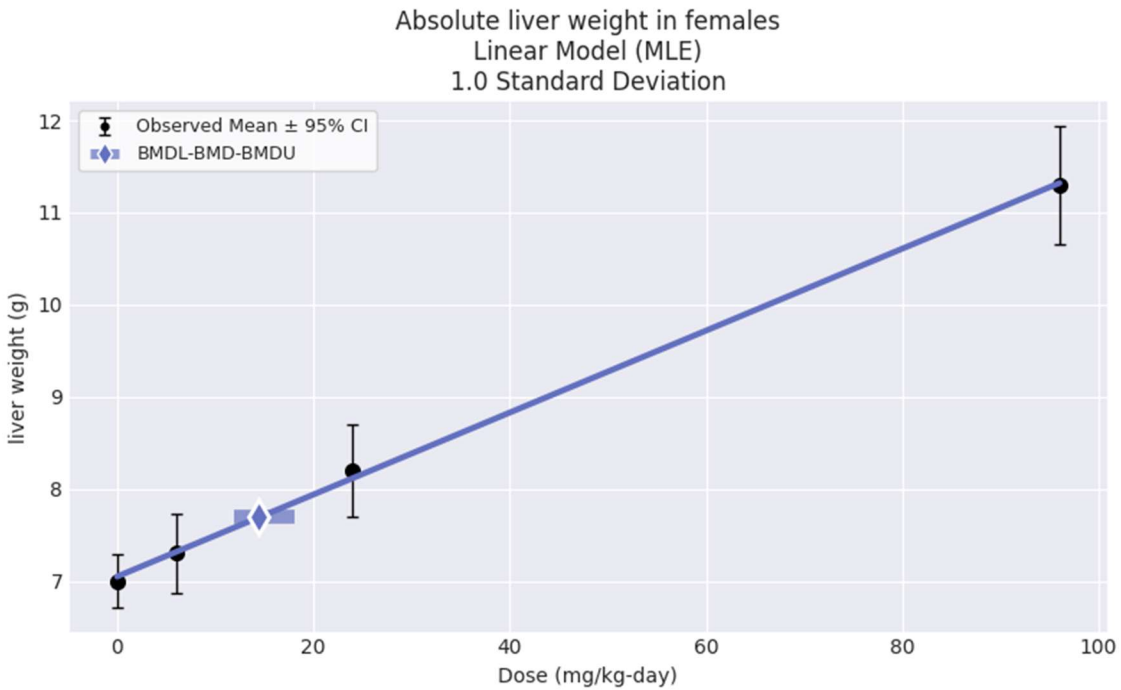
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	15.113	18.204	26.236	0.497	85.199	-0.663	0.887	<b>Viable</b> Control stdev. fit > 1.5
Exponential 5	8.218	12.719	23.953	-	87.802	-0.	<0.001	<b>Questionable</b> Zero degrees of freedom; saturated model Control stdev. fit > 1.5
Hill	8.087	12.713	23.56	-	87.802	<0.001	-0.	<b>Questionable</b> Zero degrees of freedom; saturated model Control stdev. fit > 1.5
Polynomial 2	11.887	14.435	23.009	0.886	84.046	-0.243	-0.079	<b>Viable</b> Control stdev. fit > 1.5
Polynomial 3	11.888	14.565	23.064	0.877	84.066	-0.29	-0.115	<b>Viable</b> Control stdev. fit > 1.5
Power	11.887	14.425	23.299	0.886	84.045	-0.238	-0.076	<b>Viable</b> Control stdev. fit > 1.5
Linear <sup>ab</sup>	11.887	14.425	18.124	0.886	84.045	-0.238	-0.076	<b>Recommended - Lowest AIC</b> Control stdev. fit > 1.5

<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model



**Selected Model: Linear**



Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Modeling Direction	Up (↑)
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	14.4254
BMDL	11.8871
BMDU	18.1242
AIC	84.0454
Log-Likelihood	-39.0227
P-Value	0.885553
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	7.04839	no	0.131443
b1	0.0444956	no	0.00265176
alpha	0.411996	no	0.0379555

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	10	7	7.04839	-0.238387
6	10	7.3	7.31536	-0.0756785
24	10	8.2	8.11628	0.412448
96	10	11.3	11.32	-0.0983821

Dose	N	Sample SD	Model Fitted SD
0	10	0.4	0.641869
6	10	0.6	0.641869
24	10	0.7	0.641869
96	10	0.9	0.641869

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-38.9012	5	87.8023
A2	-35.7588	8	87.5176
A3	-38.9012	5	87.8023
fitted	-39.0227	3	84.0454
reduced	-80.7086	2	165.417

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
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Test 1	89.8995	6	0
Test 2	6.28472	3	0.0985503
Test 3	6.28472	3	0.0985503
Test 4	0.243085	2	0.885553

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.

### 2.4.1.7 Relative Liver Weight, Female Rats; BMR: 10% RD; Normal Distribution + Nonconstant Variance

#### Dataset

**Name:** Relative liver wt in females

Dose (mg/kg-day)	N	Mean (percent of bw)	Std. Dev. (percent of bw)
0	10	2.54	0.19
6	10	2.51	0.13
24	10	2.86	0.25
96	10	4.2	0.39

#### Settings

Setting	Value
<b>BMR</b>	10% Relative Deviation
<b>Distribution</b>	Normal + Nonconstant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

#### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	-	22.294	-	-1	-	0.075	-0.759	<b>Unusable</b> Did not successfully execute.
Exponential 5	14.976	23.399	25.021	-	3.005	0.329	-0.126	<b>Questionable</b> Zero degrees of freedom; saturated model
Hill	22.807	23.273	24.27	-	3.005	0.329	-0.126	<b>Questionable</b> Zero degrees of freedom; saturated model
Polynomial 2	12.672	17.982	28.092	0.093	3.523	0.808	0.359	<b>Questionable</b> Goodness of fit p-value < 0.1

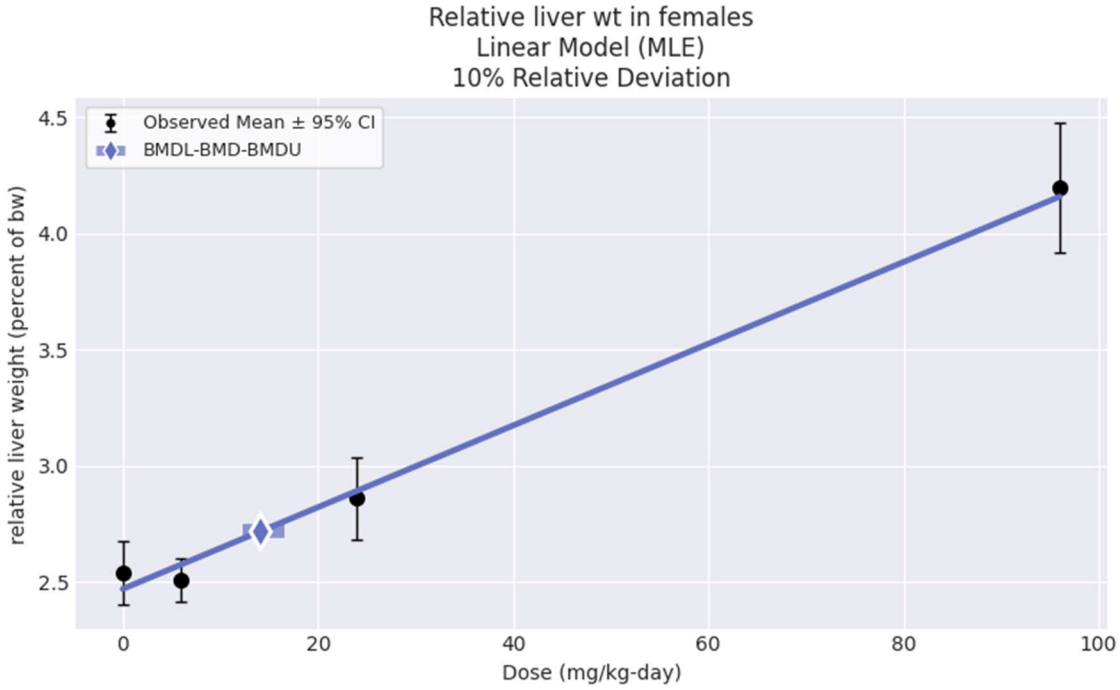
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Polynomial 3	12.673	17.991	28.092	0.093	3.523	0.807	0.36	<b>Questionable</b> Goodness of fit p-value < 0.1
Power	12.908	19.012	27.827	0.129	2.996	0.674	0.406	<b>Viable</b>
Linear <sup>ab</sup>	12.286	14.046	16.497	0.139	2.642	1.275	-1.132	<b>Recommended - Lowest AIC</b>

<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model

**Selected Model: Linear**



Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	10% Relative Deviation
Distribution	Normal + Nonconstant variance
Modeling Direction	Up (↑)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g <sub>s</sub>	0	0	1000
b <sub>1</sub>	0	-18	18
rho	0	0	18
alpha	0	-18	18

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Modeling Summary:

BMD	14.0459
BMDL	12.2859
BMDU	16.497
AIC	2.6425
Log-Likelihood	2.67875
P-Value	0.13902
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	2.47033	no	0.0386358
b1	0.0175875	no	0.0013356
rho	2.99794	no	1.16702
alpha	0.00198335	no	5.0458e-06

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	10	2.54	2.47033	1.27527
6	10	2.51	2.57586	-1.13226
24	10	2.86	2.89243	-0.468676
96	10	4.2	4.15874	0.345986

Dose	N	Sample SD	Model Fitted SD
0	10	0.19	0.172754
6	10	0.13	0.183933
24	10	0.25	0.218837
96	10	0.39	0.377142

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-0.559205	5	11.1184
A2	5.63822	8	4.72356
A3	4.65189	6	2.69623
fitted	2.67875	4	2.6425
reduced	-44.3328	2	92.6656

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	99.942	6	0
Test 2	12.3948	3	0.00614602
Test 3	1.97266	2	0.372942
Test 4	3.94627	2	0.13902

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.

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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.

### 2.4.1.8 Relative Liver Weight, Female Rats; BMR: 1 SD; Normal Distribution + Nonconstant Variance

#### Dataset

**Name:** Relative liver wt in females

Dose (mg/kg-day)	N	Mean (percent of bw)	Std. Dev. (percent of bw)
0	10	2.54	0.19
6	10	2.51	0.13
24	10	2.86	0.25
96	10	4.2	0.39

#### Settings

Setting	Value
<b>BMR</b>	1.0 Standard Deviation
<b>Distribution</b>	Normal + Nonconstant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

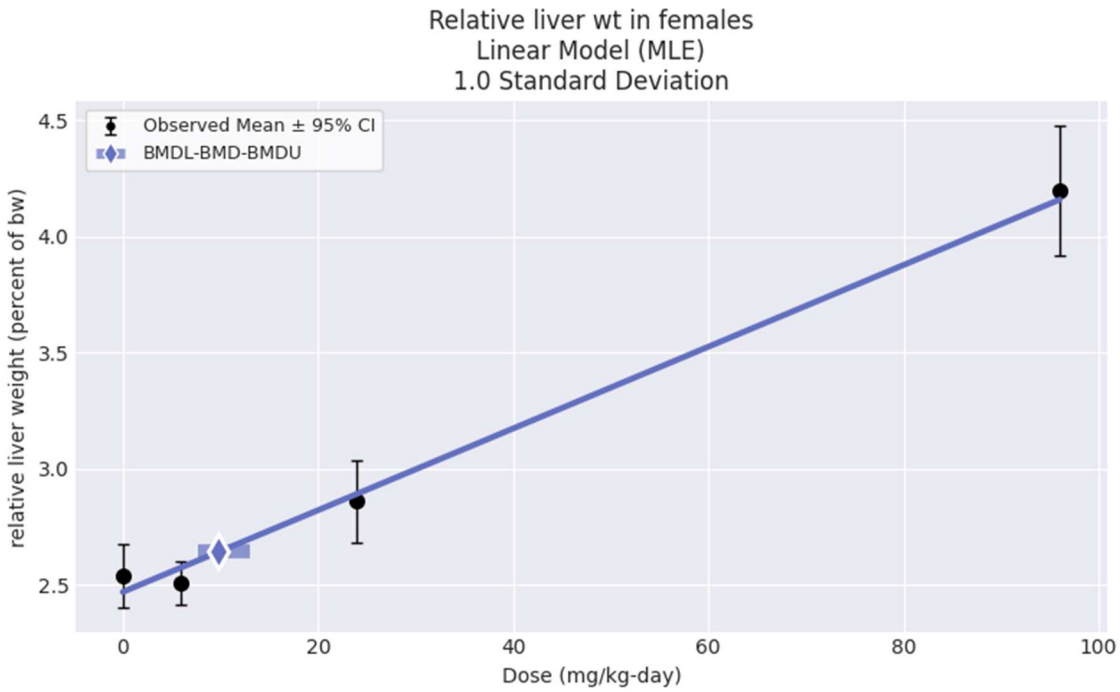
#### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	-	24.188	-	-1	-	0.075	-0.759	<b>Unusable</b> Did not successfully execute.
Exponential 5	10.528	22.647	23.761	-	3.005	0.329	-0.126	<b>Questionable</b> Zero degrees of freedom; saturated model
Hill	21.338	22.394	23.631	-	3.005	0.329	-0.126	<b>Questionable</b> Zero degrees of freedom; saturated model
Polynomial 2	8.089	12.676	22.805	0.093	3.523	0.808	-1.146	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 3	8.089	12.683	22.806	0.093	3.523	0.807	-1.146	<b>Questionable</b> Goodness of fit p-value < 0.1
Power	8.373	13.809	22.977	0.129	2.996	0.674	-1.017	<b>Viable</b>
Linear <sup>ab</sup>	7.649	9.823	13.033	0.139	2.642	1.275	-1.132	<b>Recommended - Lowest AIC</b>

<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model

**Selected Model: Linear**



Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant variance
Modeling Direction	Up (↑)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g	0	0	1000
b1	0	-18	18
rho	0	0	18
alpha	0	-18	18

Modeling Summary:

BMD	9.82254
BMDL	7.64852
BMDU	13.0332
AIC	2.6425
Log-Likelihood	2.67875
P-Value	0.13902
Model d.f.	2

Model Parameters:

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Variable	Estimate	On Bound	Std Error
g	2.47033	no	0.0386358
b1	0.0175875	no	0.0013356
rho	2.99794	no	1.16702
alpha	0.00198335	no	5.0458e-06

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	10	2.54	2.47033	1.27527
6	10	2.51	2.57586	-1.13226
24	10	2.86	2.89243	-0.468676
96	10	4.2	4.15874	0.345986

Dose	N	Sample SD	Model Fitted SD
0	10	0.19	0.172754
6	10	0.13	0.183933
24	10	0.25	0.218837
96	10	0.39	0.377142

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-0.559205	5	11.1184
A2	5.63822	8	4.72356
A3	4.65189	6	2.69623
fitted	2.67875	4	2.6425
reduced	-44.3328	2	92.6656

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	99.942	6	0
Test 2	12.3948	3	0.00614602
Test 3	1.97266	2	0.372942
Test 4	3.94627	2	0.13902

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.

## 2.4.2 Clinical Chemistry

### 2.4.2.1 Serum ALT, Male Rats; BMR: 1 SD; Normal Distribution + Nonconstant Variance

#### Dataset

Name: Serum ALT in Males

Dose (mg/kg-day)	N	Mean (IU/L)	Std. Dev. (IU/L)
0	10	26	4
6	10	26	6
24	10	53	36
96	10	42	15

#### Settings

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant variance
Adverse Direction	Up (↑)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

#### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	-	-	-	-1	-	<0.001	-	<b>Unusable</b> Did not successfully execute.
Exponential 5	5.918	7.365	19.971	-	319.448	0.392	-0.471	<b>Questionable</b> Zero degrees of freedom; saturated model
Hill	98.328	101.483	110.207	-	369.104	-1.045	-0.254	<b>Questionable</b> Zero degrees of freedom; saturated model Control stdev. fit > 1.5 BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Polynomial 2	145.42	148.547	151.589	<0.001	366.34	-0.927	-0.586	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Polynomial 3	144.069	147.166	150.179	<0.001	366.333	-0.925	-0.592	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0

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Power	105.832	108.097	110.311	<0.001	366.24	-0.867	-0.831	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 BMDL/highest dose ratio > 1.0 BMD/highest dose ratio > 1.0
Linear	3.883	6.682	15.13	<0.001	359.149	0.974	-1.256	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5

### Selected Model

No model was selected as a best-fitting model.

### 2.4.2.2 Serum ALT, Female Rats; BMR: 1 SD; Normal Distribution + Nonconstant Variance

#### Dataset

**Name:** Serum ALT in females

Dose (mg/kg-day)	N	Mean (IU/L)	Std. Dev. (IU/L)
0	10	22	7
6	10	22	5
24	10	26	8
96	10	37	23

#### Settings

Setting	Value
<b>BMR</b>	1.0 Standard Deviation
<b>Distribution</b>	Normal + Nonconstant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

#### Maximum Likelihood Approach

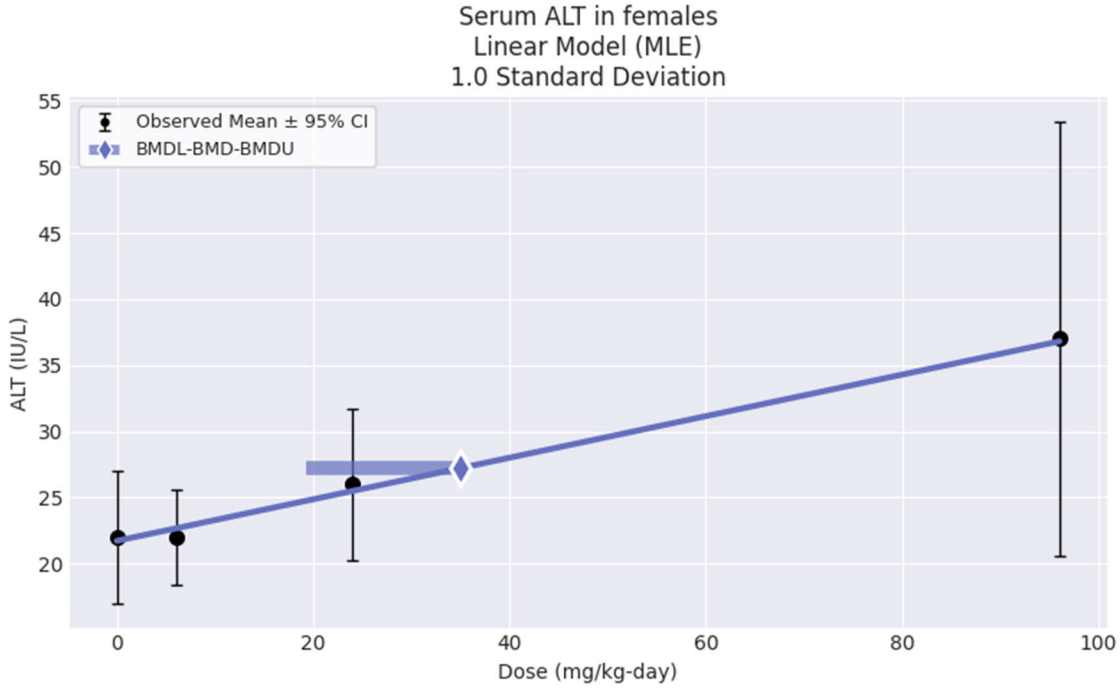
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	-	32.949	-	-1	-	-0.	-0.	<b>Unusable</b> Did not successfully execute.
Exponential 5	19.115	25.142	80.936	-	297.966	-0.072	0.238	<b>Questionable</b> Zero degrees of freedom; saturated model
Hill	23.217	25.416	80.296	-	297.966	-0.072	0.238	<b>Questionable</b> Zero degrees of freedom; saturated model
Polynomial 2	19.866	42.616	-	0.262	296.678	0.009	0.455	<b>Viable</b>
Polynomial 3	19.866	42.616	-	0.262	296.678	0.009	0.455	<b>Viable</b>
Power	20.179	41.867	85.776	0.293	296.526	-0.027	0.46	<b>Viable</b>

Linear <sup>ab</sup>	19.301	34.969	-	0.459	294.975	0.159	0.193	<b>Recommended - Lowest AIC</b>
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<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model

### Selected Model: Linear



Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant variance
Modeling Direction	Up (↑)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	1

Parameter Settings:

Parameter	Initial	Min	Max
g	0	0	1000
b1	0	-18	18
rho	0	0	18
alpha	0	-18	18

Modeling Summary:

BMD	34.9687
BMDL	19.3012
BMDU	-9999
AIC	294.975
Log-Likelihood	-143.488

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P-Value	0.459342
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	21.7236	no	1.29592
b1	0.157168	no	0.0650753
rho	5.08737	no	2.04972
alpha	4.77117e-06	no	1.49073e-10

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	10	22	21.7236	0.159033
6	10	22	22.6666	-0.344261
24	10	26	25.4956	0.193116
96	10	37	36.8118	0.0283141

Dose	N	Sample SD	Model Fitted SD
0	10	7	5.49597
6	10	5	6.12333
24	10	8	8.25881
96	10	23	21.0227

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-156.98	5	323.96
A2	-142.353	8	300.706
A3	-142.71	6	297.419
fitted	-143.488	4	294.975
reduced	-161.461	2	326.922

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	38.2159	6	1.01932e-06
Test 2	29.2542	3	1.98027e-06
Test 3	0.712867	2	0.700169
Test 4	1.55592	2	0.459342

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 {NTP, 1985, 1944492@@author-year}

### 2.1.1 Liver Weight; 13-week study

13-week oral toxicity study in rats

Report Generated: 2026-Jan-21 19:01 UTC

Analysis URL: [View](#)

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

#### 2.1.1.1 Relative Liver Weight, Male Rats; BMR: 10% RD; Normal Distribution + Nonconstant Variance

##### Dataset

Name: Male relative liver weight

Dose (mg/kg-day)	N	Mean (percent of bw)	Std. Dev. (percent of bw)
0	9	3.18	0.2
5.14	9	3.28	0.22
10.29	10	3.1	0.15
21.43	9	3.43	0.22
42.86	9	3.72	0.29
85.71	10	4.61	0.47

Test 1 Dose Response: 0

Test 2 Homogeneity of Variance: 0.005

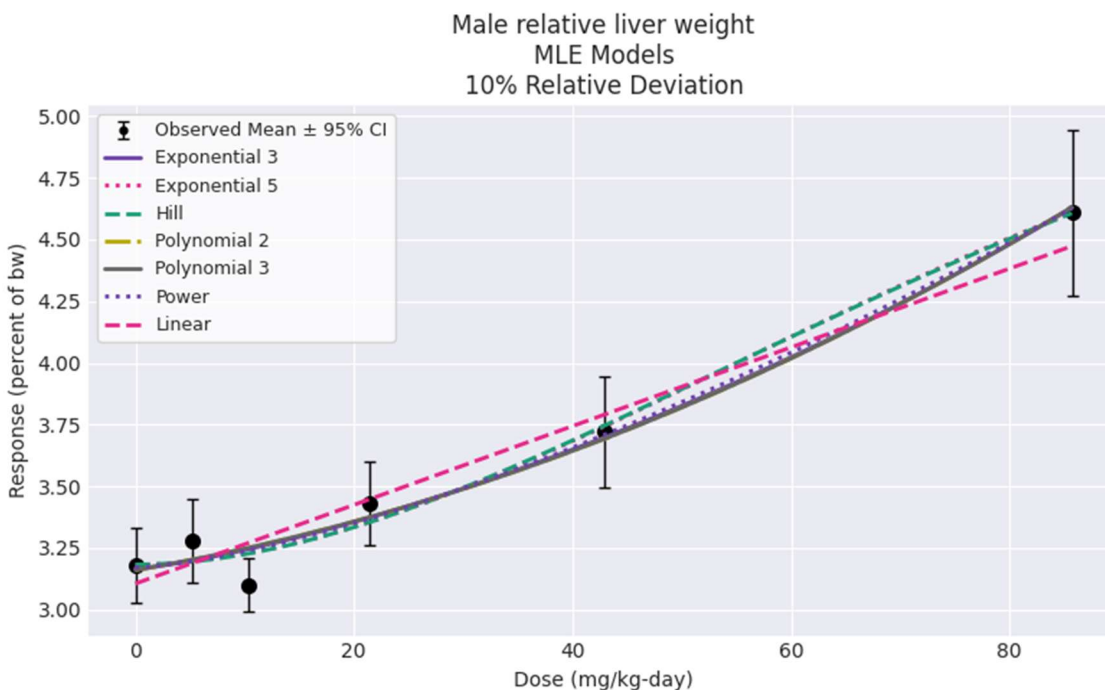
Test 3 Variance Model Selection: 0.9577

##### Settings

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

##### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	20.718	29.43	38.869	0.032	13.248	0.212	0.761	<b>Questionable</b> Goodness of fit p-value < 0.1
Exponential 5	21.842	30.416	38.453	0.016	14.664	-0.02	1.023	<b>Questionable</b> Goodness of fit p-value < 0.1
Hill	22.394	30.398	35.762	0.016	14.634	-0.034	1.033	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 2	20.358	29.053	39.269	0.028	13.521	0.315	0.739	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 3	20.198	29.054	39.269	0.028	13.521	0.315	0.739	<b>Questionable</b> Goodness of fit p-value < 0.1
Power	21.32	29.709	38.71	0.035	12.999	0.146	0.819	<b>Questionable</b> Goodness of fit p-value < 0.1
Linear	16.44	19.439	24.119	0.009	15.9	1.154	-0.205	<b>Questionable</b> Goodness of fit p-value < 0.1



### Selected Model

No model was selected as a best-fitting model.

### 2.1.1.2 Relative Liver Weight, Male Rats; BMR: 1 SD; Normal Distribution + Nonconstant Variance

#### Dataset

Name: Male relative liver weight

Dose (mg/kg-day)	N	Mean (percent of bw)	Std. Dev. (percent of bw)
0	9	3.18	0.2
5.14	9	3.28	0.22
10.29	10	3.1	0.15
21.43	9	3.43	0.22
42.86	9	3.72	0.29
85.71	10	4.61	0.47

Test 1 Dose Response: 0

Test 2 Homogeneity of Variance: 0.005

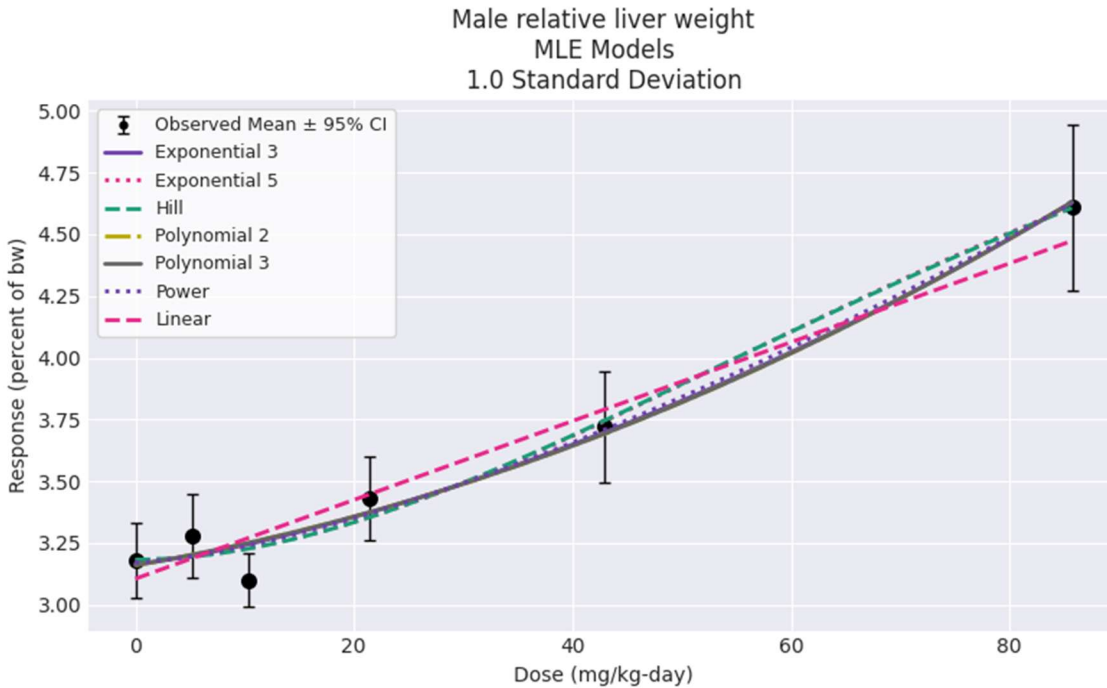
Test 3 Variance Model Selection: 0.9577

#### Settings

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant variance
Adverse Direction	Up (↑)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	12.843	20.719	30.921	0.032	13.248	0.212	0.761	<b>Questionable</b> Goodness of fit p-value < 0.1
Exponential 5	14.218	23.128	32.591	0.016	14.664	-0.02	1.023	<b>Questionable</b> Goodness of fit p-value < 0.1
Hill	14.518	23.209	32.429	0.016	14.634	-0.034	1.033	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 2	12.549	19.995	31.578	0.028	13.521	0.315	0.739	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 3	12.288	19.996	31.578	0.028	13.521	0.315	0.739	<b>Questionable</b> Goodness of fit p-value < 0.1
Power	13.672	21.384	31.115	0.035	12.999	0.146	0.819	<b>Questionable</b> Goodness of fit p-value < 0.1
Linear	9.714	12.272	15.969	0.009	15.9	1.154	-2.433	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1



### Selected Model

No model was selected as a best-fitting model.

### 2.1.1.3 Relative Liver Weight, Female Rats; BMR: 10% RD; Normal Distribution + Constant Variance

#### Dataset

**Name:** Female relative liver weight

Dose (mg/kg-day)	N	Mean (percent of bw)	Std. Dev. (percent of bw)
0	10	2.9	0.2
5.14	10	2.98	0.15
10.29	10	2.92	0.16
21.43	10	3.13	0.2
42.86	10	3.33	0.18
85.71	8	3.78	0.3

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.338

Test 3 Variance Model Selection: 0.338

#### Settings

Setting	Value
<b>BMR</b>	10% Relative Deviation
<b>Distribution</b>	Normal + Constant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

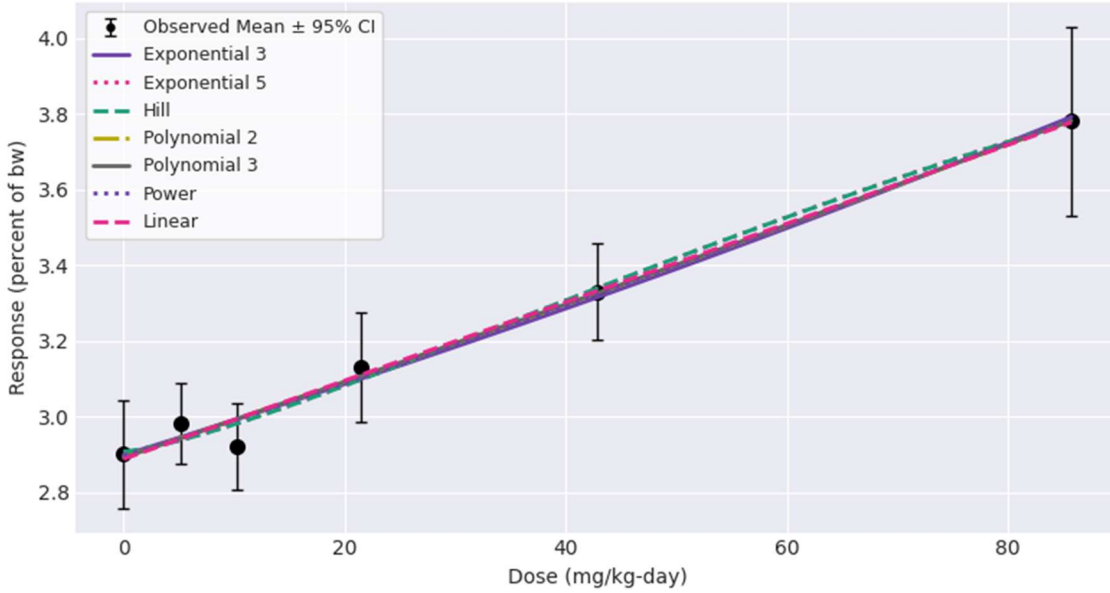
#### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	26.796	30.374	42.329	0.828	-20.436	0.038	0.504	Viable
Exponential 5	19.84	30.382	41.842	0.388	-16.69	-0.102	0.546	Viable
Hill	19.715	30.411	41.806	0.389	-16.696	-0.115	0.547	Viable
Polynomial 2	23.925	28.84	41.631	0.559	-18.518	0.137	0.402	Viable
Polynomial 3	23.934	28.712	41.632	0.559	-18.518	0.149	0.397	Viable
Power	23.956	29.569	42.111	0.568	-18.561	0.063	0.451	Viable
Linear <sup>ab</sup>	23.931	27.795	32.968	0.719	-20.492	0.216	0.338	Recommended - Lowest AIC

<sup>a</sup> BMDS recommended best fitting model

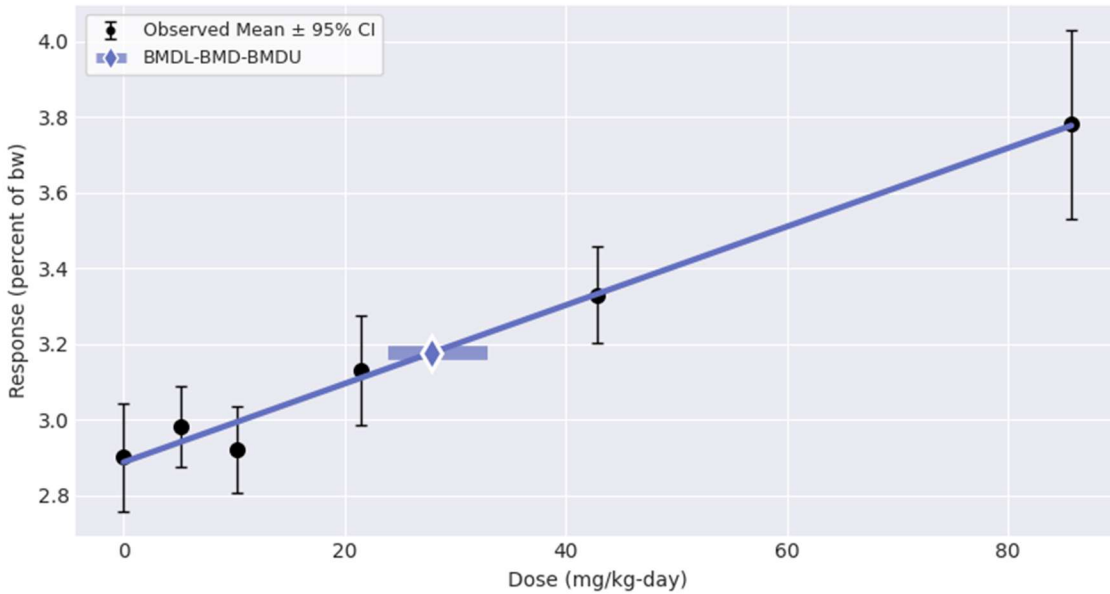
<sup>b</sup> User selected best fitting model

Female relative liver weight  
MLE Models  
10% Relative Deviation



**Selected Model: Linear**

Female relative liver weight  
Linear Model (MLE)  
10% Relative Deviation



Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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BMR Distribution	10% Relative Deviation
Modeling Direction	Normal + Constant variance
Confidence Level (one sided)	Up (↑) 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	27.7953
BMDL	23.9314
BMDU	32.9682
AIC	-20.4918
Log-Likelihood	13.2459
P-Value	0.718617
Model d.f.	4

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	2.88687	no	0.034297
b1	0.0103862	no	0.000906331
alpha	0.0370817	no	0.00025534

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	10	2.9	2.88687	0.215597
5.14	10	2.98	2.94026	0.652663
10.29	10	2.92	2.99375	-1.21103
21.43	10	3.13	3.10945	0.337513
42.86	10	3.33	3.33202	-0.033224
85.71	8	3.78	3.77707	0.0430184

Dose	N	Sample SD	Model Fitted SD
0	10	0.2	0.192566
5.14	10	0.15	0.192566
10.29	10	0.16	0.192566
21.43	10	0.2	0.192566
42.86	10	0.18	0.192566
85.71	8	0.3	0.192566

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	14.2925	7	-14.5851
A2	17.1352	12	-10.2705
A3	14.2925	7	-14.5851
fitted	13.2459	3	-20.4918
reduced	-21.0612	2	46.1224

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Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	76.3929	10	2.54696e-12
Test 2	5.68543	5	0.338041
Test 3	5.68543	5	0.338041
Test 4	2.09323	4	0.718617

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.

### 2.1.1.4 Relative Liver Weight, Female Rats; BMR: 1 SD; Normal Distribution + Constant Variance

#### Dataset

**Name:** Female relative liver weight

Dose (mg/kg-day)	N	Mean (percent of bw)	Std. Dev. (percent of bw)
0	10	2.9	0.2
5.14	10	2.98	0.15
10.29	10	2.92	0.16
21.43	10	3.13	0.2
42.86	10	3.33	0.18
85.71	8	3.78	0.3

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.338

Test 3 Variance Model Selection: 0.338

#### Settings

Setting	Value
<b>BMR</b>	1.0 Standard Deviation
<b>Distribution</b>	Normal + Constant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

#### Maximum Likelihood Approach

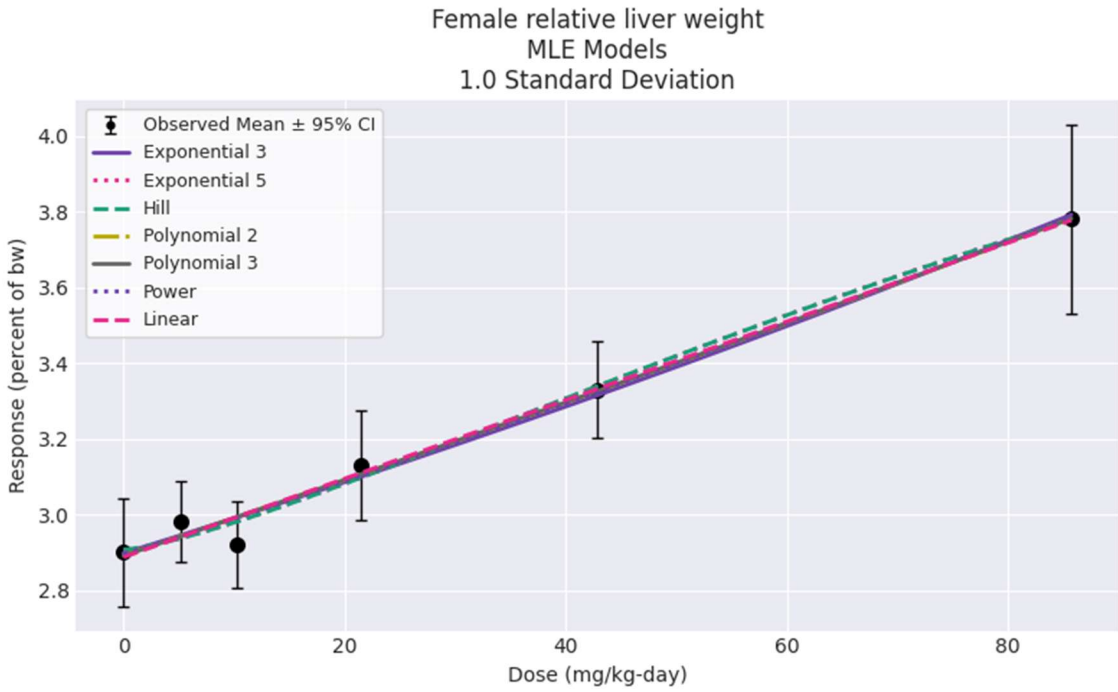
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	17.232	20.526	32.152	0.708	-20.436	0.038	0.504	<b>Viable</b>
Exponential 5	12.93	21.582	33.422	0.388	-16.69	-0.102	0.546	<b>Viable</b>
Hill	12.819	21.654	33.293	0.389	-16.696	-0.115	0.547	<b>Viable</b>
Polynomial 2	15.311	19.319	31.165	0.559	-18.518	0.137	0.402	<b>Viable</b>

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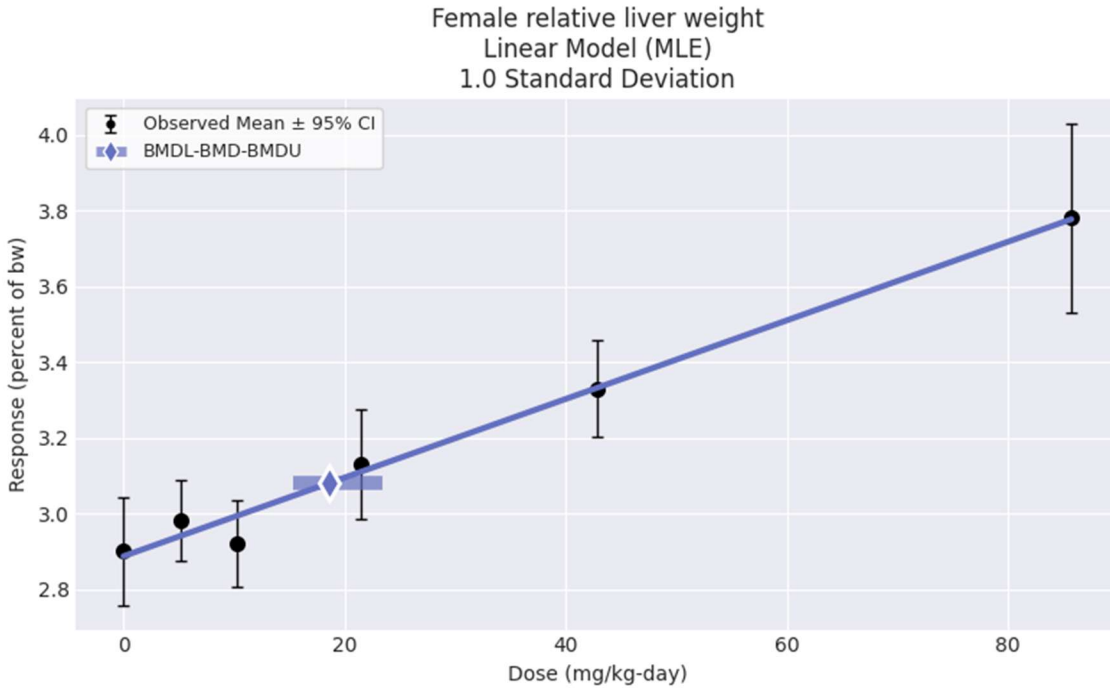
Polynomial 3	15.316	19.226	31.167	0.559	-18.518	0.149	0.397	<b>Viable</b>
Power	15.326	20.056	32.208	0.568	-18.561	0.063	0.451	<b>Viable</b>
Linear <sup>ab</sup>	15.29	18.541	23.408	0.719	-20.492	0.216	0.338	<b>Recommended - Lowest AIC</b>

<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model



**Selected Model: Linear**



Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Modeling Direction	Up (↑)
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	18.5406
BMDL	15.2903
BMDU	23.4077
AIC	-20.4918
Log-Likelihood	13.2459
P-Value	0.718617
Model d.f.	4

Model Parameters:

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April 2026

Variable	Estimate	On Bound	Std Error
g	2.88687	no	0.034297
b1	0.0103862	no	0.000906331
alpha	0.0370817	no	0.00025534

Goodness of Fit:

Dose	N	Sample Mean	Model Fitted Mean	Scaled Residual
0	10	2.9	2.88687	0.215597
5.14	10	2.98	2.94026	0.652663
10.29	10	2.92	2.99375	-1.21103
21.43	10	3.13	3.10945	0.337513
42.86	10	3.33	3.33202	-0.033224
85.71	8	3.78	3.77707	0.0430184

Dose	N	Sample SD	Model Fitted SD
0	10	0.2	0.192566
5.14	10	0.15	0.192566
10.29	10	0.16	0.192566
21.43	10	0.2	0.192566
42.86	10	0.18	0.192566
85.71	8	0.3	0.192566

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	14.2925	7	-14.5851
A2	17.1352	12	-10.2705
A3	14.2925	7	-14.5851
fitted	13.2459	3	-20.4918
reduced	-21.0612	2	46.1224

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	76.3929	10	2.54696e-12
Test 2	5.68543	5	0.338041
Test 3	5.68543	5	0.338041
Test 4	2.09323	4	0.718617

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 Kidney Histopathology; 2-year study

2-year oral toxicity study in mice

Report Generated: 2026-Jan-20 15:01 UTC

Analysis URL: [View](#)

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

### 2.1.2.1 Kidney Tubular Regeneration, Male Mice; BMR: 10% ER

#### Dataset

Name: Kidney tubular regeneration

Dose (mg/kg-day)	N	Incidence
0	48	8
5.57	50	12
11.14	49	17

#### Settings

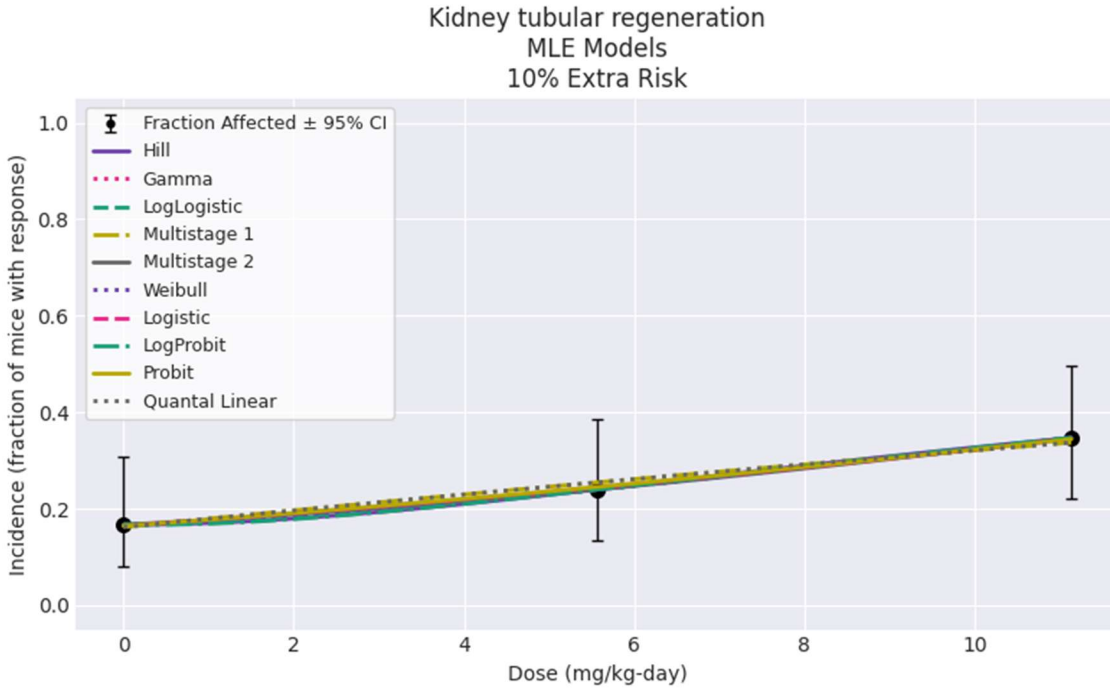
Setting	Value
BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Maximum Multistage Degree	2

#### Maximum Likelihood Approach

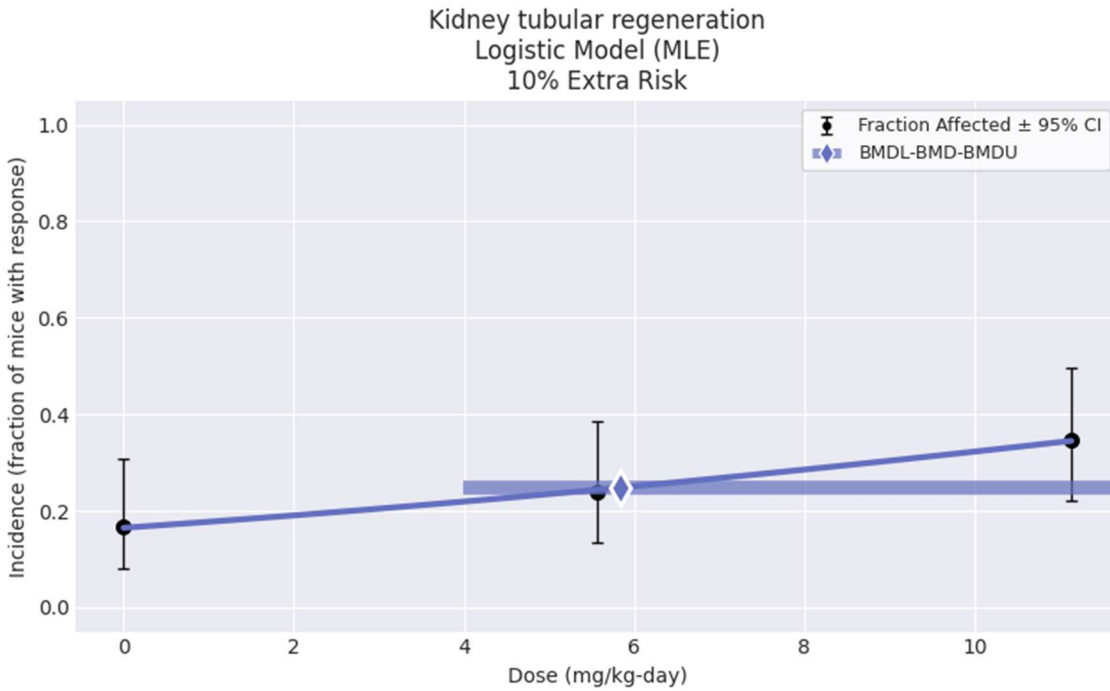
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	0	6.066	24.809	-	169.624	-0.	<0.001	<b>Unusable</b> Zero degrees of freedom; saturated model BMDL does not exist
Gamma	2.766	6.12	23.852	-	167.624	<0.001	-0.	<b>Questionable</b> Zero degrees of freedom; saturated model
LogLogistic	2.445	6.113	24.522	-	167.624	<0.001	-0.	<b>Questionable</b> Zero degrees of freedom; saturated model
Multistage 1	2.746	5.004	25.435	0.77	165.71	0.091	-0.237	<b>Viable</b>
Multistage 2	2.766	6.16	23.852	-	167.624	<0.001	<0.001	<b>Questionable</b> Zero degrees of freedom; saturated model
Weibull	2.766	6.129	23.851	-	167.624	<0.001	-0.	<b>Questionable</b> Zero degrees of freedom; saturated model
Logistic <sup>ab</sup>	3.996	5.845	22.276	0.939	165.63	0.036	-0.062	<b>Recommended - Lowest AIC</b>
LogProbit	0	6.078	-	-	167.624	-0.	<0.001	<b>Unusable</b> Zero degrees of freedom; saturated model BMDL does not exist
Probit	3.825	5.718	22.567	0.915	165.635	0.048	-0.086	<b>Viable</b>
Quantal Linear	2.746	5.004	25.435	0.77	165.71	0.091	-0.237	<b>Viable</b>

<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> Selected based on lowest AIC



### Selected Model: Logistic



Logistic Model

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Input Summary:

BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Modeling approach	frequentist_unrestricted

Parameter Settings:

Parameter	Initial	Min	Max
a	0	-18	18
b	0	0	100

Modeling Summary:

BMD	5.84505
BMDL	3.99561
BMDU	22.2756
AIC	165.63
Log-Likelihood	-80.8149
P-Value	0.938656
Overall d.f.	1
Chi <sup>2</sup>	0.0059227

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-1.62355	no	0.342712
b	0.088203	no	0.0436184

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	48	8	7.90638	0.164716	0.0364307
5.57	50	12	12.1872	0.243745	-0.0616762
11.14	49	17	16.9064	0.345028	0.0281344

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-80.812	3	-	-	-
Fitted model	-80.8149	2	0.00593115	1	0.938612
Reduced model	-82.9368	1	4.24967	2	0.119453

## 2.2 {NIEHS, 2025, 13049126@@author-year}

### 2.2.1 Liver Weight

Report Generated: 2026-Mar-11 16:03 UTC

Analysis URL: [View](#)

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

### 2.2.1.1 Absolute Liver Weight, BMR: 1 SD; Normal Distribution + Nonconstant Variance Dataset

Name: Absolute liver weight

Dose	N	Mean (g)	Std. Dev. (g)
0	10	0.94	0.05
0.25	5	0.96	0.03
2.5	5	0.9	0.03
7.5	5	0.92	0.04
25	5	1.16	0.05
62.5	7	1.41	0.04

#### Settings

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant variance
Adverse Direction	Up (↑)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

#### Maximum Likelihood Approach

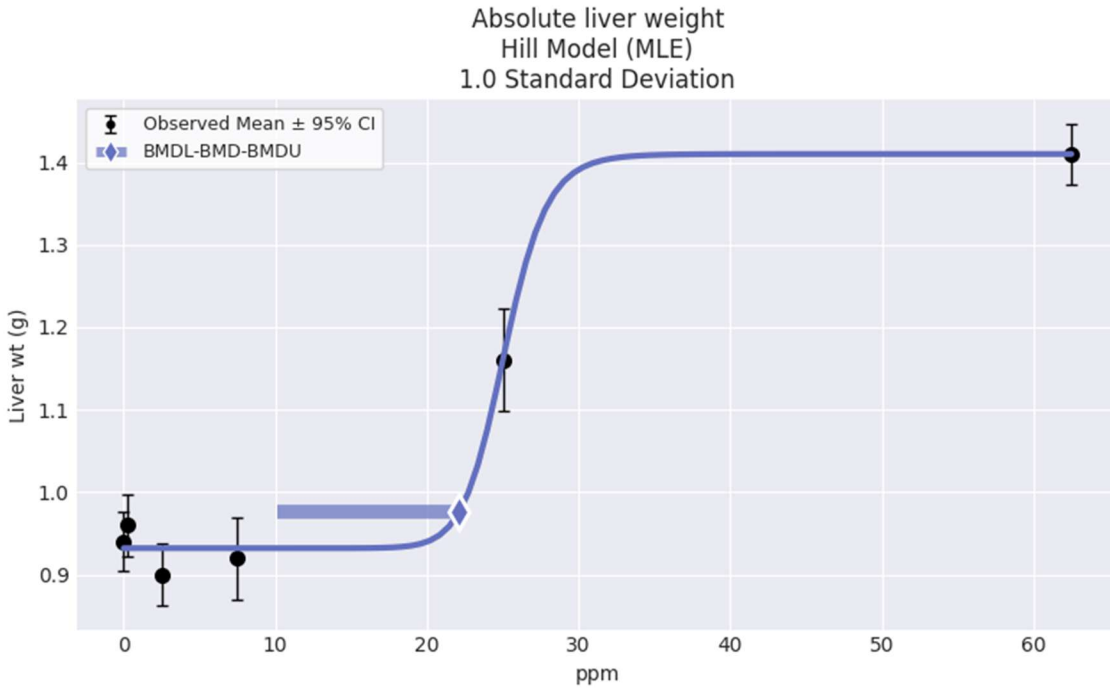
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	-	21.143	-	-1	-	0.599	-32.905	<b>Unusable</b> Did not successfully execute.
Exponential 5	10.339	22.138	23.053	0.096	-119.116	0.599	<0.001	<b>Questionable</b> Goodness of fit p-value < 0.1
Hill <sup>ab</sup>	10.137	22.115	22.625	0.103	-119.28	0.58	0.005	<b>Recommended - Lowest AIC</b>
Polynomial 2	5.447	6.638	9.616	<0.001	-107.31	1.059	-2.632	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Polynomial 3	5.447	6.638	9.616	<0.001	-107.31	1.059	-2.632	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Power	5.51	7.535	11.629	<0.001	-105.604	0.875	-2.465	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Linear	5.446	6.638	8.301	<0.001	-107.31	1.059	-2.632	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1

<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model

**Selected Model: Hill**

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Hill Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant variance
Modeling Direction	Up (↑)
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
rho	0	-18	18
alpha	0	-18	18

Modeling Summary:

BMD	22.1147
BMDL	10.1367
BMDU	22.6246
AIC	-119.28

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Log-Likelihood	64.6398
P-Value	0.102926
Model d.f.	3

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.932011	no	0.0087086
v	0.478012	no	0.0169645
k	25.1295	no	0.234772
n	18	yes	Not Reported
rho	-0.591894	no	1.43737
alpha	0.00181851	no	7.89359e-07

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	10	0.94	0.932011	0.580181
0.25	5	0.96	0.932011	1.43734
2.5	5	0.9	0.932011	-1.64393
7.5	5	0.92	0.932011	-0.616838
25	5	1.16	1.15991	0.00467435
62.5	7	1.41	1.41002	-0.00162051

Dose	N	Sample SD	Model Fitted SD
0	10	0.05	0.0435419
0.25	5	0.03	0.0435419
2.5	5	0.03	0.0435419
7.5	5	0.04	0.0435419
25	5	0.05	0.0408123
62.5	7	0.04	0.0385208

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	67.7251	7	-121.45
A2	69.4251	12	-114.85
A3	67.7326	8	-119.465
fitted	64.6398	5	-119.28
reduced	8.32247	2	-12.6449

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	122.205	10	0
Test 2	3.40003	5	0.638565

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Test 3	3.38508	4	0.495566
Test 4	6.18551	3	0.102926

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.

### 2.2.1.2 Absolute Liver Weight, BMR: 10% RD; Normal Distribution + Nonconstant Variance Dataset

**Name:** Absolute liver weight

Dose	N	Mean (g)	Std. Dev. (g)
0	10	0.94	0.05
0.25	5	0.96	0.03
2.5	5	0.9	0.03
7.5	5	0.92	0.04
25	5	1.16	0.05
62.5	7	1.41	0.04

#### Settings

Setting	Value
<b>BMR</b>	10% Relative Deviation
<b>Distribution</b>	Normal + Nonconstant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

#### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	-	22.178	-	-1	-	0.599	-32.905	<b>Unusable</b> Did not successfully execute.
Exponential 5	14.933	23.347	23.893	0.096	-119.116	0.599	<0.001	<b>Questionable</b> Goodness of fit p-value < 0.1
Hill <sup>ab</sup>	22.335	23.226	23.651	0.103	-119.28	0.58	0.005	<b>Recommended - Lowest AIC</b>
Polynomial 2	10.704	11.702	15.373	<0.001	-107.31	1.059	-2.632	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1

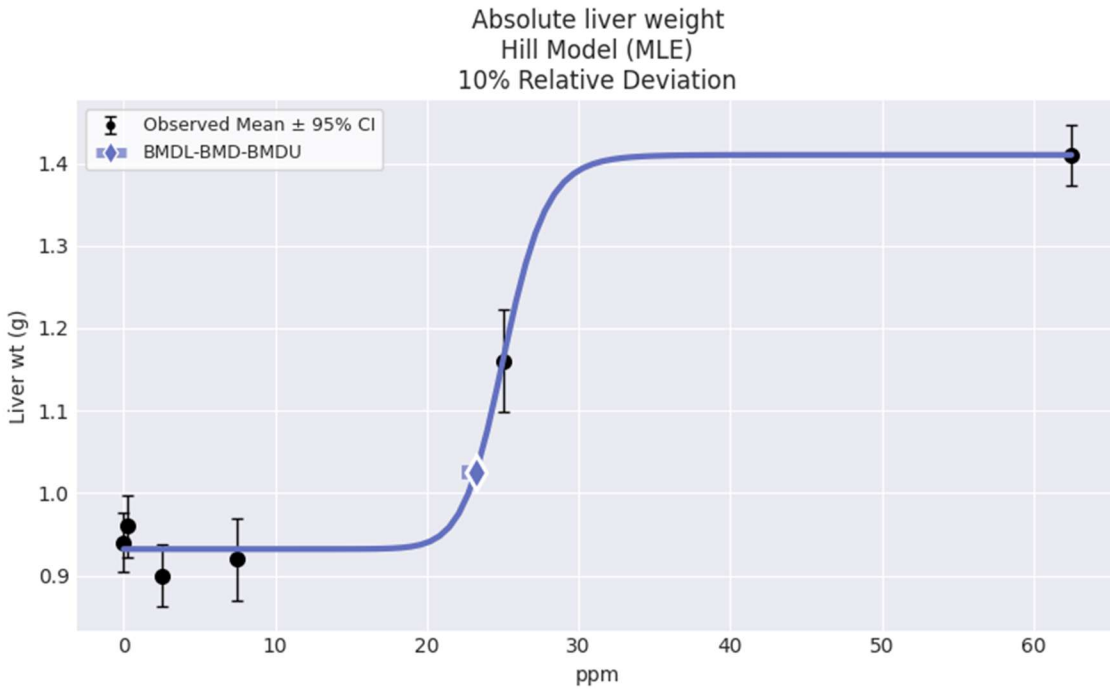
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Polynomial 3	10.704	11.702	15.375	<0.001	-107.31	1.059	-2.632	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Power	10.765	12.943	17.386	<0.001	-105.604	0.875	-2.465	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Linear	10.704	11.702	12.858	<0.001	-107.31	1.059	-2.632	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1

<sup>a</sup> BMDS recommended best fitting model

<sup>b</sup> User selected best fitting model

**Selected Model: Hill**



Hill Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	10% Relative Deviation
Distribution	Normal + Nonconstant variance
Modeling Direction	Up (↑)
Confidence Level (one sided)	0.95
Modeling Approach	MLE

Public Release Draft  
April 2026

Parameter Settings:

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

Modeling Summary:

BMD	23.2258
BMDL	22.3349
BMDU	23.6513
AIC	-119.28
Log-Likelihood	64.6398
P-Value	0.102926
Model d.f.	3

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.932011	no	0.0087086
v	0.478012	no	0.0169645
k	25.1295	no	0.234772
n	18	yes	Not Reported
rho	-0.591894	no	1.43737
alpha	0.00181851	no	7.89359e-07

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	10	0.94	0.932011	0.580181
0.25	5	0.96	0.932011	1.43734
2.5	5	0.9	0.932011	-1.64393
7.5	5	0.92	0.932011	-0.616838
25	5	1.16	1.15991	0.00467435
62.5	7	1.41	1.41002	-0.00162051

Dose	N	Sample SD	Model Fitted SD
0	10	0.05	0.0435419
0.25	5	0.03	0.0435419
2.5	5	0.03	0.0435419
7.5	5	0.04	0.0435419
25	5	0.05	0.0408123
62.5	7	0.04	0.0385208

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Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	67.7251	7	-121.45
A2	69.4251	12	-114.85
A3	67.7326	8	-119.465
fitted	64.6398	5	-119.28
reduced	8.32247	2	-12.6449

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	122.205	10	0
Test 2	3.40003	5	0.638565
Test 3	3.38508	4	0.495566
Test 4	6.18551	3	0.102926

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.

### 2.2.1.3 Relative Liver Weight, BMR: 1 SD; Normal Distribution + Constant Variance Dataset

#### Dataset

Name: Rel liver weight

Dose	N	Mean	Std. Dev.
0	10	46.05	1.74
0.25	5	46.51	1.52
2.5	5	42.25	1.25
7.5	5	44.73	0.75
25	5	55.36	1.4
62.5	7	76.01	2.05

Test 1 Dose Response: 0

Test 2 Homogeneity of Variance: 0.2894

Test 3 Variance Model Selection: 0.2894

#### Settings

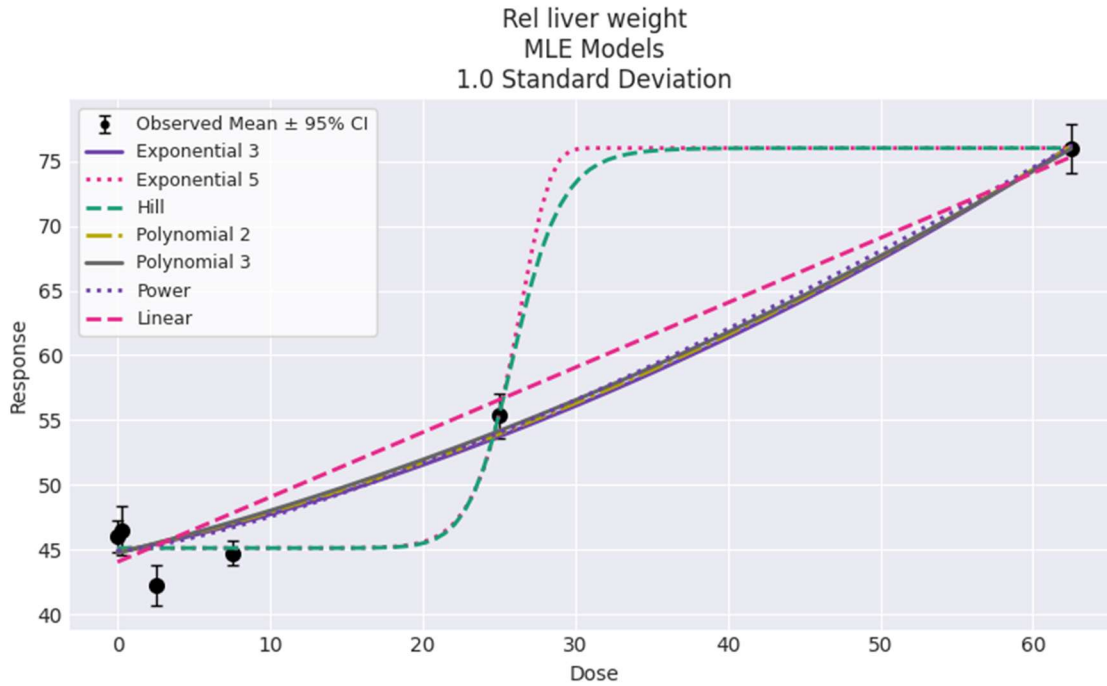
Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Up (↑)

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Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

**Maximum Likelihood Approach**

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	5.934	8.368	11.945	<0.001	173.799	1.615	-2.115	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Exponential 5	10.456	22.068	23.134	<0.001	163.786	1.524	<0.001	<b>Questionable</b> Goodness of fit p-value < 0.1
Hill	10.353	22.177	22.66	<0.001	163.786	1.524	-0.	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 2	5.52	7.584	7.741	<0.001	175.018	1.774	-2.232	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Polynomial 3	5.471	7.112	7.259	<0.001	175.188	1.849	-2.361	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Power	6.449	8.721	11.976	<0.001	171.435	1.656	-1.994	<b>Questionable</b> Goodness of fit p-value < 0.1
Linear	4.302	5.189	6.445	<0.001	181.624	2.442	-2.642	<b>Questionable</b>  Residual near BMD  > 2.0 Residual at control > 2.0 Goodness of fit p-value < 0.1



### Selected Model

No model was selected as a best-fitting model.

### 2.2.1.4 Relative Liver Weight, BMR: 10% RD; Normal Distribution + Constant Variance Dataset

#### Dataset

Name: Rel liver weight

Dose	N	Mean	Std. Dev.
0	10	46.05	1.74
0.25	5	46.51	1.52
2.5	5	42.25	1.25
7.5	5	44.73	0.75
25	5	55.36	1.4
62.5	7	76.01	2.05

Test 1 Dose Response: 0

Test 2 Homogeneity of Variance: 0.2894

Test 3 Variance Model Selection: 0.2894

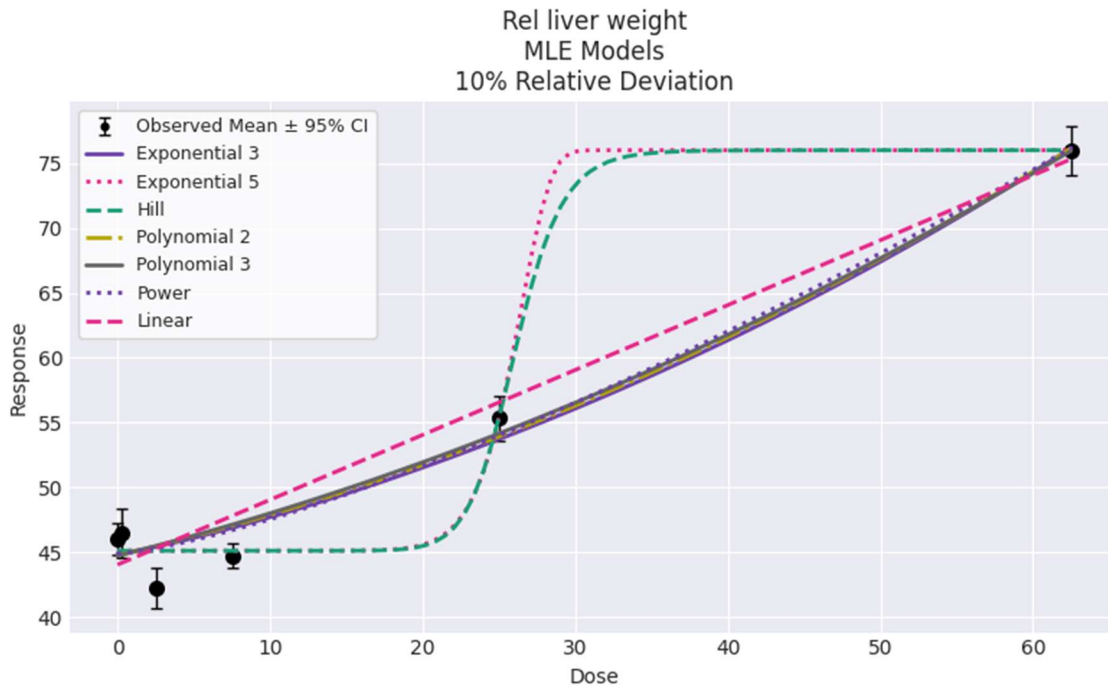
#### Settings

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

### Maximum Likelihood Approach

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Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	11.369	14.607	18.354	<0.001	173.799	1.615	-2.115	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Exponential 5	15.716	23.453	23.987	<0.001	163.786	1.524	<0.001	<b>Questionable</b> Goodness of fit p-value < 0.1
Hill	23.314	23.459	23.598	<0.001	163.786	1.524	-0.	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 2	10.629	13.695	13.979	<0.001	175.018	1.774	-2.232	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Polynomial 3	10.543	13.204	13.477	<0.001	175.188	1.849	-2.361	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Power	11.839	14.794	18.167	<0.001	171.435	1.656	-1.994	<b>Questionable</b> Goodness of fit p-value < 0.1
Linear	8.178	8.8	9.495	<0.001	181.624	2.442	-2.642	<b>Questionable</b>  Residual near BMD  > 2.0 Residual at control > 2.0 Goodness of fit p-value < 0.1



## Selected Model

No model was selected as a best-fitting model.

### 2.2.1.5 Relative Liver Weight, BMR: 1 SD; Normal Distribution + Nonconstant Variance Dataset

#### Dataset

Name: Rel liver weight

Dose	N	Mean	Std. Dev.
0	10	46.05	1.74
0.25	5	46.51	1.52
2.5	5	42.25	1.25
7.5	5	44.73	0.75
25	5	55.36	1.4
62.5	7	76.01	2.05

#### Settings

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant variance
Adverse Direction	Up (↑)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

#### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	-	30.812	-	-1	-	<0.001	-0.	<b>Unusable</b> Did not successfully execute.
Exponential 5	10.457	21.949	23.032	<0.001	163.786	1.524	<0.001	<b>Questionable</b> Goodness of fit p-value < 0.1
Hill	10.348	20.88	21.942	<0.001	165.618	1.487	-0.01	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 2	5.524	7.71	11.732	<0.001	175.011	1.745	-2.212	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Polynomial 3	15.905	16.238	16.57	<0.001	185.6	0.494	-1.42	<b>Questionable</b> Goodness of fit p-value < 0.1
Power	6.449	8.721	11.976	<0.001	171.435	1.656	-1.994	<b>Questionable</b> Goodness of fit p-value < 0.1
Linear	4.302	5.189	6.445	<0.001	181.624	2.442	-2.642	<b>Questionable</b>  Residual near BMD  > 2.0 Residual at control > 2.0 Goodness of fit p-value < 0.1

## Selected Model

No model was selected as a best-fitting model.

### 2.2.1.6 Relative Liver Weight, BMR: 1% RD; Normal Distribution + Nonconstant Variance Dataset

#### Dataset

**Name:** Rel liver weight

Dose	N	Mean	Std. Dev.
0	10	46.05	1.74
0.25	5	46.51	1.52
2.5	5	42.25	1.25
7.5	5	44.73	0.75
25	5	55.36	1.4
62.5	7	76.01	2.05

#### Settings

Setting	Value
<b>BMR</b>	10% Relative Deviation
<b>Distribution</b>	Normal + Nonconstant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

#### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	-	22.564	-	-1	-	<0.001	-0.	<b>Unusable</b> Did not successfully execute.
Exponential 5	16.24	23.389	23.922	<0.001	163.786	1.524	<0.001	<b>Questionable</b> Goodness of fit p-value < 0.1
Hill	22.236	22.688	22.919	<0.001	165.618	1.487	-0.01	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 2	10.627	13.88	18.284	<0.001	175.011	1.745	-2.212	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Polynomial 3	22.048	22.512	24.359	<0.001	185.6	0.494	3.618	<b>Questionable</b>  Residual near BMD  > 2.0 Goodness of fit p-value < 0.1
Power	11.839	14.794	18.166	<0.001	171.435	1.656	-1.994	<b>Questionable</b> Goodness of fit p-value < 0.1
Linear	8.178	8.8	9.495	<0.001	181.624	2.442	-2.642	<b>Questionable</b>  Residual near BMD  > 2.0 Residual at control > 2.0 Goodness of fit p-value < 0.1

## Selected Model

No model was selected as a best-fitting model.

### 2.2.2 Clinical Chemistry

Report Generated: 2026-Mar-11 15:03 UTC

Analysis URL: [View](#) / [Update](#)

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

#### 2.2.2.1 Serum ALT, BMR: 1 SD; Normal Distribution + Constant Variance Dataset

### Dataset

Name: NIEHS ALT Response

Dose	N	Mean	Std. Dev.
0	8	58.9	11.8
0.25	4	102.8	45.6
2.5	2	40	2
7.5	3	78.3	12.2
25	5	84.2	17.3
62.5	7	248.6	34.2

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.0002

Test 3 Variance Model Selection: 0.0002

### Settings

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

### Maximum Likelihood Approach

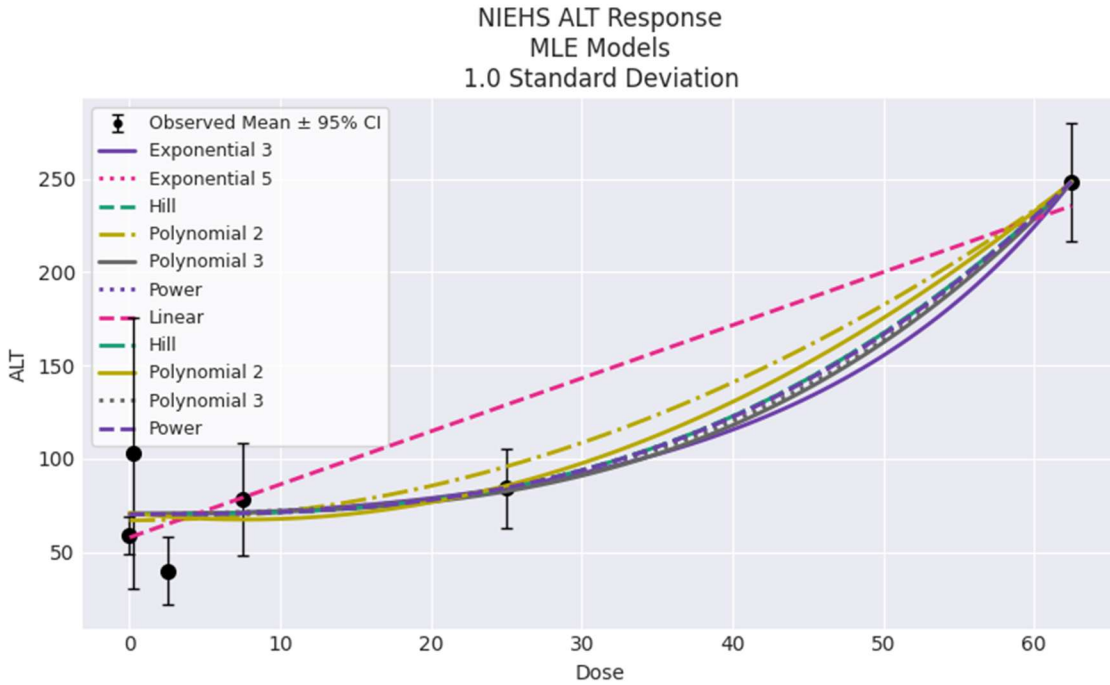
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	19.839	33.132	54.529	0.012	283.886	-1.126	-0.031	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Exponential 5	22.009	32	55.973	0.004	285.904	-1.14	-0.024	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)

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Hill	22.67	31.95	57.459	0.004	285.904	-1.14	-0.024	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Polynomial 2	18.669	24.912	28.594	0.017	282.877	-0.803	-0.912	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Polynomial 3	19.283	33.591	37.017	0.004	285.93	-1.19	0.128	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Power	20.732	32.003	34.888	0.012	283.904	-1.14	-0.024	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Linear	9.771	12.392	16.683	<0.001	294.902	0.083	-0.044	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Hill	23.551	31.95	57.457	0.004	285.904	-1.14	-0.024	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Polynomial 2	20.234	30.574	39.33	0.011	283.97	-1.208	-0.113	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Polynomial 3	6.403	32.372	50.139	0.004	285.899	-1.115	-0.026	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05) BMD/BMDL ratio > 3.0

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Power	20.732	32.003	34.888	0.012	283.904	-1.14	-0.024	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
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**Selected Model**

No model was selected as a best-fitting model.

**2.2.2.2 Serum ALT, BMR: 1 SD; Normal Distribution + Nonconstant Variance  
Dataset**

**Dataset**

**Name:** NIEHS ALT Response

Dose	N	Mean	Std. Dev.
0	8	58.9	11.8
0.25	4	102.8	45.6
2.5	2	40	2
7.5	3	78.3	12.2
25	5	84.2	17.3
62.5	7	248.6	34.2

Test 1 Dose Response: <0.0001  
Test 2 Homogeneity of Variance: 0.0002  
Test 3 Variance Model Selection: 0.0138

**Settings**

Setting	Value
<b>BMR</b>	1.0 Standard Deviation

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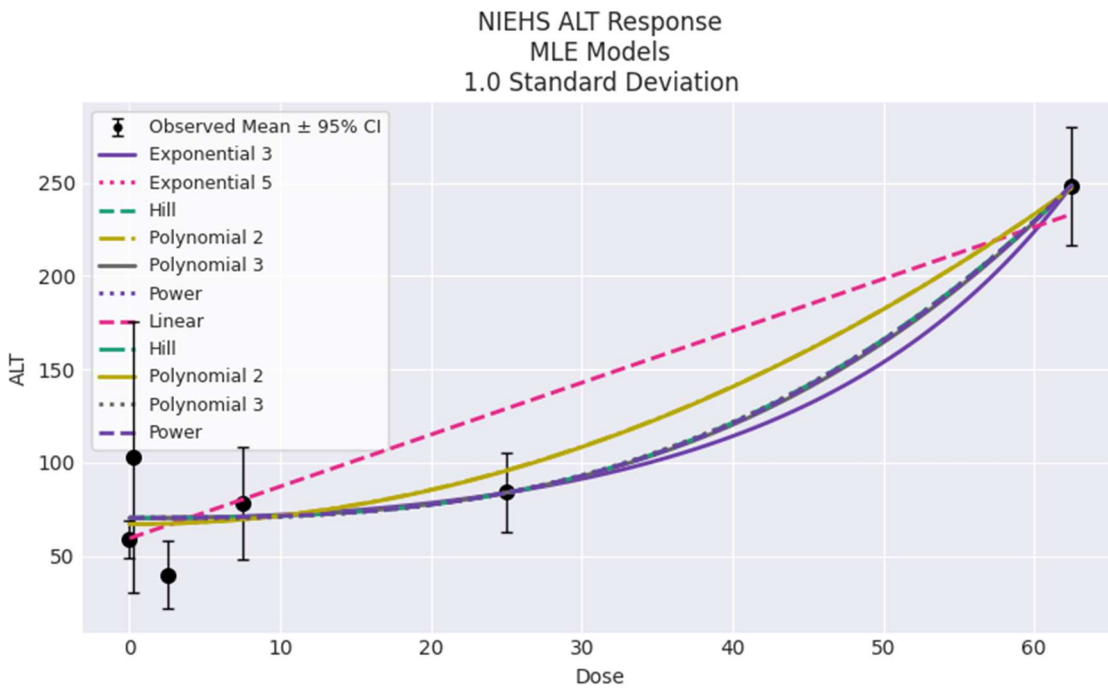
<b>Distribution</b>	Normal + Nonconstant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

**Maximum Likelihood Approach**

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	19.774	33.298	58.411	<0.001	285.737	-1.187	0.021	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5
Exponential 5	21.913	32.121	52.545	<0.001	287.751	-1.2	0.027	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5
Hill	22.266	32.068	57.636	<0.001	287.751	-1.2	0.027	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5
Polynomial 2	18.406	24.674	28.537	<0.001	284.826	-0.83	-0.918	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5
Polynomial 3	19.29	32.202	36.964	<0.001	287.748	-1.193	0.02	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5
Power	20.643	32.122	57.724	<0.001	285.751	-1.2	0.027	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5
Linear	8.856	11.82	16.451	<0.001	296.677	-0.051	-0.103	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5

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Hill	22.739	32.066	57.627	<0.001	287.751	-1.2	0.027	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5
Polynomial 2	18.449	24.76	25.273	<0.001	286.799	-0.828	-0.902	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5
Polynomial 3	6.516	31.873	49.877	<0.001	287.749	-1.186	0.01	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 BMD/BMDL ratio > 3.0
Power	20.642	32.122	57.724	<0.001	285.751	-1.2	0.027	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5



**Selected Model**

No model was selected as a best-fitting model.

**2.2.2.3 Serum ALT, BMR: 1 SD; Lognormal Distribution + Constant Variance  
Dataset**

**Dataset**

Name: NIEHS ALT Response

Dose	N	Mean	Std. Dev.
0	8	58.9	11.8
0.25	4	102.8	45.6
2.5	2	40	2
7.5	3	78.3	12.2
25	5	84.2	17.3
62.5	7	248.6	34.2

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.0241

Test 3 Variance Model Selection: 0.0241

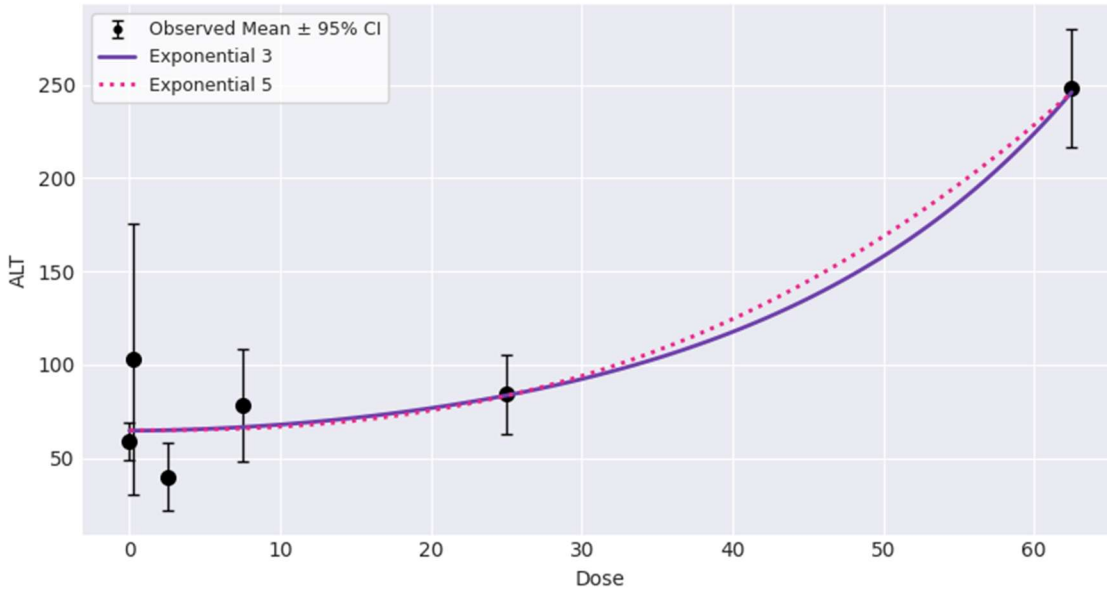
**Settings**

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Lognormal + Constant variance
Adverse Direction	Up (↑)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

**Maximum Likelihood Approach**

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	14.949	26.484	53.014	<0.001	280.646	-12.788	0.568	<b>Questionable</b> Residual at control > 2.0 Goodness of fit p-value < 0.1 Constant variance test failed (Test 2 p-value < 0.05)
Exponential 5	17.638	26.522	35.084	<0.001	282.739	-13.32	0.862	<b>Questionable</b> Residual at control > 2.0 Goodness of fit p-value < 0.1 Constant variance test failed (Test 2 p-value < 0.05)

NIEHS ALT Response  
MLE Models  
1.0 Standard Deviation



### Selected Model

No model was selected as a best-fitting model.

### 2.2.2.4 Serum ALT with 1 ppm group removed, BMR: 1 SD; Normal Distribution + Constant Variance Dataset

#### Dataset

Name: NIEHS ALT Response - 1 ppm datapoint

Dose	N	Mean	Std. Dev.
0	8	58.9	11.8
2.5	2	40	2
7.5	3	78.3	12.2
25	5	84.2	17.3
62.5	7	248.6	34.2

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.0007

Test 3 Variance Model Selection: 0.0007

#### Settings

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

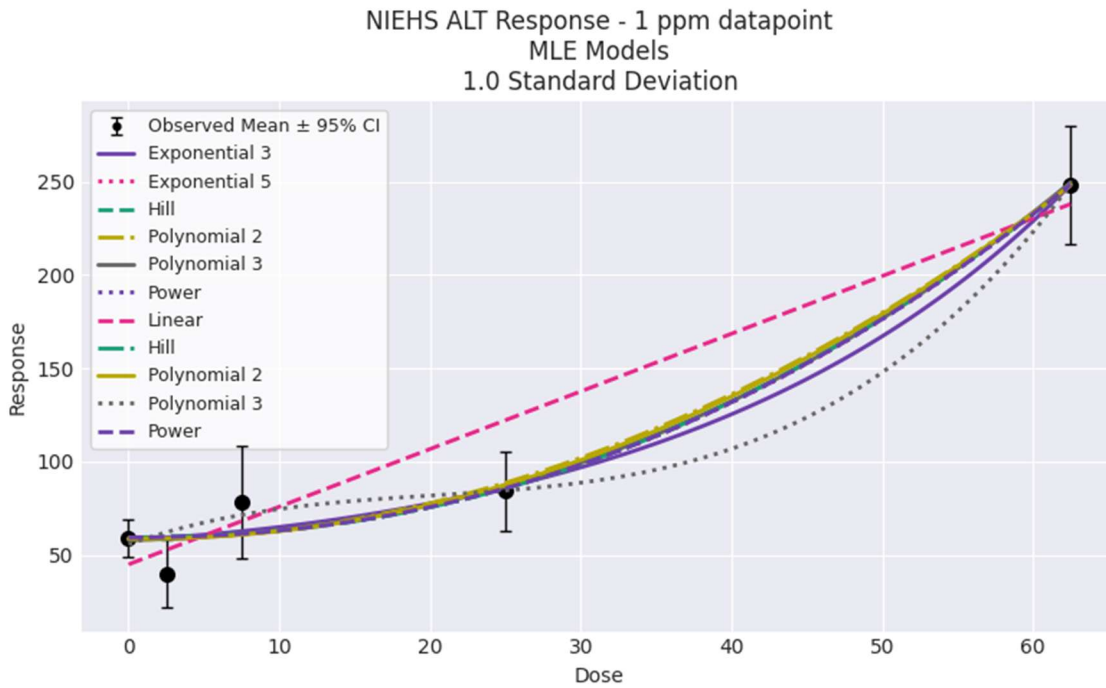
### Maximum Likelihood Approach

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Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	12.706	21.207	36.141	0.159	231.103	0.045	-0.224	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Exponential 5	18.837	22.555	32.365	0.046	233.414	-0.071	-0.165	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Hill	18.419	22.611	35.401	0.046	233.426	-0.076	-0.162	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Polynomial 2	13.456	20.858	23.94	0.251	229.527	0.082	-0.473	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Polynomial 3	11.974	21.541	21.987	0.047	233.388	0.115	-0.269	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Power	15.063	22.553	35.445	0.136	231.414	-0.071	-0.166	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Linear	7.164	9.077	12.135	<0.001	243.653	1.406	0.628	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Hill	18.352	22.611	35.402	0.046	233.426	-0.076	-0.162	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Polynomial 2	13.477	21.544	30.803	0.13	231.509	0.008	-0.36	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)

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Polynomial 3	3.16	12.067	12.317	0.083	232.432	0.432	0.563	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05) BMD/BMDL ratio > 3.0
Power	15.063	22.553	35.445	0.136	231.414	-0.071	-0.166	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)



**Selected Model**

No model was selected as a best-fitting model.

**2.2.2.5 Serum ALT with 1 ppm group removed, BMR: 1 SD; Normal Distribution + Nonconstant Variance Dataset**

**Dataset**

**Name:** NIEHS ALT Response - 1 ppm datapoint

Dose	N	Mean	Std. Dev.
0	8	58.9	11.8
2.5	2	40	2
7.5	3	78.3	12.2
25	5	84.2	17.3
62.5	7	248.6	34.2

Test 1 Dose Response: <0.0001  
Test 2 Homogeneity of Variance: 0.0007  
Test 3 Variance Model Selection: 0.1549

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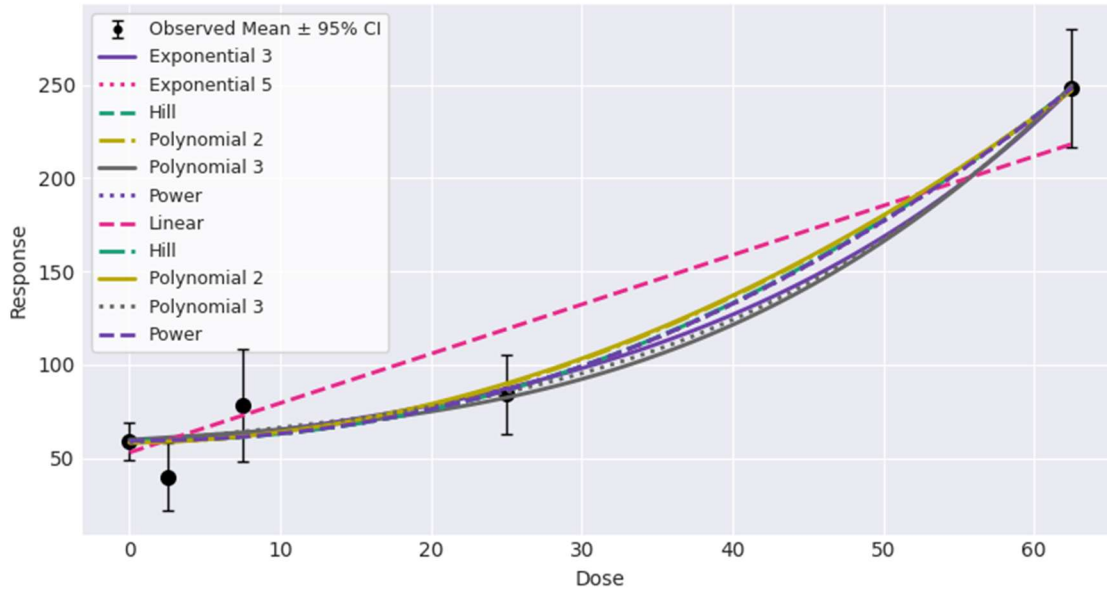
### Settings

Setting	Value
<b>BMR</b>	1.0 Standard Deviation
<b>Distribution</b>	Normal + Nonconstant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	8.615	15.799	27.239	0.004	226.387	0.128	1.852	<b>Questionable</b> Goodness of fit p-value < 0.1
Exponential 5	13.658	18.534	25.95	<0.001	229.156	-0.082	-0.277	<b>Questionable</b> Goodness of fit p-value < 0.1
Hill	14.819	18.668	28.384	<0.001	229.189	-0.092	-0.267	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 2	9.271	16.773	20.386	0.003	227.246	0.095	-0.646	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 3	7.483	19.125	27.214	<0.001	228.573	-0.186	0.236	<b>Questionable</b> Goodness of fit p-value < 0.1
Power	11.545	18.533	28.356	0.003	227.156	-0.082	-0.277	<b>Questionable</b> Goodness of fit p-value < 0.1
Linear	3.719	5.183	7.667	<0.001	237.884	1.215	0.513	<b>Questionable</b> Goodness of fit p-value < 0.1
Hill	13.859	18.691	28.395	<0.001	229.195	-0.093	-0.265	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 2	9.262	16.336	16.674	0.003	227.254	0.134	-0.722	<b>Questionable</b> Goodness of fit p-value < 0.1
Polynomial 3	2.08	15.362	15.68	0.001	227.942	0.174	1.698	<b>Questionable</b> Goodness of fit p-value < 0.1 BMD/BMDL ratio > 3.0
Power	11.545	18.533	28.356	0.003	227.156	-0.082	-0.277	<b>Questionable</b> Goodness of fit p-value < 0.1

NIEHS ALT Response - 1 ppm datapoint  
MLE Models  
1.0 Standard Deviation



### Selected Model

No model was selected as a best-fitting model.

### 2.2.2.6 Serum ALT with 1 ppm group removed, BMR: 1 SD; Lognormal Distribution + Constant Variance Dataset

#### Dataset

Name: NIEHS ALT Response - 1 ppm datapoint

Dose	N	Mean	Std. Dev.
0	8	58.9	11.8
2.5	2	40	2
7.5	3	78.3	12.2
25	5	84.2	17.3
62.5	7	248.6	34.2

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.2307

Test 3 Variance Model Selection: 0.2307

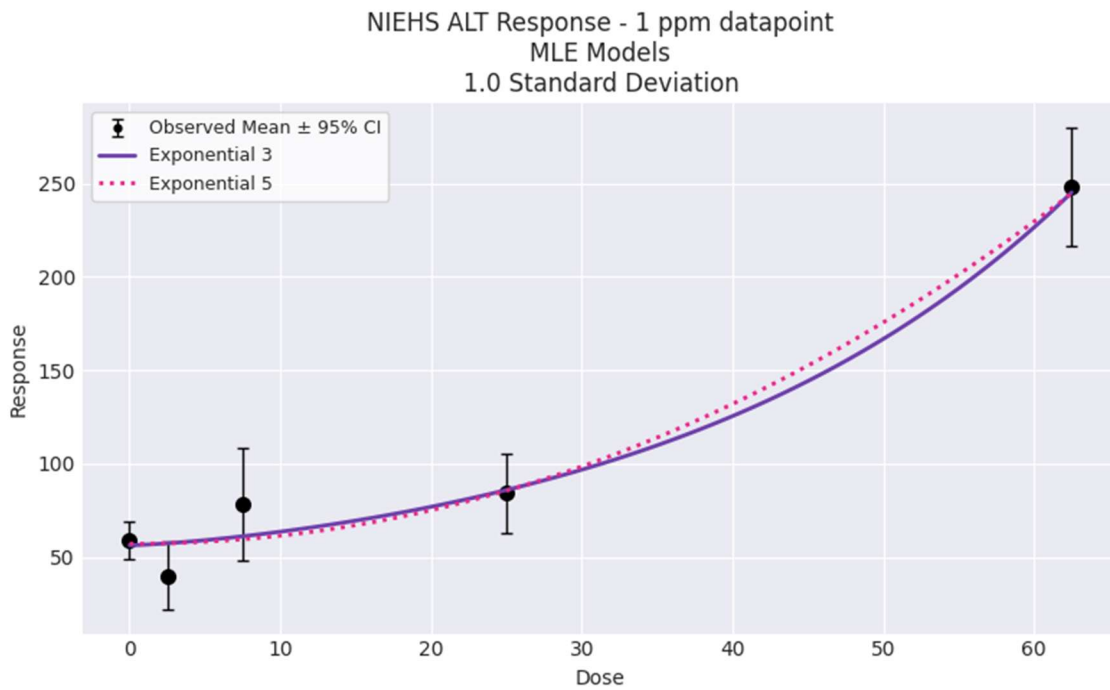
#### Settings

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Lognormal + Constant variance
Adverse Direction	Up (↑)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

### Maximum Likelihood Approach

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Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	8.209	14.687	25.171	0.001	226.545	5.761	24.123	<b>Questionable</b>  Residual near BMD  > 2.0 Residual at control > 2.0 Goodness of fit p-value < 0.1
Exponential 5	14.606	17.226	23.698	<0.001	229.365	3.868	-2.689	<b>Questionable</b>  Residual near BMD  > 2.0 Residual at control > 2.0 Goodness of fit p-value < 0.1



**Selected Model**

No model was selected as a best-fitting model.

**2.2.2.7 Serum ALT with outlier removed from 1 ppm group, BMR: 1 SD; Normal Distribution + Constant Variance Dataset**

**Dataset**

**Name:** NIEHS ALT response - remove 1ppm outlier animal

Dose	N	Mean	Std. Dev.
0	8	58.9	11.8
0.25	4	59	31.6
2.5	2	40	2
7.5	3	78.3	12.2

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25	5	84.2	17.3
62.5	7	248.6	34.2

Test 1 Dose Response: <0.0001  
 Test 2 Homogeneity of Variance: 0.0012  
 Test 3 Variance Model Selection: 0.0012

### Settings

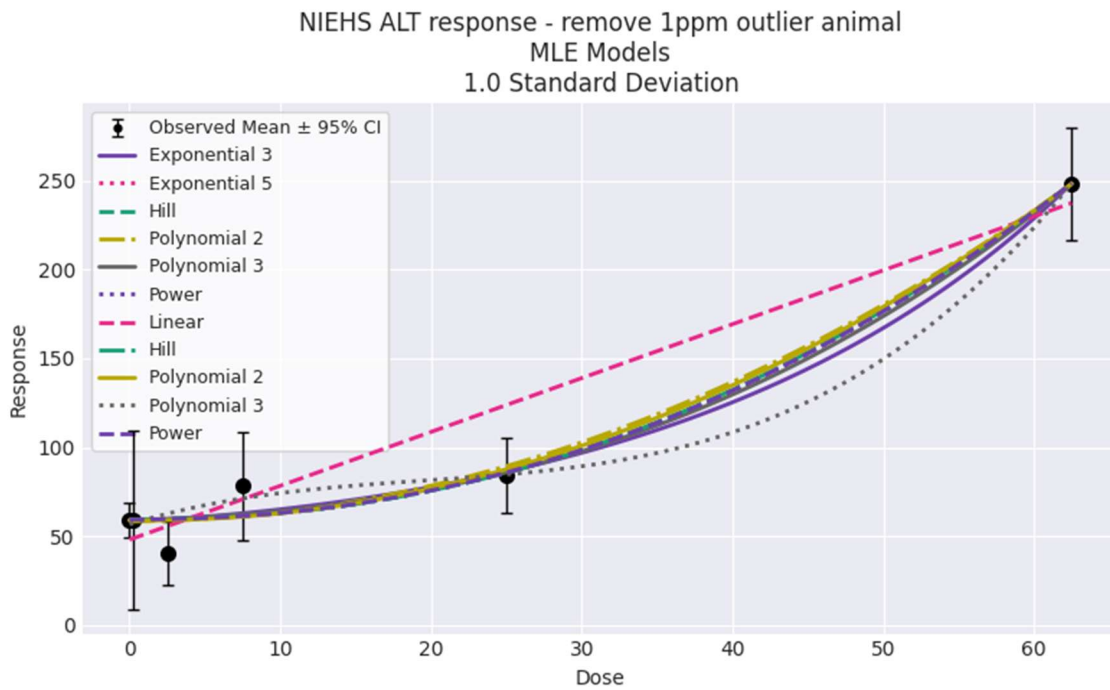
Setting	Value
<b>BMR</b>	1.0 Standard Deviation
<b>Distribution</b>	Normal + Constant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	13.318	21.869	36.534	0.348	269.484	0.029	-0.212	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Exponential 5	19.009	22.973	32.926	0.167	271.768	-0.054	-0.16	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Hill	19.065	23.023	35.573	0.166	271.78	-0.057	-0.157	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Polynomial 2	13.985	20.991	21.425	0.294	269.898	0.087	-0.521	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Polynomial 3	12.606	22.644	23.113	0.179	271.625	-0.021	-0.167	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Power	15.479	22.973	35.619	0.31	269.768	-0.054	-0.16	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Linear	7.463	9.329	12.228	0.001	282.174	1.094	0.465	<b>Questionable</b> Goodness of fit p-value < 0.1 Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Hill	18.491	23.023	35.574	0.166	271.78	-0.057	-0.156	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)

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Polynomial 2	14.041	22.087	30.945	0.3	269.853	0.001	-0.343	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Polynomial 3	3.419	14.825	46.719	0.257	270.902	0.302	0.568	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05) BMD/BMDL ratio > 3.0
Power	20.883	22.973	25.639	0.31	269.768	-0.054	-0.16	<b>Questionable</b> Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)



**Selected Model**

No model was selected as a best-fitting model.

**2.2.2.8 Serum ALT with outlier removed from 1 ppm group, BMR: 1 SD; Normal Distribution + Nonconstant Variance Dataset**

**Dataset**

**Name:** NIEHS ALT response - remove 1ppm outlier animal

Dose	N	Mean	Std. Dev.
0	8	58.9	11.8
0.25	4	59	31.6
2.5	2	40	2
7.5	3	78.3	12.2
25	5	84.2	17.3
62.5	7	248.6	34.2

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Test 1 Dose Response: <0.0001  
Test 2 Homogeneity of Variance: 0.0012  
Test 3 Variance Model Selection: 0.0091

### Settings

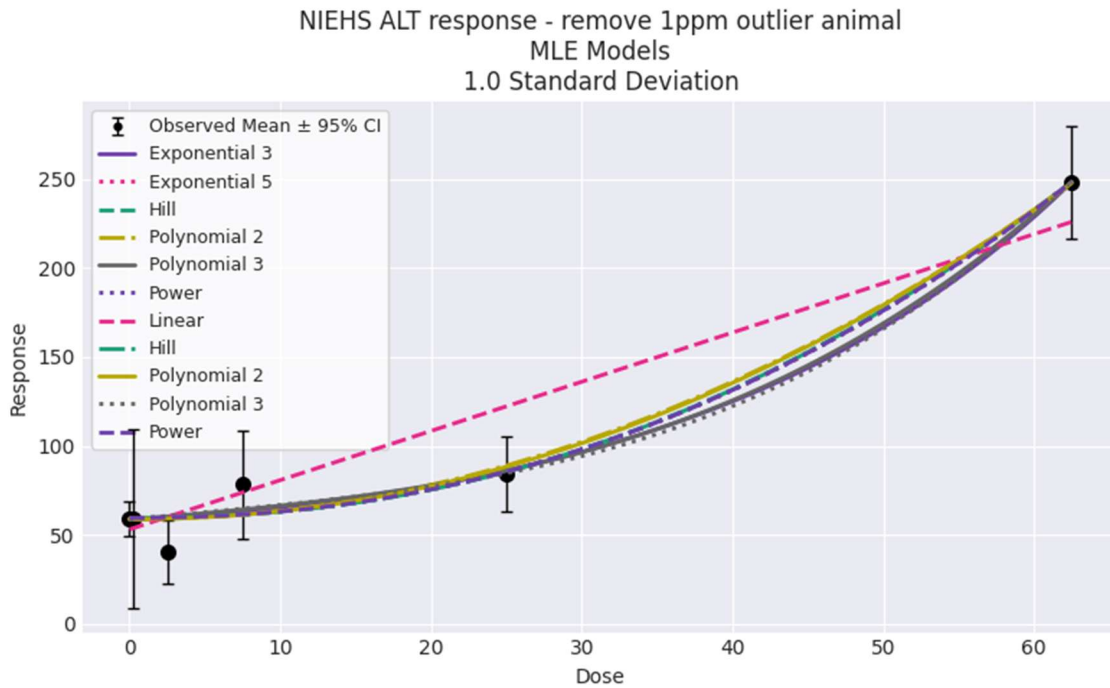
Setting	Value
<b>BMR</b>	1.0 Standard Deviation
<b>Distribution</b>	Normal + Nonconstant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

### Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	10.988	19.255	32.214	0.183	267.835	0.017	-0.208	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05)
Exponential 5	14.495	20.98	29.476	0.036	270.26	-0.09	-0.138	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5
Hill	16.929	21.056	31.999	0.036	270.277	-0.094	-0.133	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5
Polynomial 2	11.643	19.159	22.32	0.148	266.405	0.038	-0.506	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Control stdev. fit > 1.5
Polynomial 3	10.304	18.556	29.972	0.111	267.632	0.084	-0.196	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05)
Power	13.468	20.981	32.026	0.084	268.259	-0.09	-0.137	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5
Linear	5.057	6.777	9.494	<0.001	279.038	0.892	0.345	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5

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Hill	17.416	21.074	32.007	0.036	270.277	-0.095	-0.129	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5
Polynomial 2	11.657	19.626	28.511	0.079	268.393	0.001	-0.43	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5
Polynomial 3	2.781	18.978	19.37	0.052	269.529	0.067	-0.044	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 BMD/BMDL ratio > 3.0
Power	13.469	20.978	32.026	0.084	268.259	-0.09	-0.138	<b>Questionable</b> Nonconstant variance test failed (Test 3 p-value < 0.05) Goodness of fit p-value < 0.1 Control stdev. fit > 1.5



**Selected Model**

No model was selected as a best-fitting model.

**2.2.2.9 Serum ALT with outlier removed from 1 ppm group, BMR: 1 SD;  
Lognormal Distribution + Constant Variance Dataset**

**Dataset**

**Name:** NIEHS ALT response - remove 1ppm outlier animal

Dose	N	Mean	Std. Dev.
0	8	58.9	11.8
0.25	4	59	31.6
2.5	2	40	2
7.5	3	78.3	12.2
25	5	84.2	17.3
62.5	7	248.6	34.2

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.0053

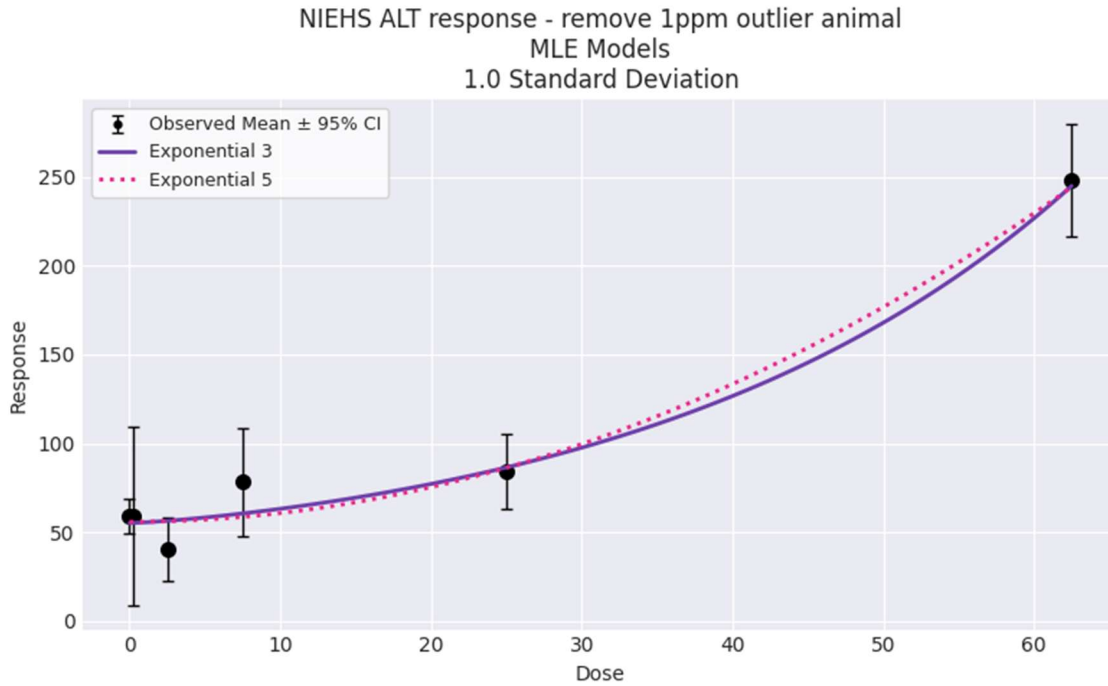
Test 3 Variance Model Selection: 0.0053

**Settings**

Setting	Value
<b>BMR</b>	1.0 Standard Deviation
<b>Distribution</b>	Lognormal + Constant variance
<b>Adverse Direction</b>	Up (↑)
<b>Maximum Polynomial Degree</b>	3
<b>Confidence Level (one sided)</b>	0.95

**Maximum Likelihood Approach**

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	9.06	15.977	27.855	0.037	268.599	8.167	23.889	<b>Questionable</b>  Residual near BMD  > 2.0 Residual at control > 2.0 Goodness of fit p-value < 0.1 Constant variance test failed (Test 2 p-value < 0.05)
Exponential 5	12.374	18.12	24.092	0.01	271.262	6.69	-3.839	<b>Questionable</b>  Residual near BMD  > 2.0 Residual at control > 2.0 Goodness of fit p-value < 0.1 Constant variance test failed (Test 2 p-value < 0.05)



### Selected Model

No model was selected as a best-fitting model.

## 3 MODEL CITATION

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U.S. Environmental Protection Agency. (2025). BMDs Online (25.1; pybmds 25.1; bmdscore 25.1) [Software]. Available from <https://bmdsonline.epa.gov> . Accessed January 20, 2026.

## 4 REFERENCES

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