

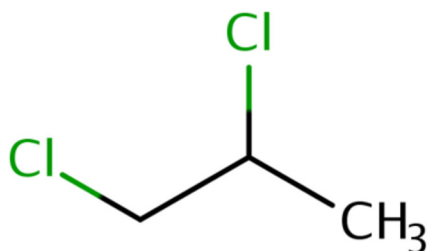


Draft Risk Evaluation for 1,2-Dichloropropane

Supplemental File Document:

Draft Benchmark Dose Modeling

CASRN 78-87-5



June 2026

BMDS Modeling – 12DCP endpoints

Dow Chemical 1983, 10610559, two-weeks: <https://bmdsonline.epa.gov/analysis/e3d2b488-e768-471a-8dc8-c4eabea9e103/x96xuvyl8kmv/#/>

1. **Olfactory mucosa degeneration, male rats** – not modeled, maximal response in all doses
2. **Olfactory mucosa degeneration, female rats** – not modeled, maximal response in all doses
3. **Nasal inflammation submucosa, male rats** – log-logistic model selected based on lowest BMDL (automated model selection logic). BMDs and BMDLs are below the lowest dose for all fitting models due to N = 5 (i.e., lowest possible observed response is 20% vs. 10% extra risk BMR used). Logistic and probit models had suspect dose response curves with control response overestimated by models; excluding these models would still result in the log-logistic model being selected based on lowest AIC.
4. **Nasal inflammation submucosa, female rats** – Hill model selected based on lowest BMDL (automated model selection logic). BMDs and BMDLs are below lowest dose for all fitting models due to reason noted in #3 above. Confidence interval for Hill model is very wide, spanning almost the entire dose range (owing to uncertainty in dose-response data with N = 5).
5. **Nasal inflammation exudate lumen, female rats** – Multistage 3 model selected based on lowest AIC.
6. **Olfactory mucosa degeneration, male mice** – not modeled, maximal response only in highest dose group
7. **Olfactory mucosa degeneration, female mice** – log-logistic model selected based on lowest BMDL, increased confidence in model results given BMD > lowest dose group.

Dow Chemical 1988, 3065001/688893, 13-weeks:

<https://bmdsonline.epa.gov/analysis/cde3d6b8-3e28-4b48-a960-e5055affb668/a5a73db1aqus/#/>

1. **Nasal respiratory epithelium hyperplasia, male rats** – Hill model selected based on lowest AIC. Response pattern in low dose group (i.e., 2 out of 9 animals responding) result in most models returning BMDs and BMDLs lower than lowest dose. If logistic and probit models were excluded due to over-estimated control responses, multiple models (Weibull, Mst1, Gamma) return the same AIC value and would be selected based on lowest AIC.
2. **Nasal respiratory epithelium hyperplasia, female rats** – Gamma model selected based on lowest AIC. All models return BMDs and BMDLs lower than lowest dose due to response pattern (i.e., 3 out of 10 animals responding in lowest dose group).

Matsumoto 2013, 1936440, 13-weeks

1. **Nasal atrophy, male mice** – not modeled due to dose-response pattern: quasi-min/max dose-response between 24.83 (0/10) and 37.27 (7/10) dose groups.
2. **Nasal atrophy, female mice** - not modeled due to dose-response pattern: quasi-min/max dose-response between 20.55 (0/10) and 30.86 (7/10) dose groups.

Umeda 2010, 866309, 2-year non-cancer endpoints

1. **Respiratory epithelium squamous cell metaplasia, male rats** – not modeled due to high response rate in the lowest dose group (31/50, 62%)
2. **Respiratory epithelium inflammation, male rats** – not modeled due to high background response rate (20/50, 40%) and high response rate in the lowest dose group (35/50, 70%)
3. **Preneoplastic lesions combined, male rats** – not modeled due to high response rate in lowest dose group (31/50, 62%)
4. **Respiratory epithelium squamous cell metaplasia, female rats** – not modeled due to high response rate in the lowest dose group (15/50, 30%); to be consistent with above modeling, results *could be* generated for this endpoint, but BMDs and BMDLs are guaranteed to be lower than lowest dose group
5. **Respiratory epithelium inflammation, female rats** – not modeled due to high background response rate (10/50, 20%) and high response rate in lowest dose group (30/50, 60%)
6. **Preneoplastic lesions combined, female rats** – not modeled due to high response rate in lowest dose group (21/50, 42%)
- 7.

Umeda 2010, 866309, 2-year cancer endpoints: <https://bmdsonline.epa.gov/analysis/d1f8c900-155d-4f42-8688-747a09dd82d6/e7jvwxf11is/#/>

1. **Neoplastic lesions, combined, male rats** – Multistage-cancer 1st degree model selected

Umeda 2010, 866309, 2-year cancer endpoints:

<https://bmdsonline.epa.gov/analysis/b595e21d-63b9-4333-a43f-c18a15202265/c8vwcmfzxkijw/#/>

1. **Neoplastic lesions, combined, female rats** – Multistage-cancer 1st degree model selected

Matsumoto 2023, 1966440, 2-year: <https://bmdsonline.epa.gov/analysis/46084957-4a44-4228-b1c9-e1f5f0932ce0/tszsgvkovr09/#/>

1. Olfactory epithelium atrophy, male rats – not modeled due to high response rates essentially equal in mid dose group (19/50, 38%) and high dose group (20/50, 40%)
2. Submucosal gland respiratory metaplasia, male rats – Multistage 1 model selected based on lowest AIC
3. Olfactory epithelium respiratory metaplasia, female rats – not modeled due to high response rate in control group (32/50, 64%) and much lower response rate in low dose group (14/50, 28%)
4. Submucosal gland respiratory metaplasia, female rats – not modeled due to high response rate in control group (16/50, 32%) and similar, lower response rates in the low dose group (11/50, 22%) and mid dose group (13/50, 26%)

Matsumoto 2013, 1936440, 2-year: <https://bmdsonline.epa.gov/analysis/c09838a0-04dc-4a26-8046-a87e93dcc0bb/7o4nr8vvat95/#/>

1. Lung + Spleen tumors, male mice

Matsumoto 2013, 1936440, 2-year: <https://bmdsonline.epa.gov/analysis/70bfe36c-c932-49a9-b569-f6a07ed718c9/7o4nr8vvat95/#/>

1. Lung + Spleen + Harderian gland tumors, male mice

Matsumoto 2013, 1936440, 2-year: <https://bmdsonline.epa.gov/analysis/b6d66518-2a22-48b1-a797-a75d0cf7f286/7o4nr8vvat95/#/output>

1. Lung tumors, female mice

BMDs Modeling – 12DCP oral endpoints¹

Dow Chemical 1989, 3064999, gestational: <https://bmdsonline.epa.gov/analysis/4e800298-8d7e-4567-a89a-48376e4d9810/lkdw55lxxbg8/#/> (Example BMD analyses were run on these datasets to see how the BMDLs compared to the NOAELs, analyses all failed due to a variety of reasons, including poor model fit to control standard deviation, variance fit, global goodness-of-fit p-values)

1. Body weight gain, GD0-16: not modeled due to non-monotonicity in low dose and statistically significant response only observed in the high dose group (as recommended by BMD TG), recommend NOAEL/LOAEL approach
2. Terminal body weight: not modeled due to response only observed in the high dose group, recommend NOAEL/LOAEL approach

Kirk et al. 1995, 688858, gestational: <https://bmdsonline.epa.gov/analysis/8708e1a6-a3bc-4761-8c8b-d182252e5a4d/awrcn5ndlqcd/#/> (Example BMD analyses were run on these datasets to see how the BMDLs compared to the NOAELs)

1. Body weight gain, GD0-21: not modeled due to response only in the high dose group, recommend NOAEL/LOAEL approach. NOAEL would be identified as 30 mg/kg-day, which is lower than the BMDL (84.5 mg/kg-day) had modeling been used and the Poly2 model selected based on lowest AIC.

Kirk et al. 1995, 688858, gestational-rats: <https://bmdsonline.epa.gov/analysis/a03f10c0-0067-44a3-bfe1-f0ec881db640/5oyonvnyo1ib/#/>

1. Delayed skull ossification: Mst1 model selected based on lowest AIC

Kirk 1995, 688858, gestational: Not modeled due to extreme non-monotonicity across dose groups: ~140% increases in body weight gain in low and mid dose groups, 440% decrease in body weight gain in high dose group. Recommend NOAEL/LOAEL approach.

Kirk 1995, 688858, gestational-rabbits: <https://bmdsonline.epa.gov/analysis/b1c311ff-7d0f-4d7e-8069-459b63a92916/y1yxqfu8qoe/#/>

¹ Unless noted otherwise, constant variance model results are presented.

1. Red blood cells: Poly3 model selected based on lowest AIC (dose response borders on only having a response in the highest dose group, possibly consider NOAEL/LOAEL approach)
2. Hemoglobin: response only observed in high dose group, recommend NOAEL/LOAEL approach; if modeling was used, Poly3 model would be selected based on lowest AIC
3. Hematocrit: Power model selected based on lowest AIC (dose response borders on only having a response in the highest dose group, possibly consider NOAEL/LOAEL approach)
4. Platelets: response at high dose is just slightly lower than BMR (model estimated mean + model estimated standard deviation), but only by a very small amount. For example, if modeling was used, the BMD (151.47 mg/kg-day) for the power model would just barely exceed highest dose group (150 mg/kg-day); possibly consider NOAEL/LOAEL approach given uncertainty. Otherwise, power model would be selected based on lowest AIC.
5. White blood cells: response only observed in high dose group, recommend NOAEL/LOAEL
6. Reticulocytes: non-constant variance model used; Poly3 model selected based on lowest AIC

Kirk 1995, 688858, gestational-rabbits: <https://bmdsonline.epa.gov/analysis/8c4f6f9a-341e-4d7c-a2d0-40820b4e077a/w23t3oa68ogc/#/>

1. Delayed skull ossification: response in highest dose (0.04) lower than BMR (0.05), recommend using NOAEL/LOAEL approach for this endpoint. There are several models that fit the data, but the BMDs are all above the highest dose and uncertainty in results is increased due to extrapolation beyond observed dose range

Bruckner 1989, 67910, 13 weeks: modeling not possible on this data given that Ns were only reported as 6-8 animals per dose group. BMD modeling requires precise dose-group-specific Ns. Recommend NOAEL/LOAEL approach for these endpoints.

NTP 1986, 67963, 13 week: <https://bmdsonline.epa.gov/analysis/b5486923-b12a-4738-9987-9f522e953c6a/2rtxx6qux9ke/#/>

1. Decreased body weight: non-monotonic response in low dose, no models return adequate fit (global goodness-of-fit p-value < 0.10, constant and non-constant variance models fail), recommend NOAEL/LOAEL approach.

NTP 1986, 67963, 2-year: <https://bmdsonline.epa.gov/analysis/c63853a0-dd84-41d3-b1bc-7f3caa80ceaa/lq652u83d52i/#/> (this dataset has only 3 dose groups and thus fewer models can be fit to the data and still return a goodness-of-fit p-value due to # dose groups vs # model parameters)

1. Mammary gland tumors, female rats: response in high dose (5/50) less than BMR (10% BMR, this is higher than 5/50 due to 1/50 response in control group:

$P(d) = ER(1 - P(0)) + P(0) = 0.10(1 - 0.018) + 0.018 = 0.116$). You could use the cancer slope factor regardless of uncertainty due to extrapolation beyond dose range or drop the BMR to be within the dose range (I am unsure about this approach though).

NTP 1986, 67963, 2 year: <https://bmdsonline.epa.gov/analysis/764d7a4b-f5af-4c2b-b617-a6f45b77ff99/n4ytnkuq0vbt/#/> (this dataset has only 3 dose groups and thus fewer models can be fit to the data and still return a goodness-of-fit p-value due to # dose groups vs # model parameters)

1. Clear cell foci (only Mst1, Mst2, logistic, and probit models considered b/c all other models did not return global goodness-of-fit p-values): Mst2 model selected based on lowest AIC
2. Necrosis (combined; Hill and log-probit models did not return global goodness-of-fit p-values and were not considered): Weibull model selected based on lowest AIC (note that typically data like this would not be modeled due to response only observed in the high dose group; however, in this case, the BMR is very close to the observed response in the high dose group and uncertainty may be reduced

NTP 1986, 67963, 2 year: <https://bmdsonline.epa.gov/analysis/7baabff9-54d0-4269-9306-6592a68db421/587tlptcy4yt/#/> (this dataset has only 3 dose groups and thus fewer models can be fit to the data and still return a goodness-of-fit p-value due to # dose groups vs # model parameters)

1. Liver tumors, female mice: Mst1 model selected based on cancer model selection workflow (Mst2 model had b2 parameter on bound [i.e., estimated to be 0] and Mst1 model thus selected based on lowest BMDL; note that because b2 parameter = 0 for Mst2 model, it returned identical results as Mst1 model)

NTP 1986, 67963, 2 year: <https://bmdsonline.epa.gov/analysis/18bfccfd-4728-4673-8748-d3d4dec7c634/o33buko02wtk/#/> (this dataset has only 3 dose groups and thus fewer models can be fit to the data and still return a goodness-of-fit p-value due to # dose groups vs # model parameters)

1. Liver tumors, male mice: Mst1 model selected based on cancer model selection workflow (no model had a parameter estimated on a bound [i.e., estimated to be 0] and Mst1 model thus selected based on lowest AIC). Response at BMR is lower than response at BMD, consider raising BMR to response at low dose to avoid underestimation of cancer slope factor.

NTP 1986, 67963, 2 year: <https://bmdsonline.epa.gov/analysis/82cad661-d1fa-447b-862c-8079db5f135b/1hz99uad2h8x/#/> (this dataset has only 3 dose groups and thus fewer models can be fit to the data and still return a goodness-of-fit p-value due to # dose groups vs # model parameters)

1. Hepatocytomegaly (only Mst1, Mst2, weibull, logistic, and probit models considered b/c all other models did not return global goodness-of-fit p-values): Weibull model selected based on lowest AIC
2. Necrosis (only Mst1, logistic, and probit models considered b/c all other models did not return global goodness-of-fit p-values): probit model selected based on lowest AIC

Kirk 1995, 688858-rabbits: <https://bmdsonline.epa.gov/analysis/69f03d26-3e5c-4fbf-9495-5024e66faee3/95xavtigriek/#/> (response only observed in high dose group, modeling results generated for comparison, recommend NOAEL/LOAEL approach)

1. Fetal body weight: Power model would be selected based on lowest AIC if modeling results were used.

Decreased body weight

NTP, 1986 67963

Decreased body weight

1,2-DCP

Report Generated: 2026-Jan-26 16:01 UTC

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

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

Session for Decreased body weight

Dataset

Name: Decreased body weight

Dose (mg/kg-day)	N	Mean (g)	Std. Dev. (g)
0	10	300.1	24.7
43	10	334.3	24.3
89.3	10	308.2	26.2
179	10	297.7	12.7
357	10	252.4	46.5

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.0031

Test 3 Variance Model Selection: 0.0031

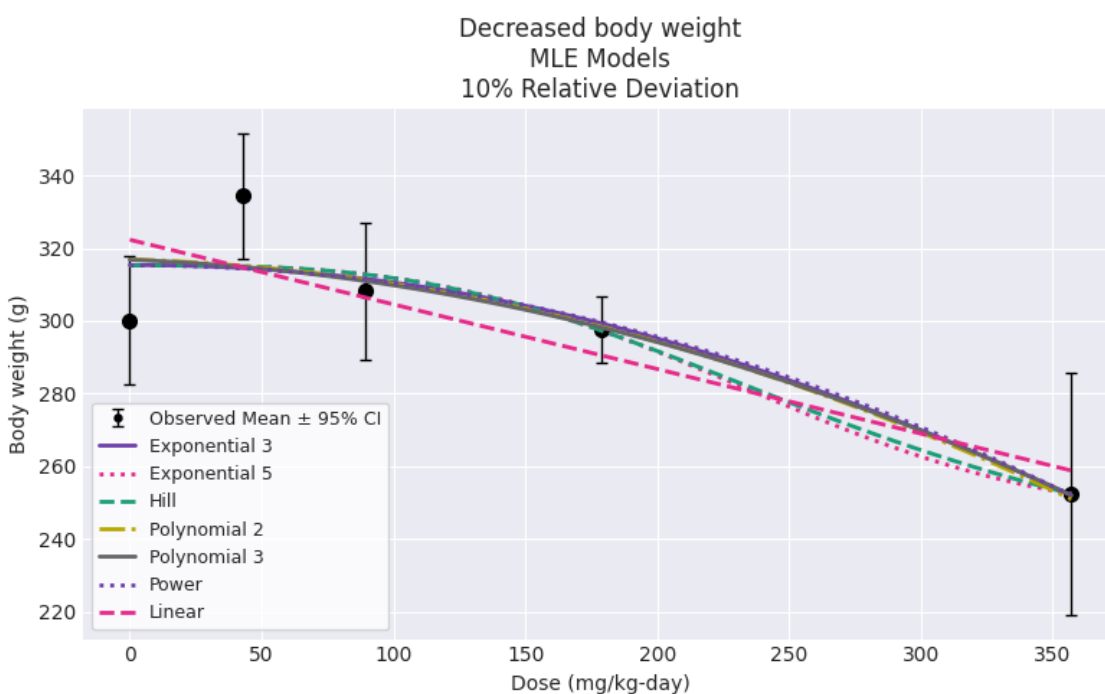
Settings

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	175.267	249.446	347.535	0.021	489.192	-1.62	-0.164	Questionable Goodness of fit p-value < 0.1 Constant variance test failed (Test 2 p-value < 0.05)
Exponential 5	163.191	226.045	346.682	0.006	491.043	-1.612	0.042	Questionable Goodness of fit p-value < 0.1 Constant variance test failed (Test 2 p-value < 0.05)
Hill	161.509	228.315	315.441	0.006	491.037	-1.614	0.049	Questionable Goodness of fit p-value < 0.1 Constant variance test failed (Test 2 p-value < 0.05)

Polynomial 2	178.488	240.772	245.756	0.018	489.51	-1.747	-0.072	Questionable Goodness of fit p-value < 0.1 Constant variance test failed (Test 2 p-value < 0.05)
Polynomial 3	178.396	241.431	246.429	0.017	489.516	-1.762	-0.047	Questionable Goodness of fit p-value < 0.1 Constant variance test failed (Test 2 p-value < 0.05)
Power	177.582	252.656	346.074	0.02	489.231	-1.615	-0.197	Questionable Goodness of fit p-value < 0.1 Constant variance test failed (Test 2 p-value < 0.05)
Linear	140.031	181.273	261.779	0.01	490.874	-2.275	0.74	Questionable 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.

Session for Decreased body weight

Dataset

Name: Decreased body weight

Dose (mg/kg-day)	N	Mean (g)	Std. Dev. (g)
0	10	300.1	24.7
43	10	334.3	24.3
89.3	10	308.2	26.2
179	10	297.7	12.7
357	10	252.4	46.5

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.0031

Test 3 Variance Model Selection: 0.0031

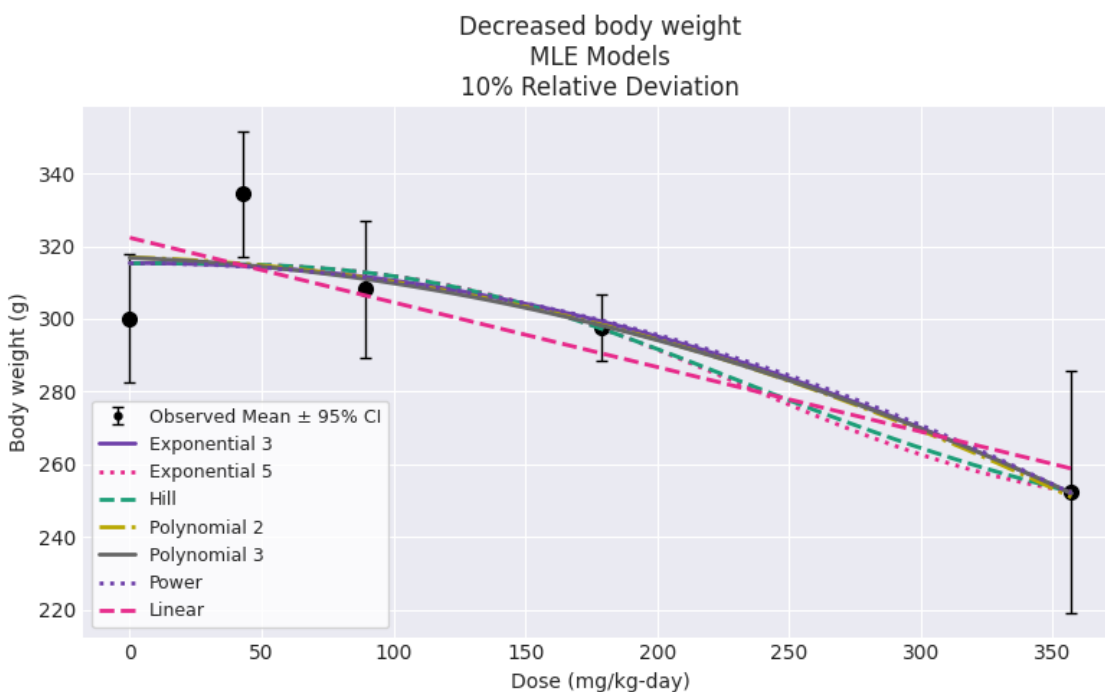
Settings

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

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Linear	140.031	181.273	261.779	0.01	490.874	-2.275	0.74	Questionable Residual at control > 2.0 Goodness of fit p-value < 0.1 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.

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.

Delayed skull ossification

Kirk 1995

Delayed skull ossification

1,2-DCP

Report Generated: 2026-Jan-26 16:01 UTC

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

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

Session for Delayed skull ossification

Dataset

Name: Delayed skull ossification

Dose (mg/kg-day)	N	Incidence
0	149	0
15	146	0
50	131.4	1.85
150	97.4	4.17

Settings

Setting	Value
BMR	5% 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
Hill	-	-	-	0.998	59.885	-0.002	-	Unusable Did not successfully execute.
LogLogistic	103.783	160.118	-	0.773	58.635	-0.002	-0.139	Viable BMD/highest dose ratio > 1.0
Multistage 1 ^a	107.164	196.047	-	0.888	57.09	-0.002	0.222	Recommended - Lowest AIC BMD/highest dose ratio > 1.0
Multistage 2	107.717	160.33	-	0.735	58.808	-0.002	-0.113	Viable BMD/highest dose ratio > 1.0
Multistage 3	107.707	160.33	-	0.735	58.808	-0.002	-0.113	Viable BMD/highest dose ratio > 1.0
Weibull	104.373	160.059	-	0.771	58.643	-0.002	-0.138	Viable BMD/highest dose ratio > 1.0
Logistic	126.911	156.268	247.031	0.334	60.435	-0.566	-0.15	Viable BMD/highest dose ratio > 1.0
LogProbit	99.653	160.656	-	0.819	58.46	-0.002	-0.153	Viable BMD/highest dose ratio > 1.0

Probit	122.396	155.863	254.776	0.368	60.2	-0.52	-0.187	Viable BMD/highest dose ratio > 1.0
Quantal Linear	107.252	196.047	-	0.888	57.09	-0.002	0.222	Viable BMD/highest dose ratio > 1.0

^a BMDS recommended best fitting model

Selected Model

No model was selected as a best-fitting model.

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.

Delayed skull ossification

Kirk 1995

Delayed skull ossification 1,2-DCP

Report Generated: 2026-Jan-26 14:01 UTC

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

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

Session for Delayed skull ossification

Dataset

Name: Delayed skull ossification

Dose (mg/kg-day)	N	Incidence
0	227.165	5.409
10	286.144	5.262
30	214.678	9.27
125	174.689	14.395

Settings

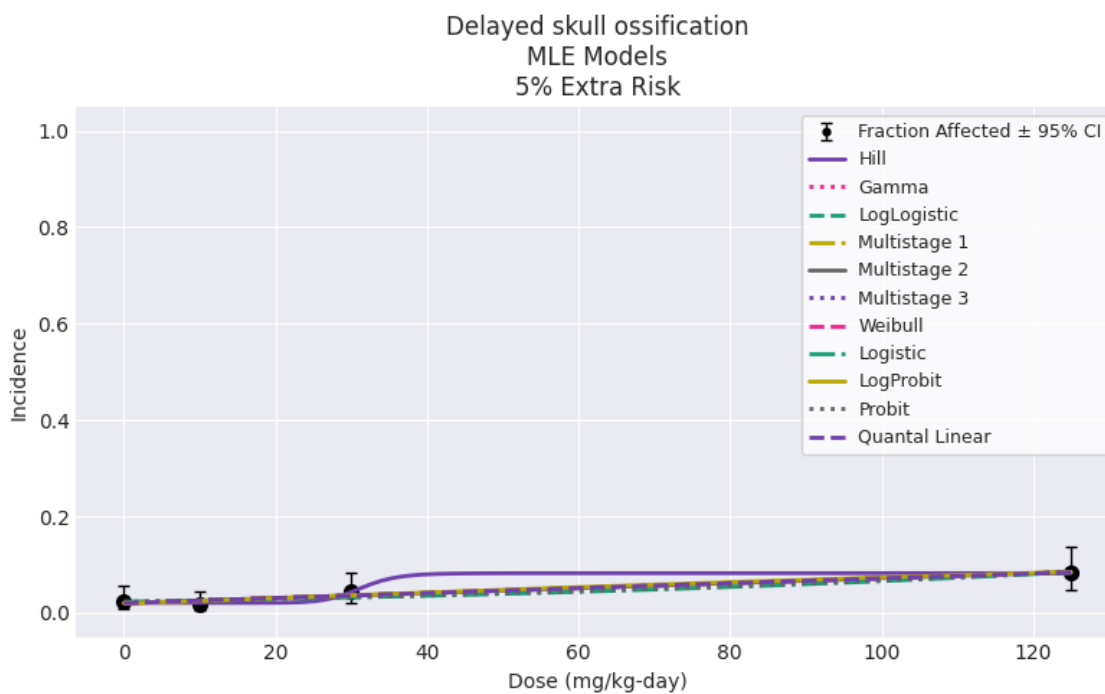
Setting	Value
BMR	5% Extra Risk
Confidence Level (one sided)	0.95
Maximum Multistage Degree	3

Maximum Likelihood Approach

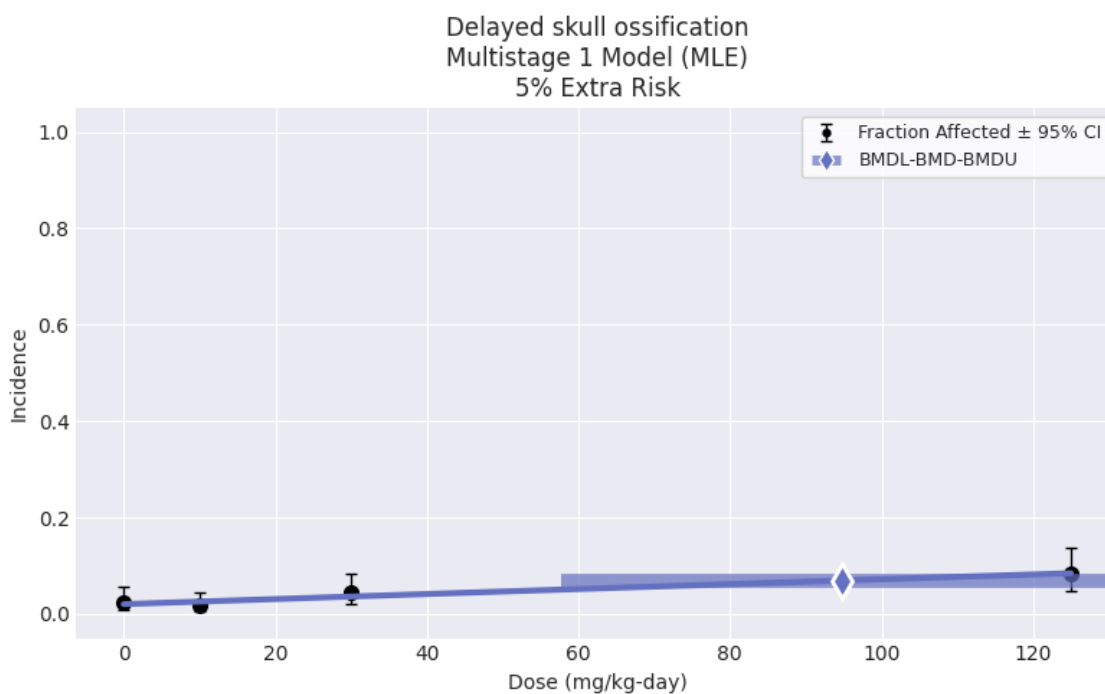
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	29.119	34.755	118.241	-	287.614	0.319	<0.001	Questionable Zero degrees of freedom; saturated model
Gamma	57.803	95.246	203.401	0.303	286.522	0.36	-0.108	Viable
LogLogistic	56.378	94.715	205.089	0.306	286.512	0.366	-0.107	Viable
Multistage 1 ^{ab}	57.786	94.75	203.533	0.589	284.526	0.387	-0.09	Recommended - Lowest AIC
Multistage 2	57.784	94.75	203.528	0.589	284.526	0.387	-0.09	Viable
Multistage 3	57.783	94.75	203.512	0.589	284.526	0.387	-0.09	Viable
Weibull	57.798	95.188	203.44	0.303	286.523	0.365	-0.105	Viable
Logistic	83.263	108.847	182.516	0.466	284.944	0.056	-0.111	Viable
LogProbit	48.927	91.457	251.271	0.342	286.357	0.364	-0.122	Viable
Probit	79.532	106.896	185.042	0.485	284.87	0.094	-0.121	Viable
Quantal Linear	57.788	94.75	203.53	0.589	284.526	0.387	-0.09	Viable

^a BMDS recommended best fitting model

^b User selected best fitting model; Mst1 model selected based on lowest AIC



Selected Model: Multistage 1



Multistage 1 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	5% 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	94.7495
BMDL	57.7856
BMDU	203.533
AIC	284.526
Log-Likelihood	-140.263
P-Value	0.58889
Overall d.f.	2
Chi²	1.05903

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0201965	no	0.0207681
b1	0.000541357	no	0.0228641

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	227.165	5.4087	4.58795	0.0201965	0.387108
10	286.144	5.2624	7.29278	0.0254864	-0.761616
30	214.678	9.2702	7.72428	0.0359807	0.56652
125	174.689	14.3953	14.7273	0.0843058	-0.0904165

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-139.716	4	-	-	-
Fitted model	-140.263	2	1.09351	2	0.578825
Reduced model	-145.927	1	12.4212	3	0.00607113

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.

Dow 1983 - 1,2-DCP

Dow Chemical 1983, 10610559

Two-week exposure, male and female rats, female mice

Report Generated: 2026-Jan-27 12:01 UTC

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

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

Session for Nasal inflammation submucosa - male rats

Dataset

Name: Nasal inflammation submucosa - male rats

Dose (mg/m3)	N	Incidence
0	5	0
15.5	5	1
45.6	5	3
151.1	5	3

Settings

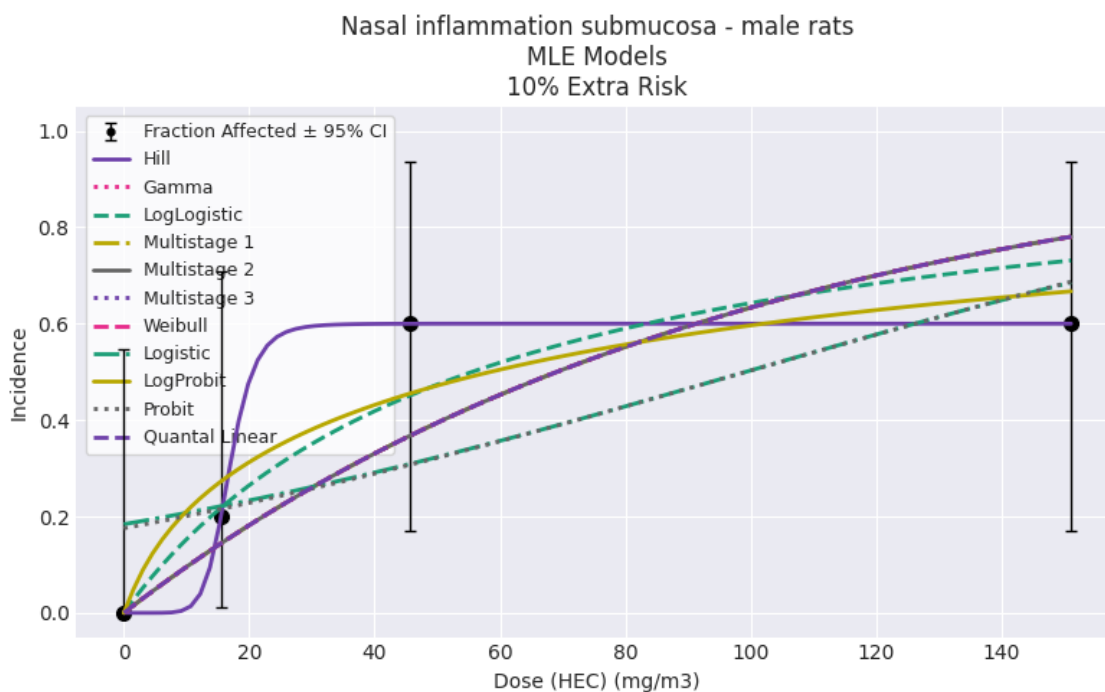
Setting	Value
BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Maximum Multistage Degree	3

Maximum Likelihood Approach

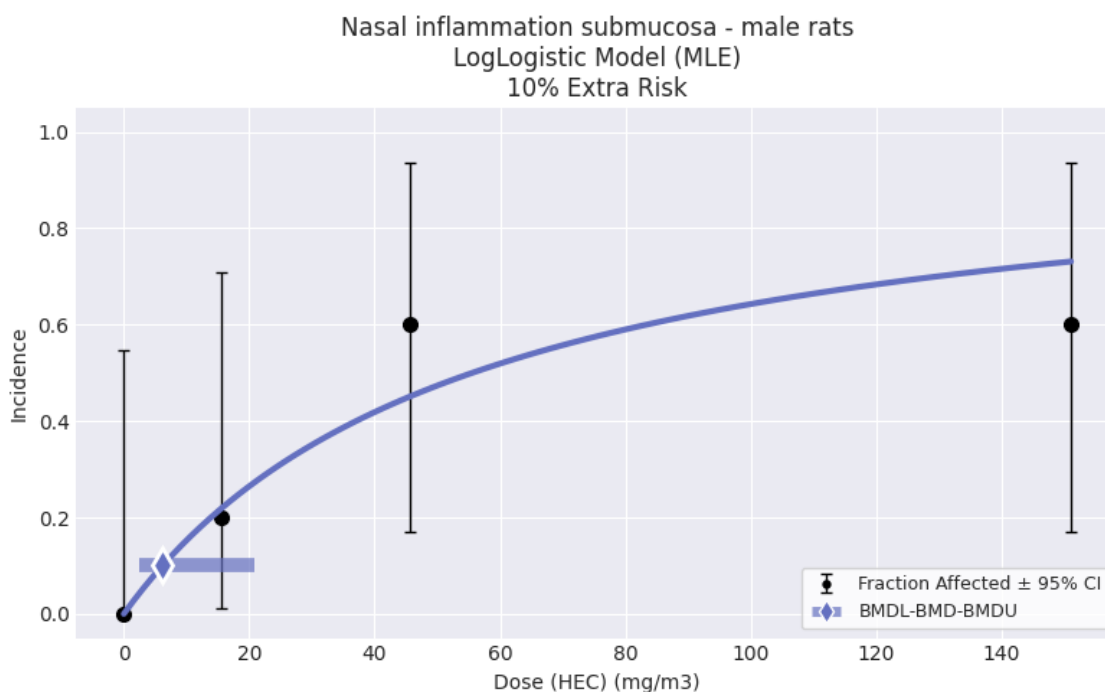
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	0	13.863	22.38	1.	24.464	-0.	-0.	Unusable BMDL does not exist
Gamma	5.788	10.5	53.594	0.523	22.513	-0.	0.356	Viable
LogLogistic ^{ab}	2.411	6.174	20.759	0.826	21.325	-0.	-0.	Recommended - Lowest BMDL lowest dose/BMDL ratio > 3.0
Multistage 1	5.788	10.5	41.655	0.523	22.513	-0.	0.356	Viable
Multistage 2	5.788	10.5	54.473	0.523	22.513	-0.	0.356	Viable
Multistage 3	5.788	10.5	56.141	0.523	22.513	-0.	0.356	Viable
Weibull	5.788	10.5	54.077	0.523	22.513	-0.	0.356	Viable
Logistic	16.757	31.459	179.842	0.193	26.469	-1.062	1.408	Viable
LogProbit	0	3.5	20.472	0.719	23.128	-0.	-0.	Unusable lowest dose/BMD ratio > 3.0 BMDL does not exist
Probit	17.154	30.115	162.779	0.196	26.391	-1.032	-0.085	Viable
Quantal Linear	5.788	10.5	41.655	0.523	22.513	-0.	0.356	Viable

^a BMDS recommended best fitting model

^b User selected best fitting model



Selected Model: LogLogistic



LogLogistic Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-18	18
a	0	-18	18
b	1	1	18

Modeling Summary:

BMD	6.17383
BMDL	2.41109
BMDU	20.7591
AIC	21.3248
Log-Likelihood	-9.66242
P-Value	0.826177
Overall d.f.	3
Chi²	0.896897

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
a	-4.01754	no	0.570388
b	1	yes	Not Reported

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	5	0	7.61499e-08	1.523e-08	-0.000275953
15.5	5	1	1.09056	0.218112	-0.0980701
45.6	5	3	2.25376	0.450751	0.670722
151.1	5	3	3.65568	0.731137	-0.661371

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-9.23213	4	-	-	-
Fitted model	-9.66242	1	0.860578	3	0.834929
Reduced model	-12.9489	1	7.43361	3	0.0592891

Session for Nasal inflammation submucosa - male rats

Dataset

Name: Nasal inflammation submucosa - male rats

Dose (mg/m3)	N	Incidence
0	5	0

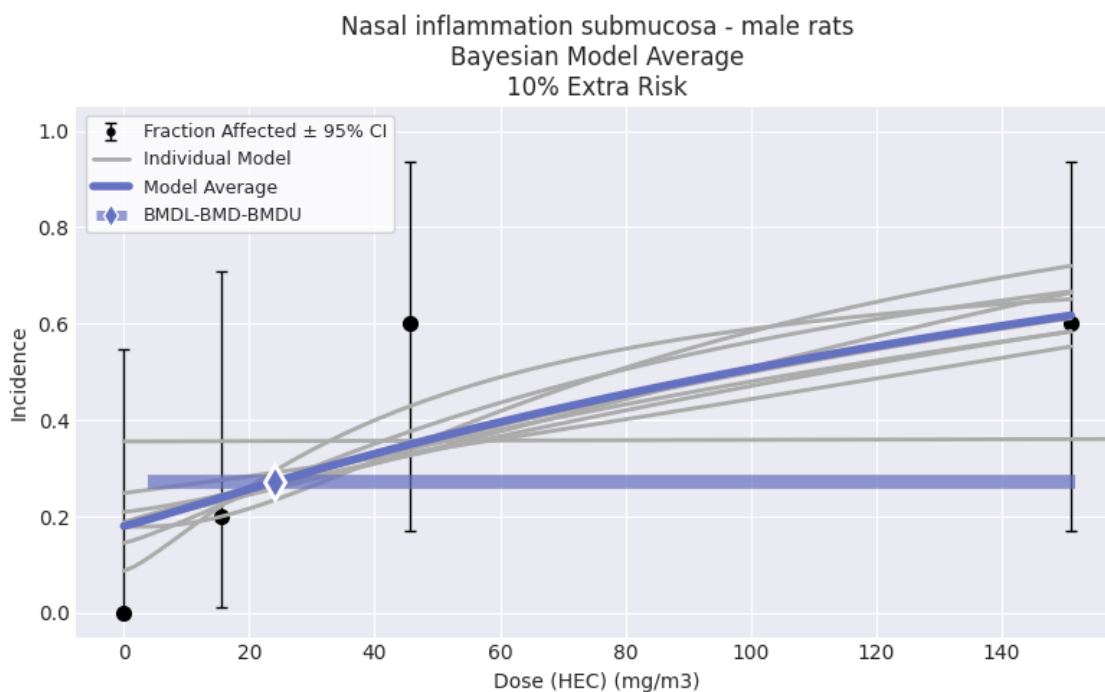
15.5	5	1
45.6	5	3
151.1	5	3

Settings

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

Bayesian Summary

Model	Prior Weights	Posterior Weights	BMDL	BMD	BMDU	Unnormalized Log Posterior Probability	Scaled Residual near BMD	Scaled Residual at Control
Hill	0.111	0.071	1.132	10.81	166.842	-21.449	-0.69	-0.118
Gamma	0.111	0.063	5.712	31.966	-	-11.018	-1.151	1.303
Logistic	0.111	0	27.749	1982.957	-	-7.101	-1.662	1.115
LogLogistic	0.111	0.113	1.947	16.794	76.909	-16.172	-0.922	-0.126
LogProbit	0.111	0.044	5.331	29.601	131.369	-16.32	-1.044	0.002
Multistage 2	0.111	0.076	9.731	26.689	71.1	-14.464	-1.064	-0.165
Probit	0.111	0.13	19.428	41.269	219.343	-9.127	-1.286	1.272
Quantal Linear	0.111	0.415	8.674	21.228	104.607	-9.442	-1.038	-0.2
Weibull	0.111	0.089	1.628	22.947	701.074	-15.749	-1.077	-0.232
Model Average	-	-	3.736	23.978	151.65	-	-	-



Session for Nasal inflammation submucosa - female rats

Dataset

Name: Nasal inflammation submucosa - female rats

Dose (mg/m3)	N	Incidence
0	5	0
11.7	5	1
34.4	5	1
113.9	5	4

Settings

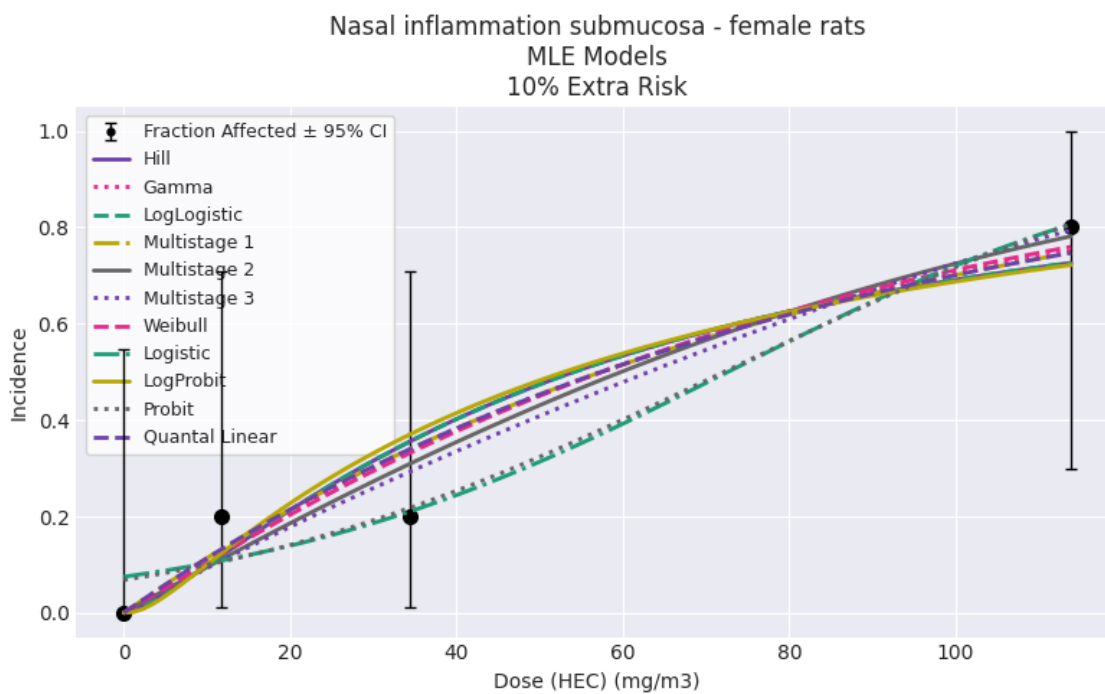
Setting	Value
BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Maximum Multistage Degree	3

Maximum Likelihood Approach

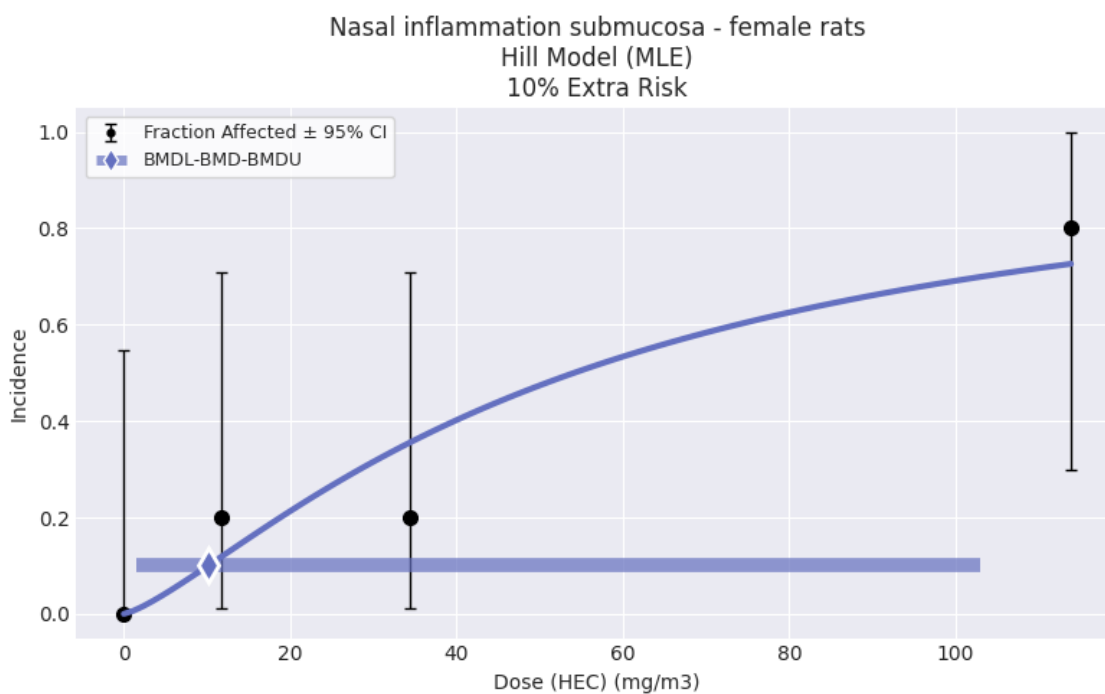
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill ^{ab}	1.507	10.142	103.054	0.611	20.01	-0.	0.567	Recommended - Lowest BMDL lowest dose/BMDL ratio > 3.0 BMD/BMDL ratio > 3.0
Gamma	4.567	9.112	27.546	0.697	19.745	-0.	0.488	Viable
LogLogistic	2.615	10.142	28.02	0.611	20.01	-0.	0.567	Viable lowest dose/BMDL ratio > 3.0 BMD/BMDL ratio > 3.0
Multistage 1	4.566	8.731	22.379	0.87	17.747	-0.	0.452	Viable
Multistage 2	4.609	10.557	48.681	0.706	19.663	-0.	0.637	Viable
Multistage 3	4.64	10.823	63.718	0.884	17.602	-0.	0.666	Viable
Weibull	4.571	9.653	29.49	0.695	19.736	-0.	0.541	Viable
Logistic	13.789	26.284	48.043	0.656	20.154	-0.637	-0.057	Viable
LogProbit	0.018	9.981	107.579	0.592	20.094	-0.	0.523	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0
Probit	13.576	24.256	43.239	0.656	20.11	-0.605	-0.097	Viable
Quantal Linear	4.566	8.731	22.379	0.87	17.747	-0.	0.452	Viable

^a BMDS recommended best fitting model

^b User selected best fitting model



Selected Model: Hill



Hill Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-18	18
v	0	-18	18
a	0	-18	18
b	1	1	18

Modeling Summary:

BMD	10.1423
BMDL	1.50697
BMDU	103.054
AIC	20.0099
Log-Likelihood	-8.00493
P-Value	0.610906
Overall d.f.	2
Chi ²	0.985624

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
v	1	yes	Not Reported
a	-5.23669	no	2.81817
b	1.31197	no	0.728832

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	5	0	7.61499e-08	1.523e-08	-0.000275953
11.7	5	1	0.590901	0.11818	0.566737
34.4	5	1	1.77761	0.355521	-0.726504
113.9	5	4	3.63149	0.726299	0.369628

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-7.50604	4	-	-	-
Fitted model	-8.00493	2	0.997794	2	0.6072
Reduced model	-12.2173	1	9.4225	3	0.0241703

Session for Nasal inflammation submucosa - female rats

Dataset

Name: Nasal inflammation submucosa - female rats

Dose (mg/m3)	N	Incidence
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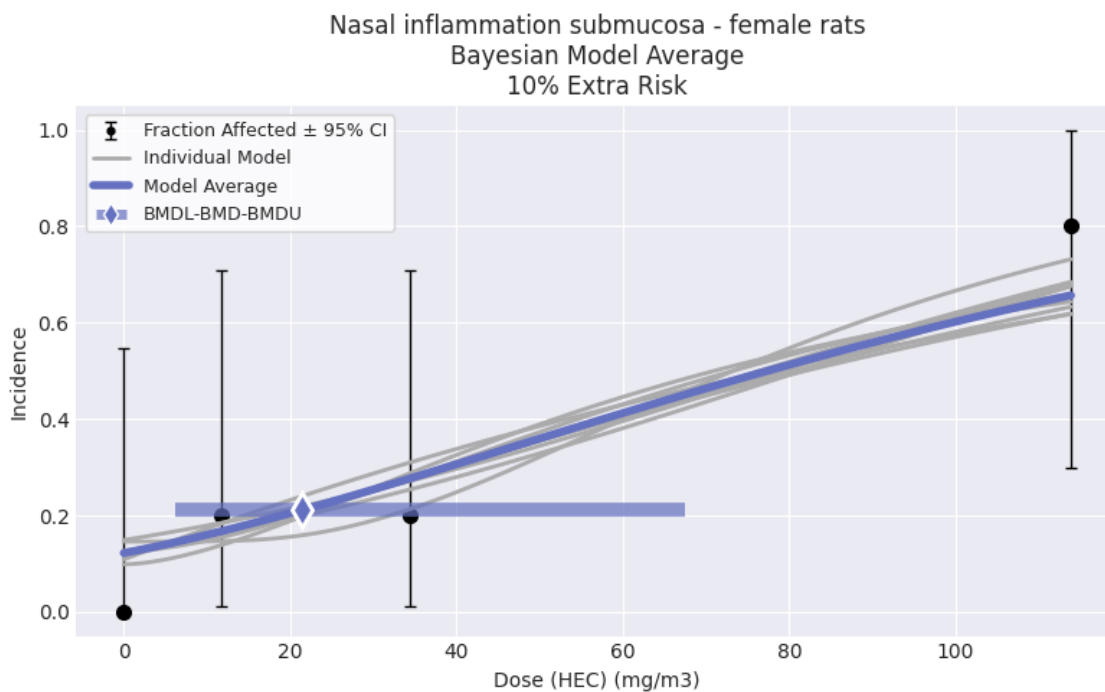
0	5	0
11.7	5	1
34.4	5	1
113.9	5	4

Settings

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

Bayesian Summary

Model	Prior Weights	Posterior Weights	BMDL	BMD	BMDU	Unnormalized Log Posterior Probability	Scaled Residual near BMD	Scaled Residual at Control
Hill	0.111	0.051	3.316	20.02	68.488	-19.988	-0.739	0.399
Gamma	0.111	0.055	5.829	21.438	90.476	-9.386	-0.844	0.205
Logistic	0.111	0.091	13.602	25.341	-	-10.032	-0.936	-0.36
LogLogistic	0.111	0.109	4.382	23.51	60.163	-14.38	-0.847	-0.387
LogProbit	0.111	0.083	10.774	37.421	76.834	-13.718	-0.925	-0.071
Multistage 2	0.111	0.124	7.751	20.689	45.224	-12.555	-0.81	0.221
Probit	0.111	0.142	13.999	24.969	72.534	-7.525	-0.849	-0.277
Quantal Linear	0.111	0.269	6.453	14.165	48.631	-7.858	-0.781	0.098
Weibull	0.111	0.076	3.351	21.49	95.19	-13.943	-0.838	0.212
Model Average	-	-	6.24	21.353	67.494	-	-	-



Session for Nasal inflammation exudate lumen - female rats

Dataset

Name: Nasal inflammation exudate lumen - female rats

Dose (mg/m3)	N	Incidence
0	5	0
11.7	5	1
34.4	5	1
113.9	5	5

Settings

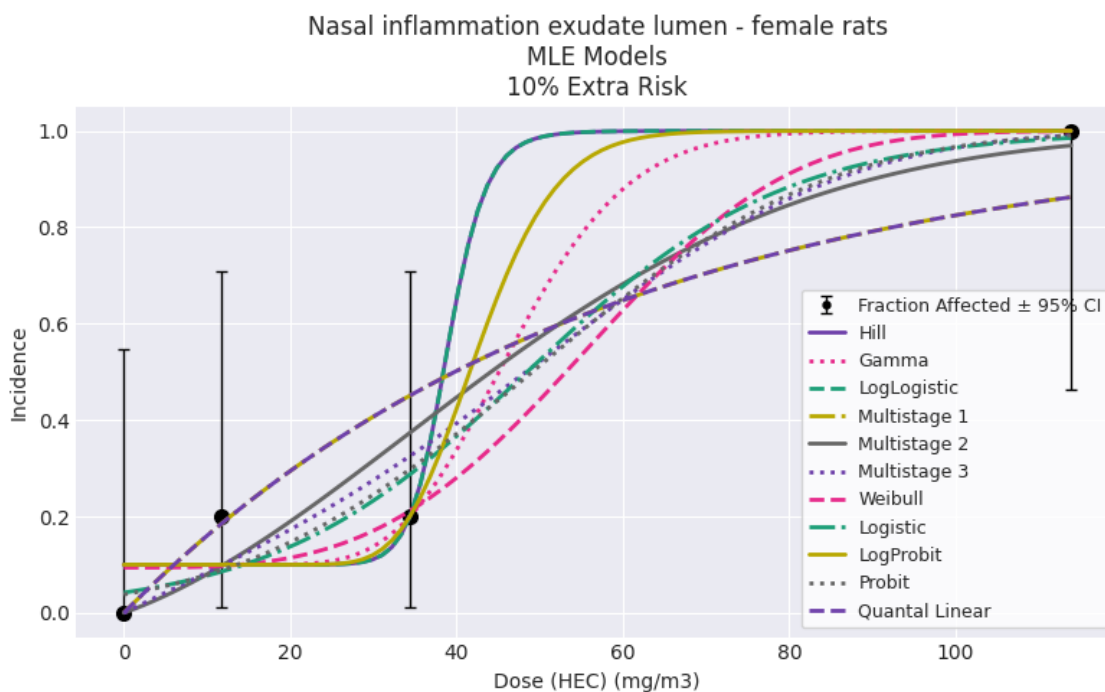
Setting	Value
BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Maximum Multistage Degree	3

Maximum Likelihood Approach

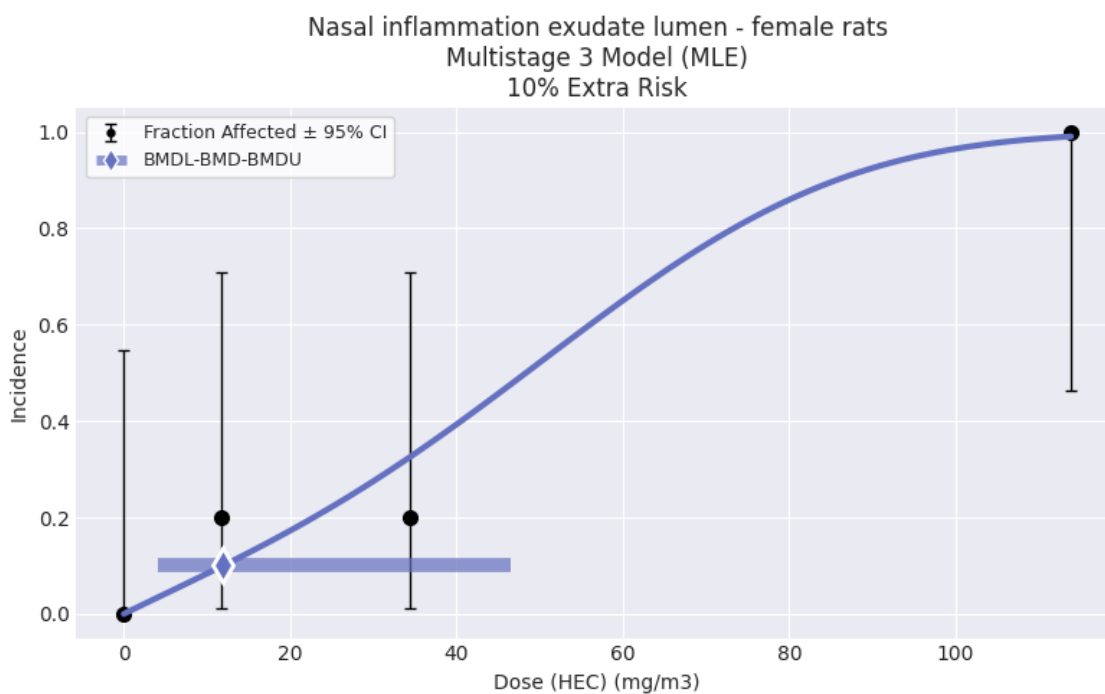
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	5.06	34.159	-	0.292	17.506	-0.745	-0.	Viable BMD/BMDL ratio > 3.0
Gamma	3.793	33.852	70.762	0.574	15.506	-0.745	-0.	Viable lowest dose/BMDL ratio > 3.0 BMD/BMDL ratio > 3.0
LogLogistic	5.062	34.159	94.851	0.292	17.506	-0.745	-0.	Viable BMD/BMDL ratio > 3.0
Multistage 1	3.147	6.047	13.026	0.557	14.879	-0.	0.09	Viable lowest dose/BMDL ratio > 3.0
Multistage 2	3.795	12	32.473	0.495	15.502	-0.	0.779	Viable lowest dose/BMDL ratio > 3.0 BMD/BMDL ratio > 3.0
Multistage 3 ^a	4.071	11.93	46.495	0.609	14.959	-0.	0.767	Viable
Weibull	3.811	31.644	98.601	0.57	15.477	-0.72	-0.064	Viable lowest dose/BMDL ratio > 3.0 BMD/BMDL ratio > 3.0
Logistic	10.032	20.059	38.327	0.516	15.416	-0.468	0.918	Viable
LogProbit	5.416	34.034	102.123	0.292	17.506	-0.745	0	Viable BMD/BMDL ratio > 3.0
Probit	9.389	18.468	34.486	0.536	15.328	-0.445	0.879	Viable
Quantal Linear ^b	3.147	6.047	13.026	0.557	14.879	-0.	0.09	Recommended - Lowest BMDL lowest dose/BMDL ratio > 3.0

^a User selected best fitting model

^b BMDS recommended best fitting model



Selected Model: Multistage 3



Multistage 3 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Modeling approach	frequentist_restricted
Degree	3

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-18	18
b1	0	0	10000
b2	0	0	10000
b3	0	0	10000

Modeling Summary:

BMD	11.9302
BMDL	4.07058
BMDU	46.4951
AIC	14.9589
Log-Likelihood	-5.47944
P-Value	0.608568
Overall d.f.	2
Chi ²	0.993295

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
b1	0.0084748	no	0.849639
b2	0	yes	Not Reported
b3	2.50546e-06	no	4.70516

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	5	0	7.61499e-08	1.523e-08	-0.000275953
11.7	5	1	0.490123	0.0980245	0.76686
34.4	5	1	1.62663	0.325325	-0.59816
113.9	5	5	4.95302	0.990604	0.217774

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-5.00402	4	-	-	-
Fitted model	-5.47944	2	0.95083	2	0.621627
Reduced model	-12.9489	1	15.8898	3	0.00119452

Session for Nasal inflammation exudate lumen - female rats

Dataset

Name: Nasal inflammation exudate lumen - female rats

Dose (mg/m3)	N	Incidence
0	5	0
11.7	5	1
34.4	5	1
113.9	5	5

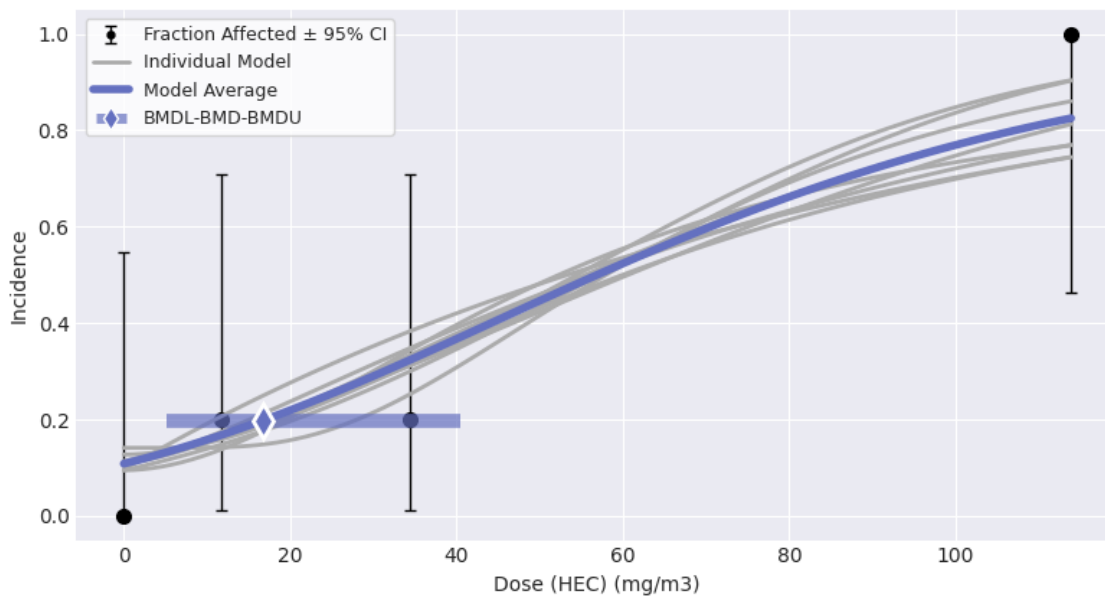
Settings

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

Bayesian Summary

Model	Prior Weights	Posterior Weights	BMDL	BMD	BMDU	Unnormalized Log Posterior Probability	Scaled Residual near BMD	Scaled Residual at Control
Hill	0.111	0.028	3.562	17.854	49.209	-19.105	-0.723	0.404
Gamma	0.111	0.044	4.294	14.749	42.896	-8.988	-0.777	0.15
Logistic	0.111	0.126	9.49	18.088	33.423	-9.045	-0.8	0.204
LogLogistic	0.111	0.062	4.262	21.182	53.445	-13.58	-0.854	0.252
LogProbit	0.111	0.079	10.053	31.546	65.025	-12.399	-0.907	-0.27
Multistage 2	0.111	0.214	5.638	17.289	35.592	-12.436	-0.79	0.192
Probit	0.111	0.178	9.88	18.197	33.243	-6.535	-0.722	0.328
Quantal Linear	0.111	0.185	4.547	9.491	26.928	-7.453	-0.729	-0.034
Weibull	0.111	0.085	3.226	17.067	48.11	-13.565	-0.784	0.228
Model Average	-	-	5.097	16.734	40.533	-	-	-

Nasal inflammation exudate lumen - female rats
Bayesian Model Average
10% Extra Risk



Session for Olfactory mucosa degeneration - female mice

Dataset

Name: Olfactory mucosa degeneration - female mice

Dose (mg/m3)	N	Incidence
0	5	0
5	5	0
16.7	5	2
49.1	5	4

Settings

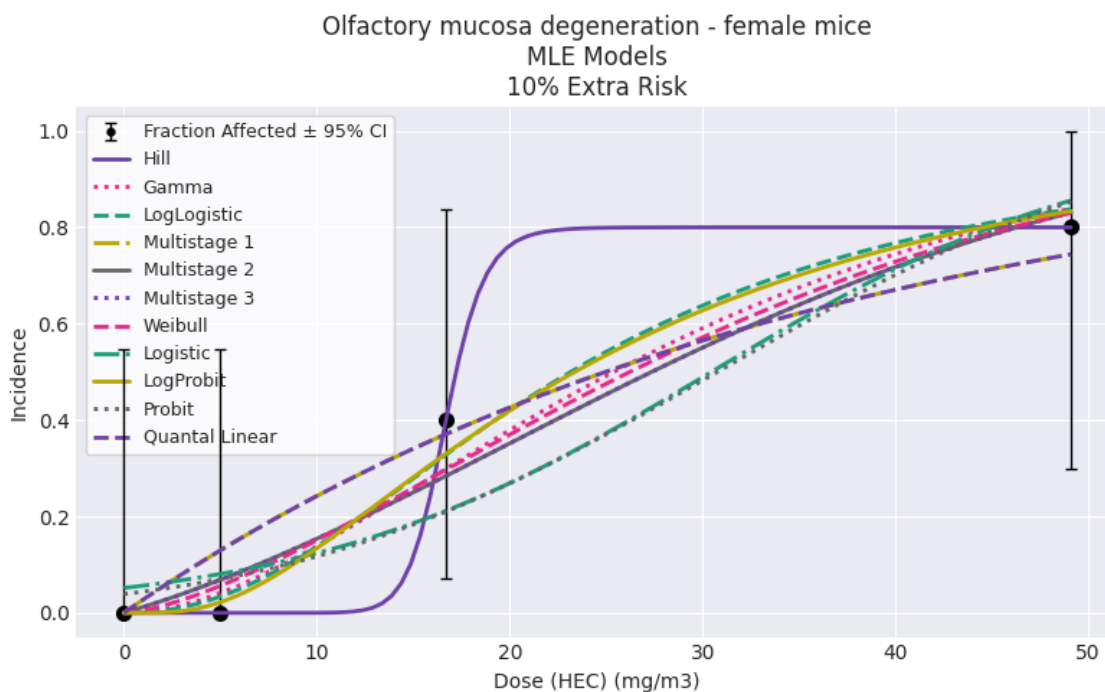
Setting	Value
BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Maximum Multistage Degree	3

Maximum Likelihood Approach

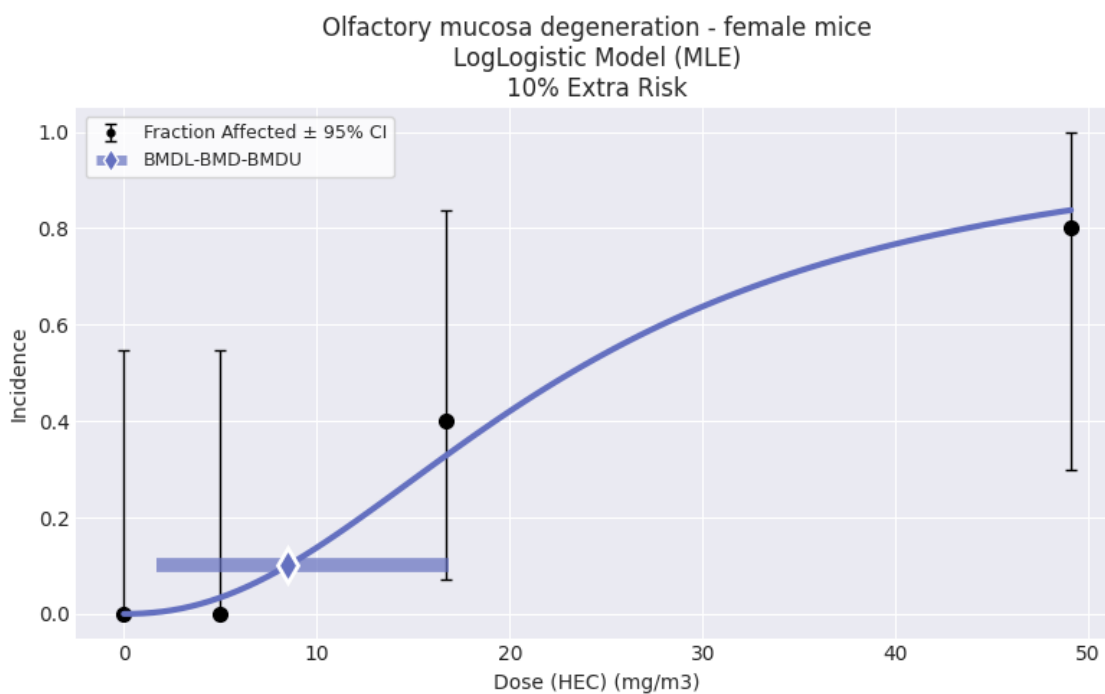
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	2.005	14.858	-	1.	17.734	-0.	<0.001	Viable BMD/BMDL ratio > 3.0
Gamma	2.182	8.231	17.18	0.774	16.438	-0.	-0.464	Viable BMD/BMDL ratio > 3.0
LogLogistic ^{ab}	1.677	8.48	16.834	0.842	16.241	-0.	-0.418	Recommended - Lowest BMDL BMD/BMDL ratio > 3.0
Multistage 1	1.983	3.796	8.316	0.839	15.227	-0.	-0.863	Viable
Multistage 2	2.088	6.948	16.567	0.694	16.784	-0.	-0.606	Viable BMD/BMDL ratio > 3.0
Multistage 3	2.088	6.948	19.684	0.694	16.784	-0.	-0.606	Viable BMD/BMDL ratio > 3.0
Weibull	2.141	7.466	17.517	0.747	16.584	-0.	-0.545	Viable BMD/BMDL ratio > 3.0
Logistic	6.17	12.011	21.89	0.387	18.128	-0.522	1.03	Viable
LogProbit	1.758	8.755	16.642	0.877	16.102	-0.	-0.336	Viable BMD/BMDL ratio > 3.0
Probit	6.195	11.518	20.518	0.411	17.885	-0.451	1.042	Viable
Quantal Linear	1.983	3.796	8.315	0.839	15.227	-0.	-0.863	Viable

^a BMDS recommended best fitting model

^b User selected best fitting model



Selected Model: LogLogistic



LogLogistic Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-18	18
a	0	-18	18
b	1	1	18

Modeling Summary:

BMD	8.48013
BMDL	1.67712
BMDU	16.8339
AIC	16.2406
Log-Likelihood	-6.1203
P-Value	0.841954
Overall d.f.	2
Chi²	0.34406

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
a	-6.87082	no	3.37119
b	2.18625	no	1.06579

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	5	0	7.61499e-08	1.523e-08	-0.000275953
5	5	0	0.169117	0.0338235	-0.418375
16.7	5	2	1.64177	0.328354	0.341144
49.1	5	4	4.18911	0.837823	-0.22944

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-5.86707	4	-	-	-
Fitted model	-6.1203	2	0.506464	2	0.776288
Reduced model	-12.2173	1	12.7004	3	0.00533133

Session for Olfactory mucosa degeneration - female mice

Dataset

Name: Olfactory mucosa degeneration - female mice

Dose (mg/m3)	N	Incidence
0	5	0

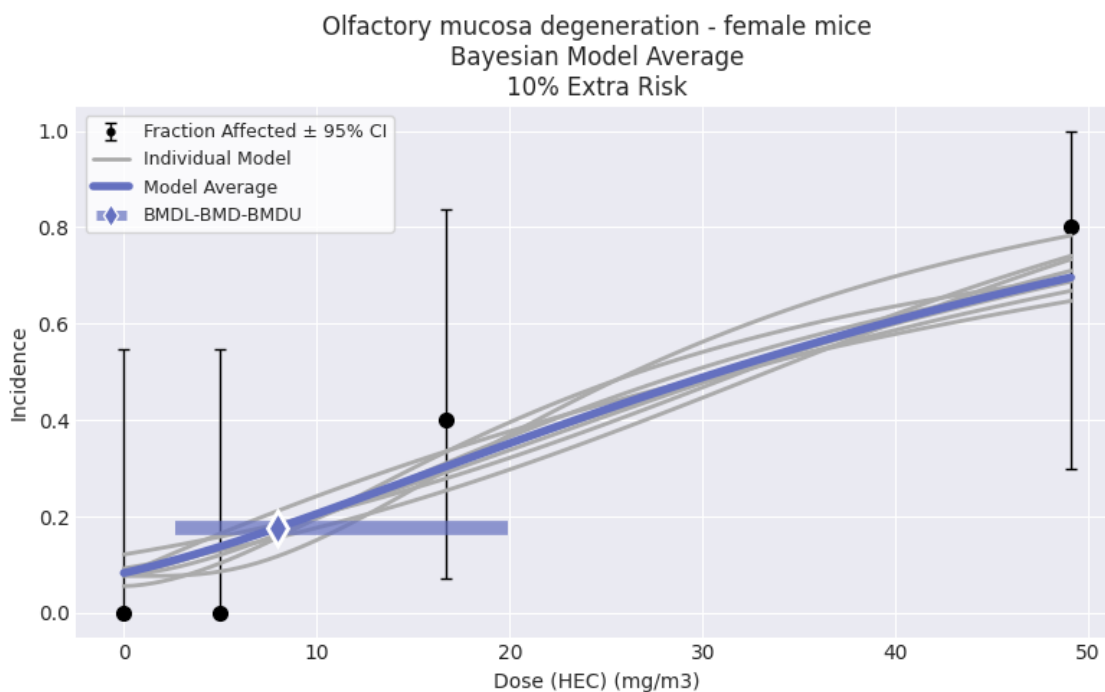
5	5	0
16.7	5	2
49.1	5	4

Settings

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

Bayesian Summary

Model	Prior Weights	Posterior Weights	BMDL	BMD	BMDU	Unnormalized Log Posterior Probability	Scaled Residual near BMD	Scaled Residual at Control
Hill	0.111	0.057	1.942	7.655	19.521	-18.637	-0.542	-0.758
Gamma	0.111	0.06	2.482	7.807	23.483	-9.514	-0.667	-0.882
Logistic	0.111	0.074	5.772	10.538	-	-10.331	-0.83	-0.969
LogLogistic	0.111	0.102	2.136	8.493	21.063	-13.282	-0.655	-0.827
LogProbit	0.111	0.068	4.161	10.932	25.695	-12.432	-0.644	0.513
Multistage 2	0.111	0.162	3.119	7.853	17.291	-12.113	-0.664	-0.893
Probit	0.111	0.13	6.051	10.644	22.12	-7.767	-0.714	-0.864
Quantal Linear	0.111	0.273	2.63	5.387	15.394	-7.997	-0.652	-0.991
Weibull	0.111	0.074	1.608	7.833	23.721	-13.128	-0.662	-0.879
Model Average	-	-	2.677	7.993	19.916	-	-	-



Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 27, 2026.

Dow 1988 - 1,2-DCP

Dow Chemical 1988, 3065001/688893

13-week exposure, male and female rats

Report Generated: 2026-Jan-26 14:01 UTC

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

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

Session for Nasal respiratory epithelium hyperplasia, male rats

Dataset

Name: Nasal respiratory epithelium hyperplasia, male rats

Dose (mg/m3)	N	Incidence
0	10	0
1.6	9	2
5.4	10	5
16.5	10	9

Settings

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

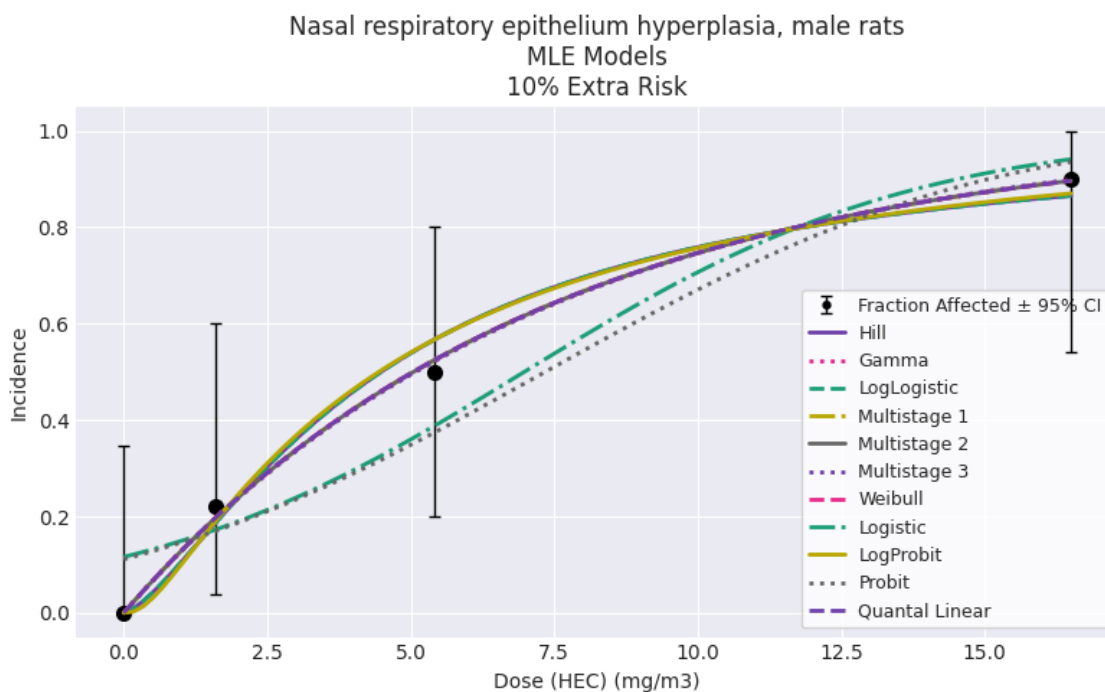
Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill ^{ab}	0.247	0.961	2.18	0.837	34.258	-0.	0.271	Recommended - Lowest BMDL lowest dose/BMDL ratio > 3.0 BMD/BMDL ratio > 3.0
Gamma	0.493	0.767	2.058	0.996	31.958	-0.	-0.	Viable lowest dose/BMDL ratio > 3.0
LogLogistic	0.262	0.961	2.18	0.837	34.258	-0.	0.271	Viable lowest dose/BMDL ratio > 3.0 BMD/BMDL ratio > 3.0
Multistage 1	0.493	0.767	1.25	0.996	31.958	-0.	-0.	Viable lowest dose/BMDL ratio > 3.0
Multistage 2	0.493	0.767	2.176	0.971	33.958	-0.	-0.	Viable lowest dose/BMDL ratio > 3.0
Multistage 3	0.493	0.775	2.175	0.971	33.956	-0.	-0.	Viable lowest dose/BMDL ratio > 3.0
Weibull	0.493	0.767	2.015	0.996	31.958	-0.	-0.	Viable lowest dose/BMDL ratio > 3.0
Logistic	1.446	2.308	3.664	0.315	37.286	-1.145	0.391	Viable

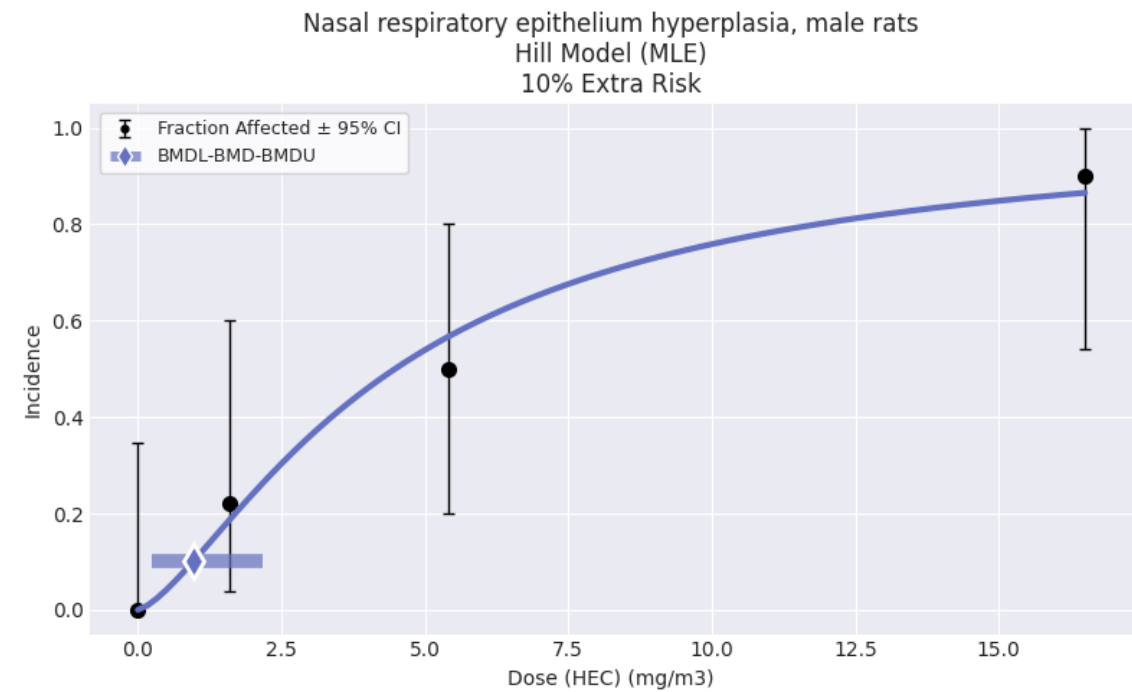
LogProbit	0.125	1.	2.091	0.852	34.22	-0.	0.246	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 BMD/BMDL ratio > 3.0
Probit	1.509	2.279	3.476	0.313	37.267	-1.119	0.416	Viable
Quantal Linear	0.493	0.767	1.25	0.996	31.958	-0.	-0.	Viable lowest dose/BMDL ratio > 3.0

^a BMDS recommended best fitting model

^b User selected best fitting model; Hill model selected based on lowest BMDL.



Selected Model: Hill



Hill Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-18	18
v	0	-18	18
a	0	-18	18
b	1	1	18

Modeling Summary:

BMD	0.961257
BMDL	0.247322
BMDU	2.18017
AIC	34.2581
Log-Likelihood	-15.129
P-Value	0.837363
Overall d.f.	2
Chi²	0.354996

Model Parameters:

Variable	Estimate	On Bound	Std Error
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g	1.523e-08	yes	Not Reported
v	1	yes	Not Reported
a	-2.14082	no	0.977193
b	1.42761	no	0.538307

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
1.6	9	2	1.68271	0.186968	0.271268
5.4	10	5	5.66283	0.566283	-0.422941
16.5	10	9	8.65446	0.865446	0.320203

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-14.9497	4	-	-	-
Fitted model	-15.129	2	0.358749	2	0.835793
Reduced model	-26.4011	1	22.9029	3	4.23089e-05

Session for Nasal respiratory epithelium hyperplasia, male rats

Dataset

Name: Nasal respiratory epithelium hyperplasia, male rats

Dose (mg/m3)	N	Incidence
0	10	0
1.6	9	2
5.4	10	5
16.5	10	9

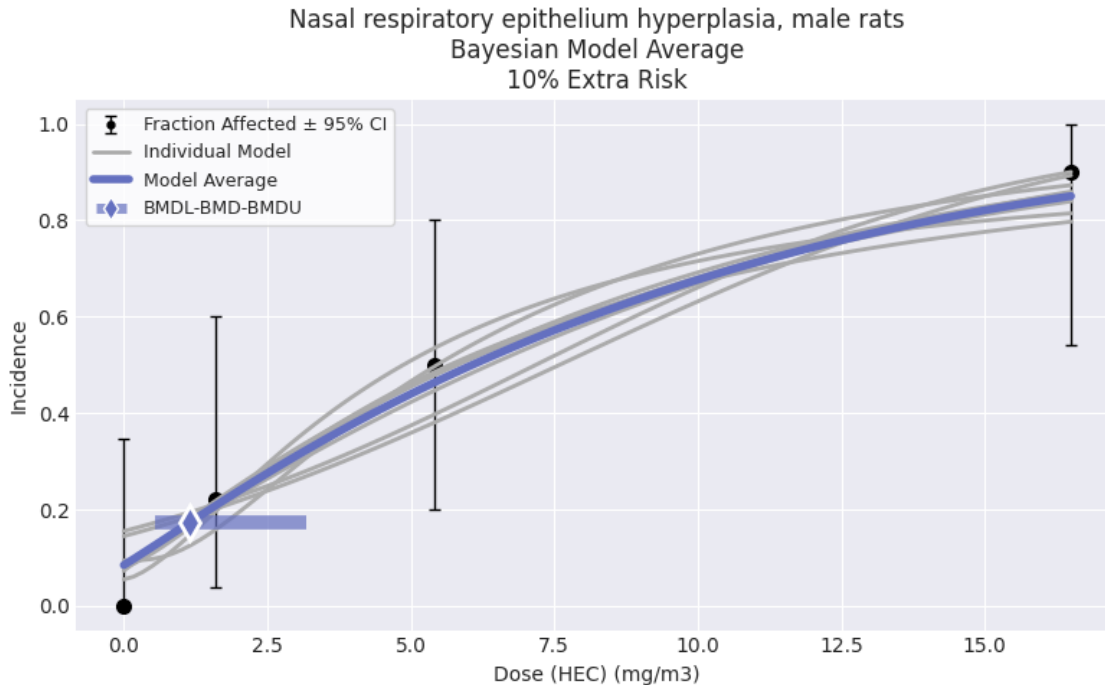
Settings

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

Bayesian Summary

Model	Prior Weights	Posterior Weights	BMDL	BMD	BMDU	Unnormalized Log Posterior Probability	Scaled Residual near BMD	Scaled Residual at Control
Hill	0.111	0.031	0.277	1.178	3.297	-27.168	-0.763	0.197
Gamma	0.111	0.053	0.371	1.26	3.143	-19.782	-0.933	0.175
Logistic	0.111	0.051	1.454	2.287	3.576	-20.422	-1.355	0.08
LogLogistic	0.111	0.049	0.268	1.268	3.948	-22.234	-0.938	0.149
LogProbit	0.111	0.034	0.595	1.905	5.147	-21.477	-1.022	0.525
Multistage 2	0.111	0.217	0.664	1.226	3.542	-21.632	-0.945	0.161
Probit	0.111	0.061	1.541	2.302	3.477	-17.899	-1.301	0.155
Quantal Linear	0.111	0.438	0.605	0.992	1.879	-18.372	-0.89	0.029
Weibull	0.111	0.066	0.2	1.077	3.491	-21.976	-0.893	0.085

Model	-	-	0.534	1.158	3.166	-	-	-
Average								



Session for Nasal respiratory epithelium hyperplasia, female rats

Dataset

Name: Nasal respiratory epithelium hyperplasia, female rats

Dose (mg/m3)	N	Incidence
0	10	0
1.2	10	3
4	10	7
12.1	10	9

Settings

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

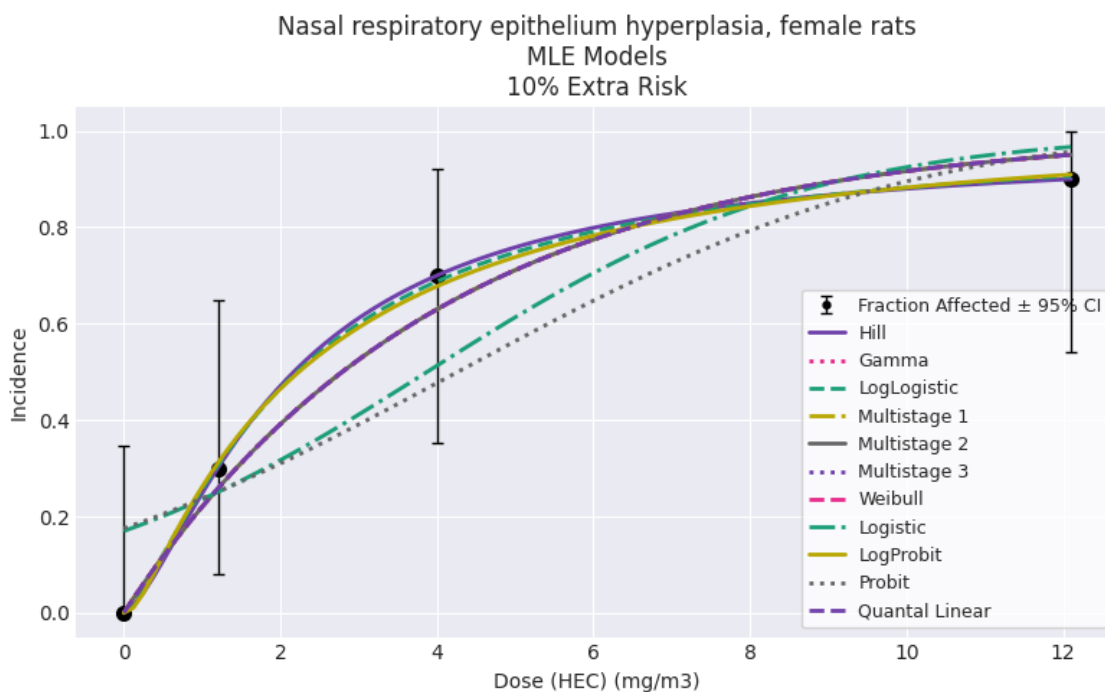
Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	0.1	0.473	1.229	1.	36.936	-0.	-0.	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 BMD/BMDL ratio > 3.0

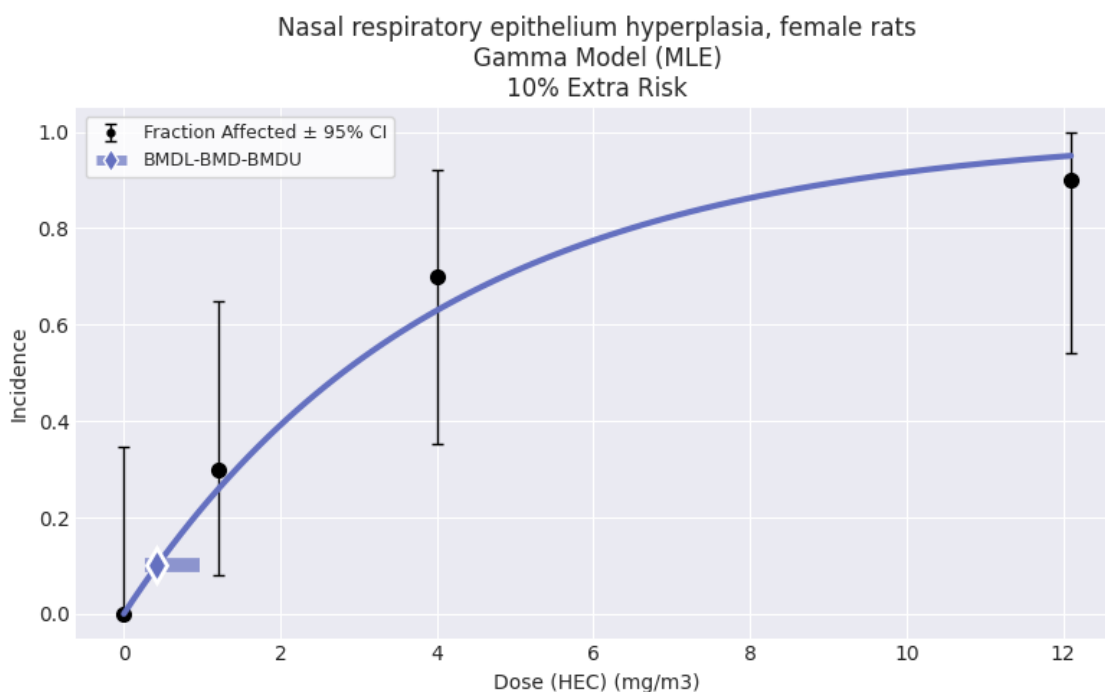
Gamma ^{ab}	0.277	0.424	0.963	0.838	33.668	-0.	-0.	Recommended - Lowest AIC lowest dose/BMDL ratio > 3.0
LogLogistic	0.117	0.428	1.073	0.993	34.949	-0.	-0.	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 BMD/BMDL ratio > 3.0
Multistage 1	0.277	0.424	0.678	0.838	33.668	-0.	-0.	Viable lowest dose/BMDL ratio > 3.0
Multistage 2	0.277	0.424	0.774	0.838	33.668	-0.	-0.	Viable lowest dose/BMDL ratio > 3.0
Multistage 3	0.277	0.424	0.774	0.838	33.668	-0.	-0.	Viable lowest dose/BMDL ratio > 3.0
Weibull	0.277	0.424	0.891	0.838	33.668	-0.	-0.	Viable lowest dose/BMDL ratio > 3.0
Logistic	0.774	1.229	1.957	0.084	41.143	-1.43	0.361	Questionable Goodness of fit p-value < 0.1
LogProbit	0.024	0.444	1.069	0.98	34.976	-0.	-0.	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 BMD/BMDL ratio > 3.0
Probit	0.872	1.294	1.941	0.081	41.527	-1.458	0.356	Questionable Goodness of fit p-value < 0.1
Quantal Linear	0.277	0.424	0.678	0.838	33.668	-0.	-0.	Viable lowest dose/BMDL ratio > 3.0

^a BMDS recommended best fitting model

^b User selected best fitting model; Gamma model selected based on lowest dose group.



Selected Model: Gamma



Gamma Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-18	18
a	1.1	1	18
b	0	0	100

Modeling Summary:

BMD	0.424155
BMDL	0.277084
BMDU	0.963133
AIC	33.6682
Log-Likelihood	-15.8341
P-Value	0.838271
Overall d.f.	3
Chi²	0.846687

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
a	1	yes	Not Reported
b	0.248401	no	0.0666627

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
1.2	10	3	2.57759	0.257759	0.305391
4	10	7	6.2976	0.62976	0.459998
12.1	10	9	9.50493	0.950493	-0.736087

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-15.4681	4	-	-	-
Fitted model	-15.8341	1	0.731977	3	0.865658
Reduced model	-27.6759	1	24.4155	3	2.04559e-05

Session for Nasal respiratory epithelium hyperplasia, female rats

Dataset

Name: Nasal respiratory epithelium hyperplasia, female rats

Dose (mg/m3)	N	Incidence
0	10	0

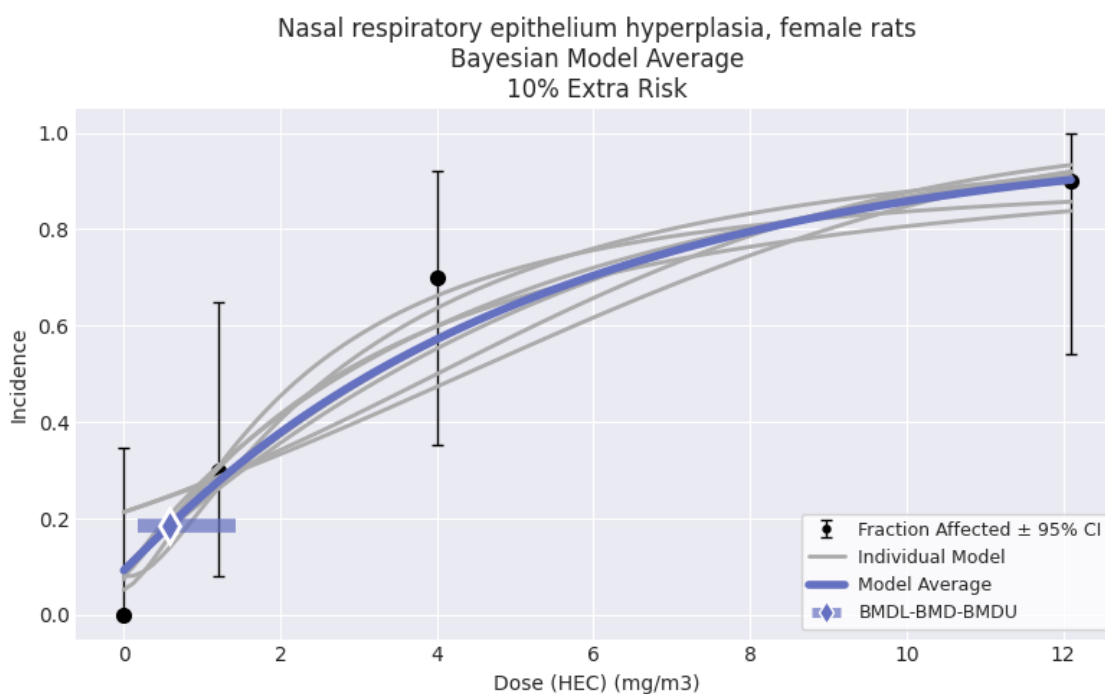
1.2	10	3
4	10	7
12.1	10	9

Settings

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

Bayesian Summary

Model	Prior Weights	Posterior Weights	BMDL	BMD	BMDU	Unnormalized Log Posterior Probability	Scaled Residual near BMD	Scaled Residual at Control
Hill	0.111	0.05	0.1	0.515	1.386	-27.587	-0.741	-0.741
Gamma	0.111	0.047	0.141	0.575	1.626	-21.396	-0.983	-0.983
Logistic	0.111	0.03	0.808	1.286	2.093	-22.574	-1.646	0.097
LogLogistic	0.111	0.046	0.078	0.484	1.672	-23.021	-0.932	-0.932
LogProbit	0.111	0.028	0.216	0.753	2.182	-22.048	-0.932	0.274
Multistage 2	0.111	0.15	0.365	0.629	1.677	-22.971	-1.02	0.285
Probit	0.111	0.027	0.913	1.359	2.12	-20.167	-1.647	0.125
Quantal Linear	0.111	0.552	0.346	0.562	1.069	-20.14	-0.979	-0.979
Weibull	0.111	0.069	0.051	0.377	1.416	-22.862	-0.893	-0.893
Model Average	-	-	0.177	0.581	1.426	-	-	-



Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.

Hematological endpoints

Kirk 1995

Hematological endpoints

1,2-DCP

Report Generated: 2026-Jan-27 13:01 UTC

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

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

Session for Red blood cells

Dataset

Name: Red blood cells

Dose (mg/kg-day)	N	Mean (x 10 ⁶ /mm ³)	Std. Dev. (x 10 ⁶ /mm ³)
0	18	5.69	0.45
15	16	5.4	0.39
50	17	5.46	0.39
150	15	4.54	0.57

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.37

Test 3 Variance Model Selection: 0.37

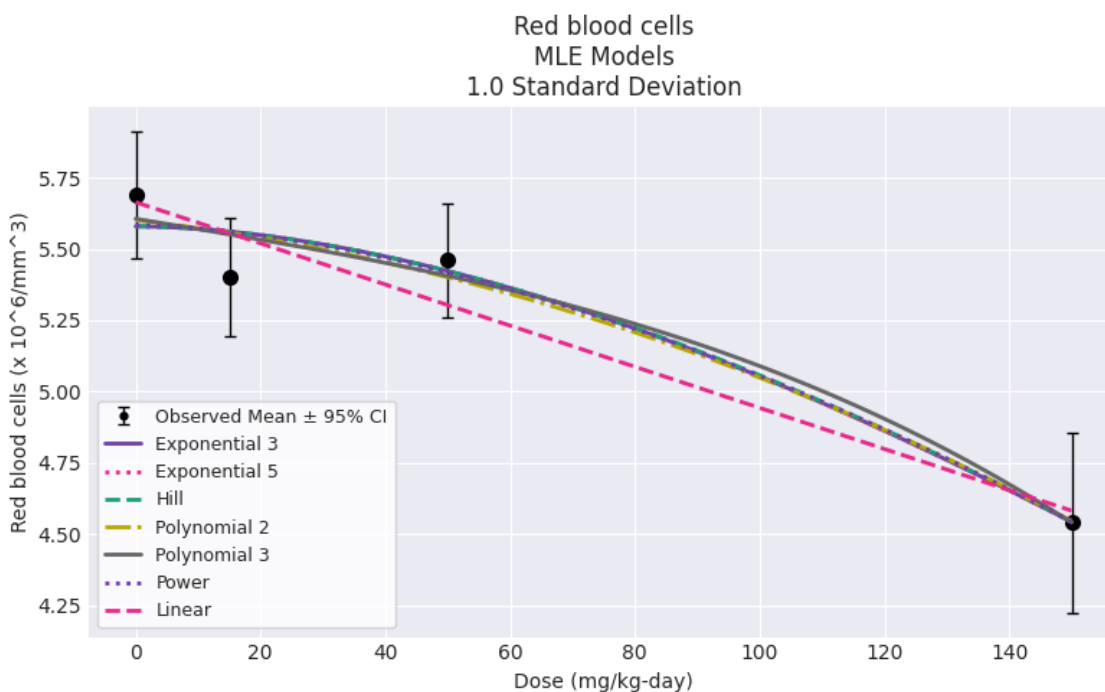
Settings

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	49.261	91.332	145.282	0.188	89.901	1.045	0.342	Viable
Exponential 5	49.261	91.332	145.346	-	91.901	1.045	0.342	Questionable Zero degrees of freedom; saturated model
Hill	47.82	91.66	145.951	-	91.884	1.039	0.344	Questionable Zero degrees of freedom; saturated model
Polynomial 2	52.499	87.35	114.394	0.082	89.587	0.839	0.544	Questionable Goodness of fit p-value < 0.1
Polynomial 3 ^a	53.323	91.335	93.225	0.251	87.322	0.797	0.499	Recommended - Lowest AIC
Power	51.746	90.798	146.623	0.069	89.859	1.004	0.391	Questionable Goodness of fit p-value < 0.1
Linear	49.618	62.85	85.447	0.12	88.806	0.244	1.424	Viable

^a BMDS recommended best fitting model



Selected Model

No model was selected as a best-fitting model.

Session for Red blood cells

Dataset

Name: Red blood cells

Dose (mg/kg-day)	N	Mean ($\times 10^6/\text{mm}^3$)	Std. Dev. ($\times 10^6/\text{mm}^3$)
0	18	5.69	0.45
15	16	5.4	0.39
50	17	5.46	0.39
150	15	4.54	0.57

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.37

Test 3 Variance Model Selection: 0.5794

Settings

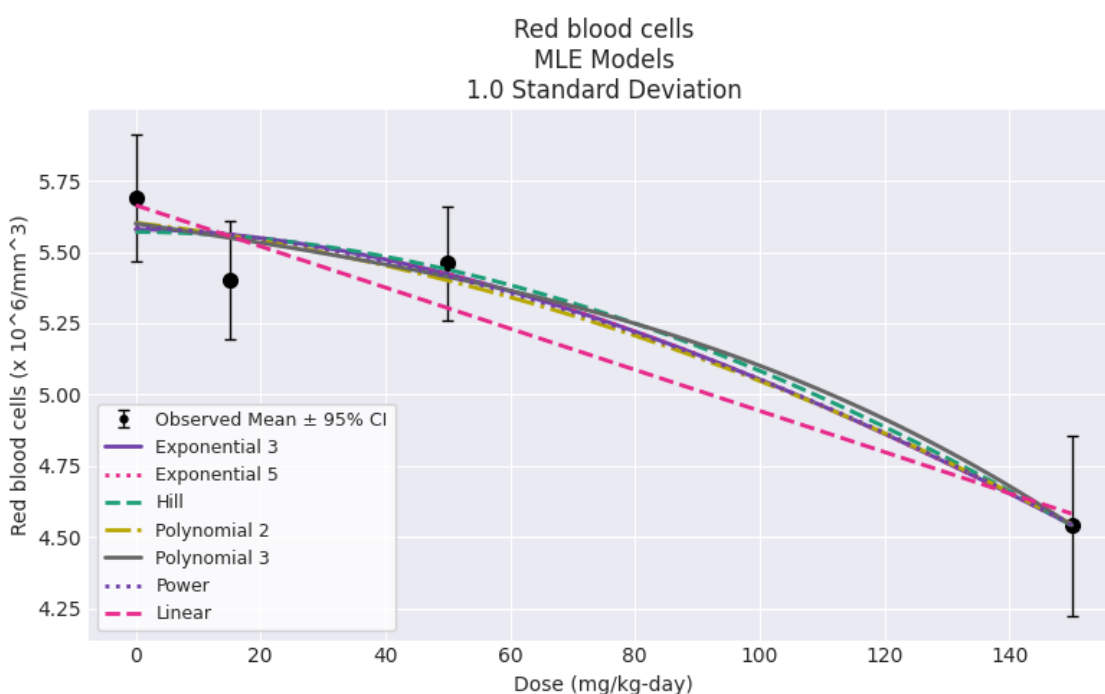
Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant variance
Adverse Direction	Down ($\downarrow$)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	49.261	91.332	145.594	0.145	89.901	1.045	0.342	Viable

Exponential 5	49.261	91.332	142.222	0.02	91.901	1.045	0.342	Questionable Goodness of fit p-value < 0.1
Hill	44.001	91.656	143.144	-	92.106	1.229	0.209	Questionable Zero degrees of freedom; saturated model
Polynomial 2	52.502	87.127	114.411	0.079	89.587	0.832	0.55	Questionable Goodness of fit p-value < 0.1
Polynomial 3 ^a	53.348	93.708	124.643	0.187	87.314	0.852	0.433	Recommended - Lowest AIC
Power	51.752	90.414	147.174	0.069	89.86	0.995	0.405	Questionable Goodness of fit p-value < 0.1
Linear	49.618	62.85	85.445	0.098	88.806	0.244	1.424	Questionable Goodness of fit p-value < 0.1

^a BMDS recommended best fitting model



Selected Model

No model was selected as a best-fitting model.

Session for Hemoglobin

Dataset

Name: Hemoglobin

Dose (mg/kg-day)	N	Mean (g/dL)	Std. Dev. (g/dL)
0	18	12.5	0.8
15	16	12.2	0.9
50	17	12.3	0.8
150	15	10.2	1.4

Test 1 Dose Response: <0.0001
 Test 2 Homogeneity of Variance: 0.0573
 Test 3 Variance Model Selection: 0.0573

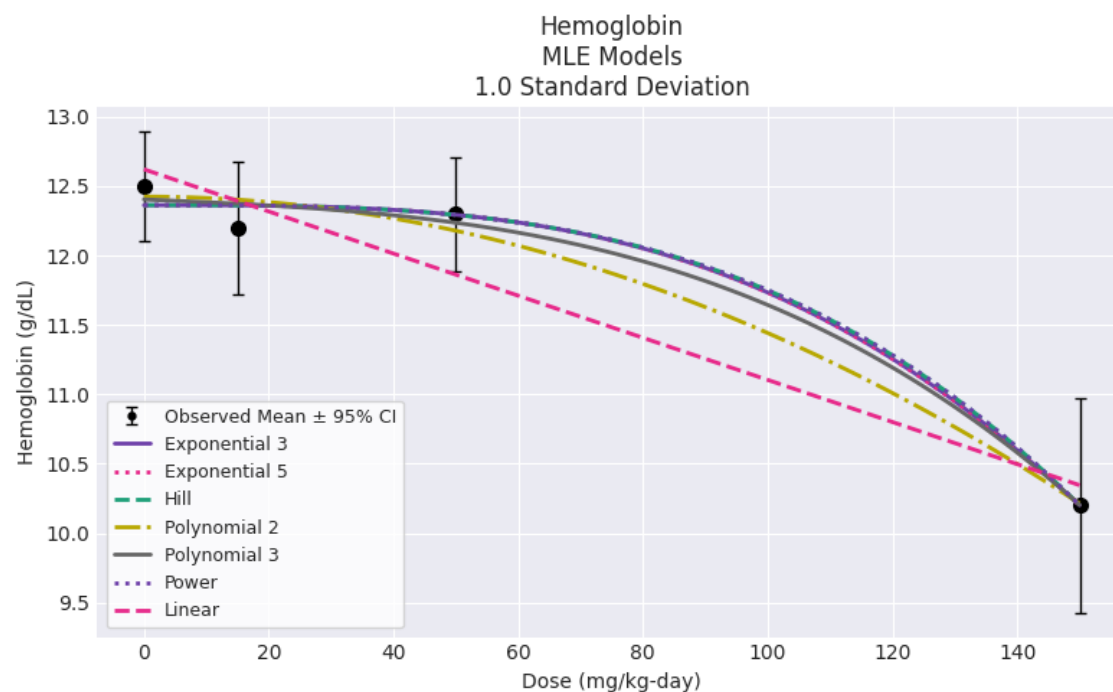
Settings

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	69.222	114.734	146.499	0.366	190.603	0.603	-0.001	Viable
Exponential 5	69.222	114.734	145.649	-	192.603	0.603	-0.001	Questionable Zero degrees of freedom; saturated model
Hill	69.239	115.647	145.767	-	192.602	0.601	-0.001	Questionable Zero degrees of freedom; saturated model
Polynomial 2	66.685	99.185	115.385	0.58	188.875	0.332	0.518	Viable
Polynomial 3 ^a	68.974	109.892	126.695	0.68	188.558	0.421	-0.012	Recommended - Lowest AIC
Power	110.445	115.732	147.348	0.366	190.602	0.601	-0.001	Viable
Linear	51.36	65.47	89.938	0.098	192.438	-0.517	1.817	Questionable Goodness of fit p-value < 0.1

^a BMDS recommended best fitting model



Selected Model

No model was selected as a best-fitting model.

Session for Hemoglobin

Dataset

Name: Hemoglobin

Dose (mg/kg-day)	N	Mean (g/dL)	Std. Dev. (g/dL)
0	18	12.5	0.8
15	16	12.2	0.9
50	17	12.3	0.8
150	15	10.2	1.4

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.0573

Test 3 Variance Model Selection: 0.9346

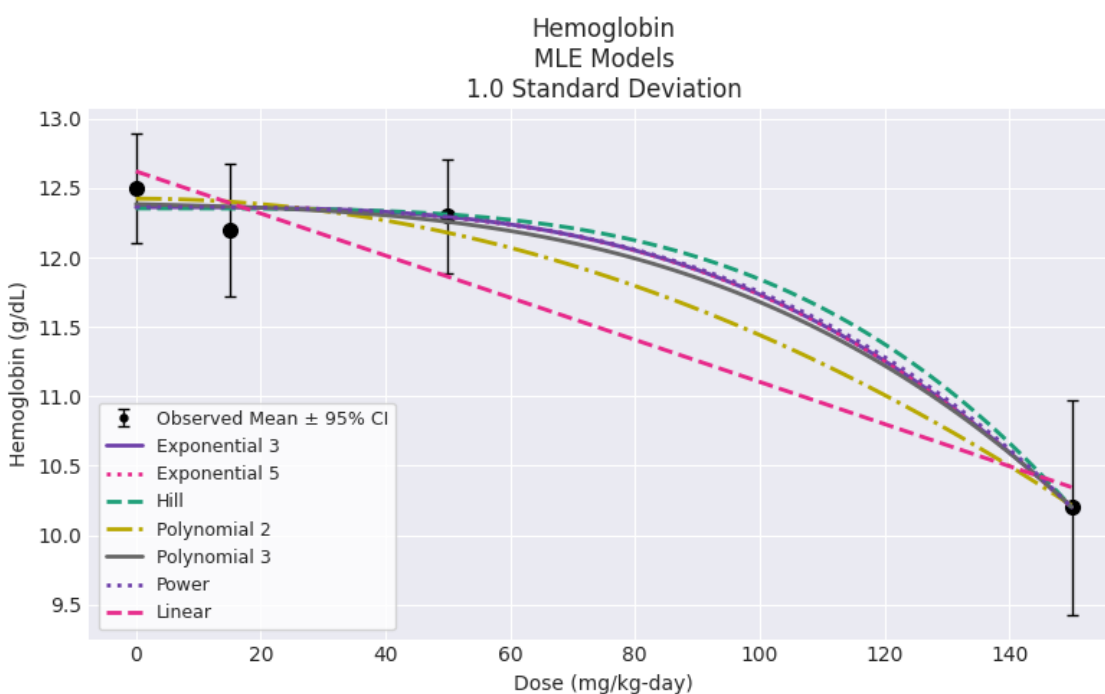
Settings

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant 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	69.224	114.734	146.522	0.017	190.603	0.603	-0.001	Questionable Goodness of fit p-value < 0.1

Exponential 5	69.222	114.734	144.052	0.004	192.603	0.603	-0.001	Questionable Goodness of fit p-value < 0.1
Hill	65.544	113.995	145.484	-	187.76	0.761	0.003	Questionable Zero degrees of freedom; saturated model
Polynomial 2	66.684	99.201	115.383	0.037	188.875	0.333	0.518	Questionable Goodness of fit p-value < 0.1
Polynomial 3	68.958	112.205	126.626	0.043	188.56	0.505	-0.015	Questionable Goodness of fit p-value < 0.1
Power	69.146	115.72	147.347	0.017	190.602	0.601	-0.001	Questionable Goodness of fit p-value < 0.1
Linear	51.361	65.47	89.939	0.007	192.438	-0.517	1.817	Questionable Goodness of fit p-value < 0.1



Selected Model

No model was selected as a best-fitting model.

Session for Hematocrit

Dataset

Name: Hematocrit

Dose (mg/kg-day)	N	Mean (%)	Std. Dev. (%)
0	18	42.9	3.2
15	16	41.2	2.3
50	17	41.9	2.9
150	15	34.9	4.3

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.0986

Test 3 Variance Model Selection: 0.0986

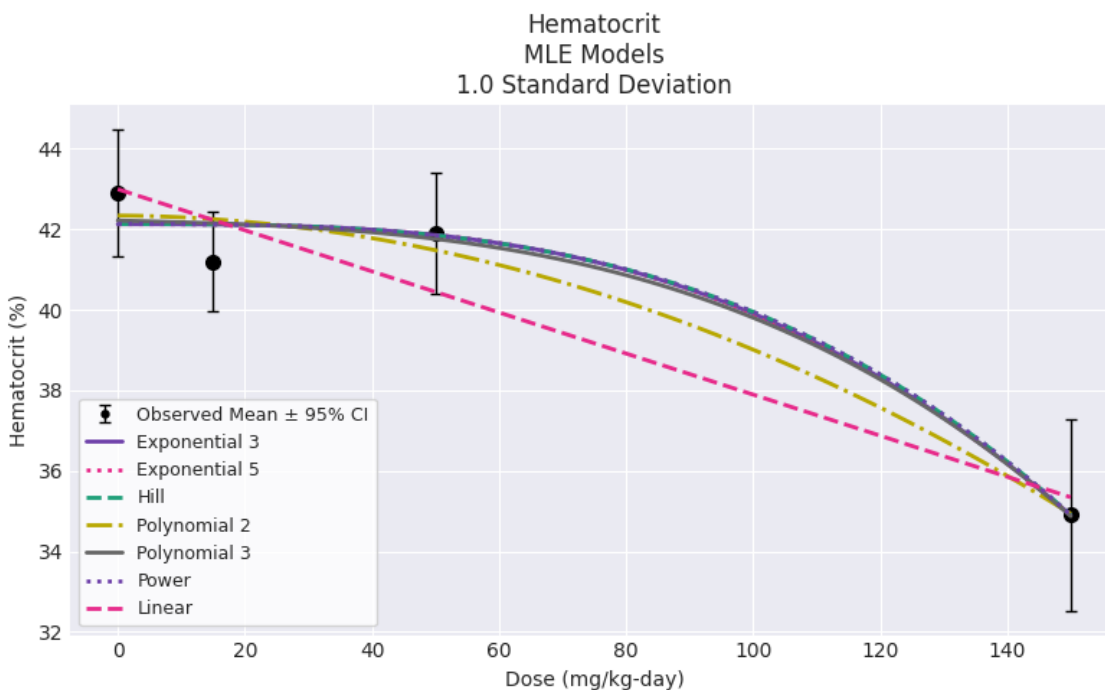
Settings

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	64.333	112.956	144.341	0.296	348.38	1.031	-0.001	Viable
Exponential 5	64.333	112.957	144.309	-	350.38	1.031	-0.001	Questionable Zero degrees of freedom; saturated model
Hill	97.964	113.694	145.936	-	350.378	1.026	-0.001	Questionable Zero degrees of freedom; saturated model
Polynomial 2	61.308	97.863	114.716	0.105	348.576	0.744	0.545	Viable
Polynomial 3	63.343	110.916	125.912	-	350.265	0.912	0.036	Questionable Zero degrees of freedom; saturated model
Power ^a	63.629	113.735	146.1	0.119	348.378	1.026	-0.001	Recommended - Lowest AIC
Linear	50.359	63.961	87.361	0.064	349.431	-0.123	1.841	Questionable Goodness of fit p-value < 0.1

^a BMDS recommended best fitting model



Selected Model

No model was selected as a best-fitting model.

Session for Hematocrit

Dataset

Name: Hematocrit

Dose (mg/kg-day)	N	Mean (%)	Std. Dev. (%)
0	18	42.9	3.2
15	16	41.2	2.3
50	17	41.9	2.9
150	15	34.9	4.3

Test 1 Dose Response: <0.0001

Test 2 Homogeneity of Variance: 0.0986

Test 3 Variance Model Selection: 0.2573

Settings

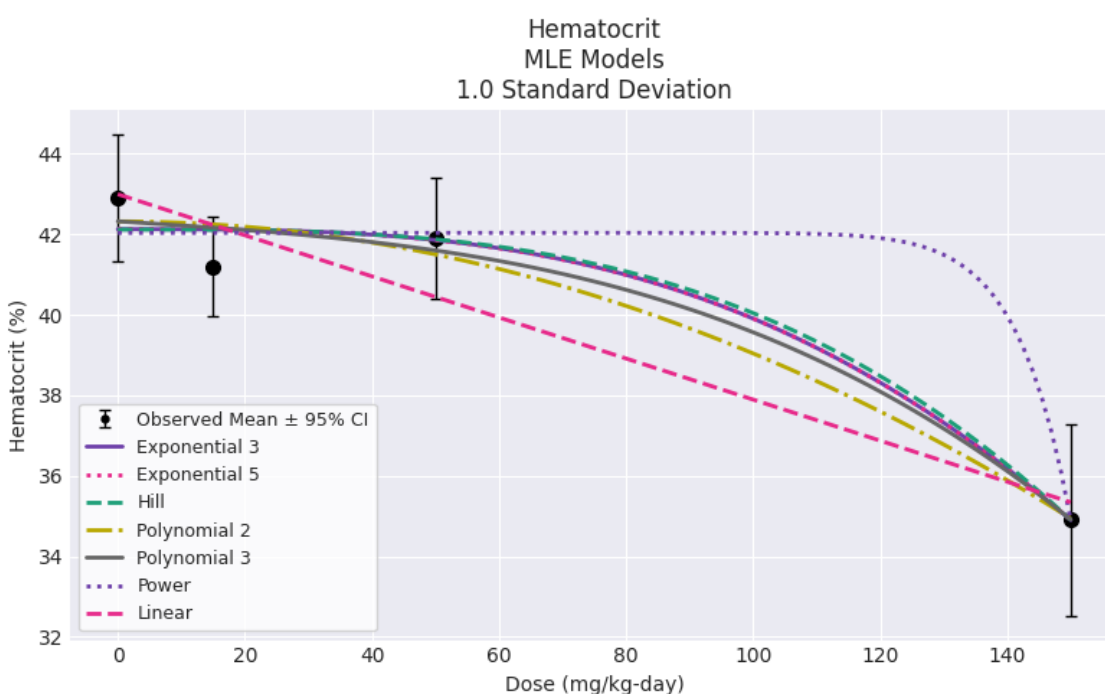
Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant variance
Adverse Direction	Down (↓)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	64.333	112.956	145.586	0.05	348.38	1.031	-0.001	Questionable Goodness of fit p-value < 0.1

Exponential 5	64.333	112.956	147.122	0.014	350.38	1.031	-0.001	Questionable Goodness of fit p-value < 0.1
Hill	61.367	110.632	137.709	-	348.626	1.175	-0.	Questionable Zero degrees of freedom; saturated model
Polynomial 2 ^a	61.333	98.683	114.62	0.102	346.574	0.773	0.519	Recommended - Lowest AIC
Polynomial 3	63.86	106.495	125.831	0.054	348.194	0.772	-0.014	Questionable Goodness of fit p-value < 0.1
Power	63.129	143.439	146.76	0.048	348.438	1.153	<0.001	Questionable Goodness of fit p-value < 0.1
Linear	50.359	63.961	87.361	0.029	349.431	-0.123	1.841	Questionable Goodness of fit p-value < 0.1

^a BMDS recommended best fitting model



Selected Model

No model was selected as a best-fitting model.

Session for Platelets

Dataset

Name: Platelets

Dose (mg/kg-day)	N	Mean (x 10 ³ /mm ³)	Std. Dev. (x 10 ³ /mm ³)
0	18	427	94
15	16	396	93
50	17	468	120
150	15	512	103

Test 1 Dose Response: 0.0524
 Test 2 Homogeneity of Variance: 0.6873
 Test 3 Variance Model Selection: 0.6873

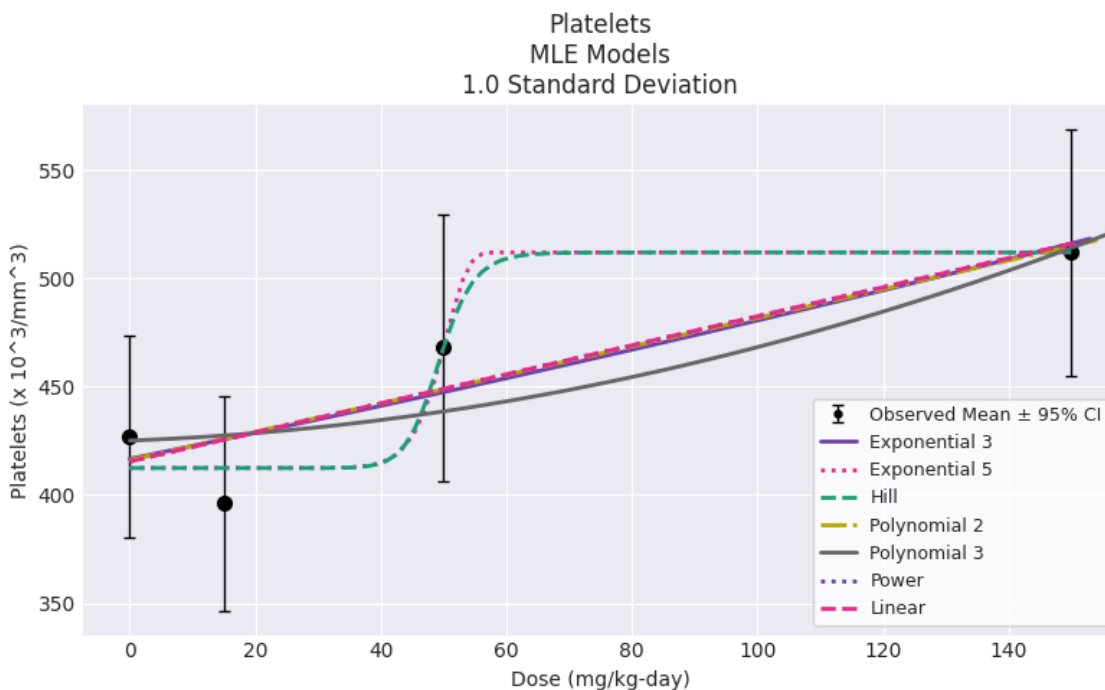
Settings

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	103.7	152.984	325.813	0.511	803.376	0.432	-0.157	Viable BMD/highest dose ratio > 1.0
Exponential 5	-	-	-	-	805.88	0.616	-	Unusable Did not successfully execute.
Hill	-	-	-	-	805.88	0.616	-	Unusable Did not successfully execute.
Polynomial 2	97.225	154.11	342.178	0.134	805.318	0.455	-0.113	Viable BMD/highest dose ratio > 1.0
Polynomial 3	92.899	161.934	165.286	0.083	806.072	0.079	-0.079	Questionable Goodness of fit p-value < 0.1 BMD/highest dose ratio > 1.0
Power ^a	97.268	151.466	341.389	0.327	803.308	0.484	-0.154	Recommended - Lowest AIC BMD/highest dose ratio > 1.0
Linear	97.268	151.466	341.389	0.327	803.308	0.484	-0.154	Viable BMD/highest dose ratio > 1.0

^a BMDS recommended best fitting model



Selected Model

No model was selected as a best-fitting model.

Session for Platelets

Dataset

Name: Platelets

Dose (mg/kg-day)	N	Mean ($\times 10^3/\text{mm}^3$)	Std. Dev. ($\times 10^3/\text{mm}^3$)
0	18	427	94
15	16	396	93
50	17	468	120
150	15	512	103

Settings

Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant variance
Adverse Direction	Up ($\uparrow$)
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	-	Unusable Did not successfully execute.

Exponential 5	50.886	53.678	-	-	807.384	0.689	-0.168	Questionable Zero degrees of freedom; saturated model
Hill	18.891	58.973	-	-	807.384	0.689	-0.168	Questionable Zero degrees of freedom; saturated model BMD/BMDL ratio > 3.0
Polynomial 2 ^a	88.492	146.585	337.878	0.255	805.21	0.505	-0.16	Recommended - Lowest AIC
Polynomial 3	88.493	146.633	339.164	0.255	805.21	0.505	-0.16	Viable
Power	88.478	146.584	339.171	0.255	805.21	0.505	-0.16	Viable
Linear	88.478	146.585	339.092	0.255	805.21	0.505	-0.16	Viable

^a BMDS recommended best fitting model

Selected Model

No model was selected as a best-fitting model.

Session for White blood cells

Dataset

Name: White blood cells

Dose (mg/kg-day)	N	Mean (x 10 ³ /mm ³)	Std. Dev. (x 10 ³ /mm ³)
0	18	6.8	1.5
15	16	7.2	1.7
50	17	6.9	1.6
150	15	8.6	2.7

Test 1 Dose Response: 0.011

Test 2 Homogeneity of Variance: 0.0549

Test 3 Variance Model Selection: 0.0549

Settings

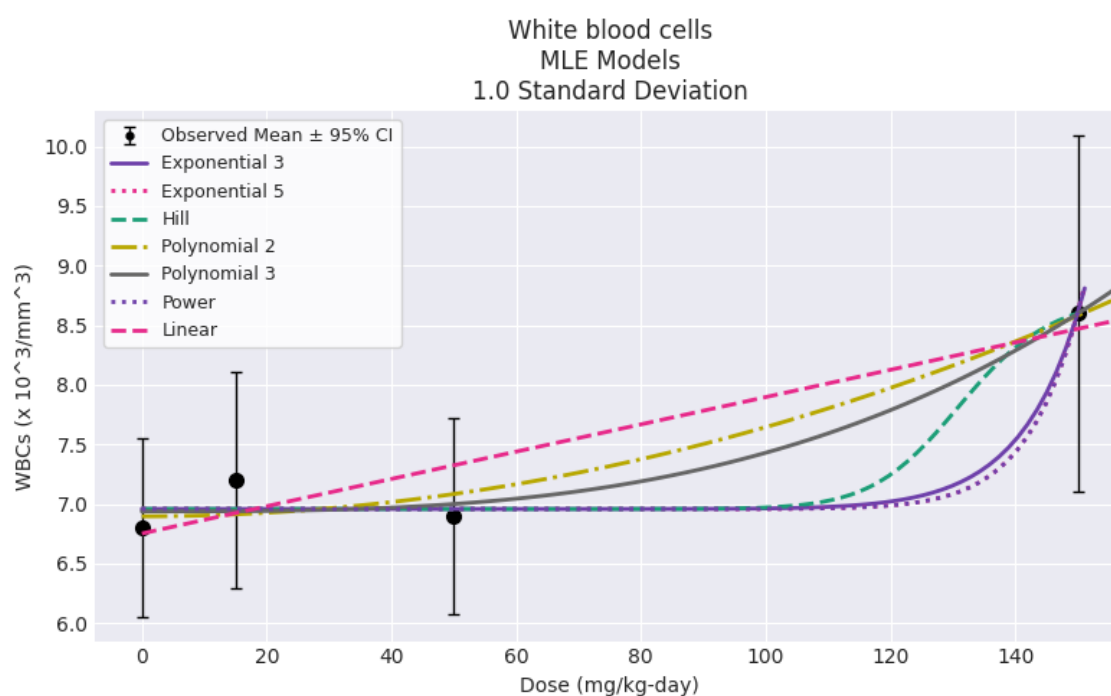
Setting	Value
BMR	1.0 Standard Deviation
Distribution	Normal + Constant variance
Adverse Direction	Up (↑)
Maximum Polynomial Degree	3
Confidence Level (one sided)	0.95

Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	112.399	151.143	300.83	0.809	276.557	-0.364	-0.	Viable BMD/highest dose ratio > 1.0
Exponential 5	147.314	151.006	156.961	-	278.557	-0.364	-0.	Questionable Zero degrees of freedom; saturated model BMD/highest dose ratio > 1.0

Hill	-	-	-	0.516	276.557	-0.364	-	Unusable Did not successfully execute.
Polynomial 2	107.924	157.421	331.829	0.74	274.737	-0.222	0.042	Viable BMD/highest dose ratio > 1.0
Polynomial 3 ^a	109.213	155.637	320.219	0.926	272.601	-0.318	0.008	Recommended - Lowest AIC BMD/highest dose ratio > 1.0
Power	109.637	151.005	316.522	0.809	274.557	-0.364	-0.	Viable BMD/highest dose ratio > 1.0
Linear	102.034	162.897	402.909	0.514	275.466	0.107	0.273	Viable BMD/highest dose ratio > 1.0

^a BMDS recommended best fitting model



Selected Model

No model was selected as a best-fitting model.

Session for White blood cells

Dataset

Name: White blood cells

Dose (mg/kg-day)	N	Mean (x 10 ³ /mm ³)	Std. Dev. (x 10 ³ /mm ³)
0	18	6.8	1.5
15	16	7.2	1.7
50	17	6.9	1.6
150	15	8.6	2.7

Test 1 Dose Response: 0.011

Test 2 Homogeneity of Variance: 0.0549

Test 3 Variance Model Selection: 0.9892

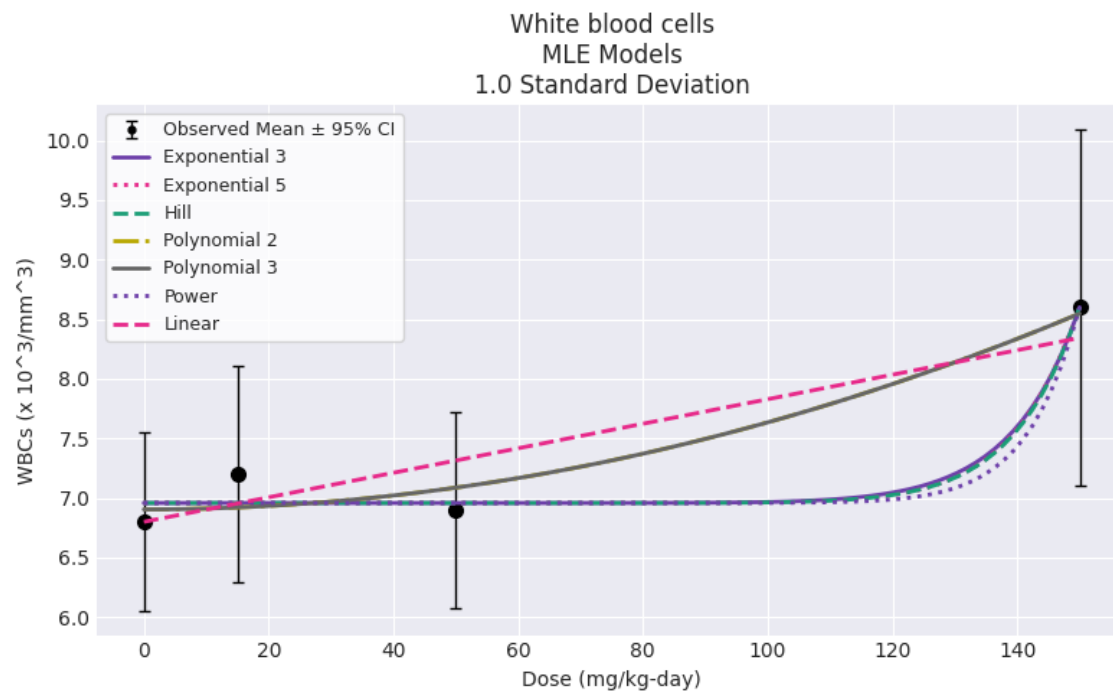
Settings

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	92.429	149.456	290.326	0.662	271.375	-0.432	<0.001	Viable
Exponential 5	54.51	149.442	-	-	273.375	-0.432	<0.001	Questionable Zero degrees of freedom; saturated model
Hill	123.909	149.464	188.569	-	273.375	-0.432	<0.001	Questionable Zero degrees of freedom; saturated model
Polynomial 2	87.039	144.777	-	0.567	269.683	-0.291	0.079	Viable
Polynomial 3 ^a	87.039	144.777	147.774	0.567	269.683	-0.291	0.079	Recommended - Lowest AIC
Power	90.601	149.574	299.907	0.363	271.375	-0.432	<0.001	Viable
Linear	78.155	142.079	-	0.338	270.72	-0.001	0.391	Viable

^a BMDS recommended best fitting model



Selected Model

No model was selected as a best-fitting model.

Session for Reticulocytes

Dataset

Name: Reticulocytes

Dose (mg/kg-day)	N	Mean (%)	Std. Dev. (%)
0	18	3.2	0.6
15	16	3.6	0.7
50	17	3.8	0.9
150	15	6.7	1.7

Test 1 Dose Response: 0

Test 2 Homogeneity of Variance: <0.0001

Test 3 Variance Model Selection: <0.0001

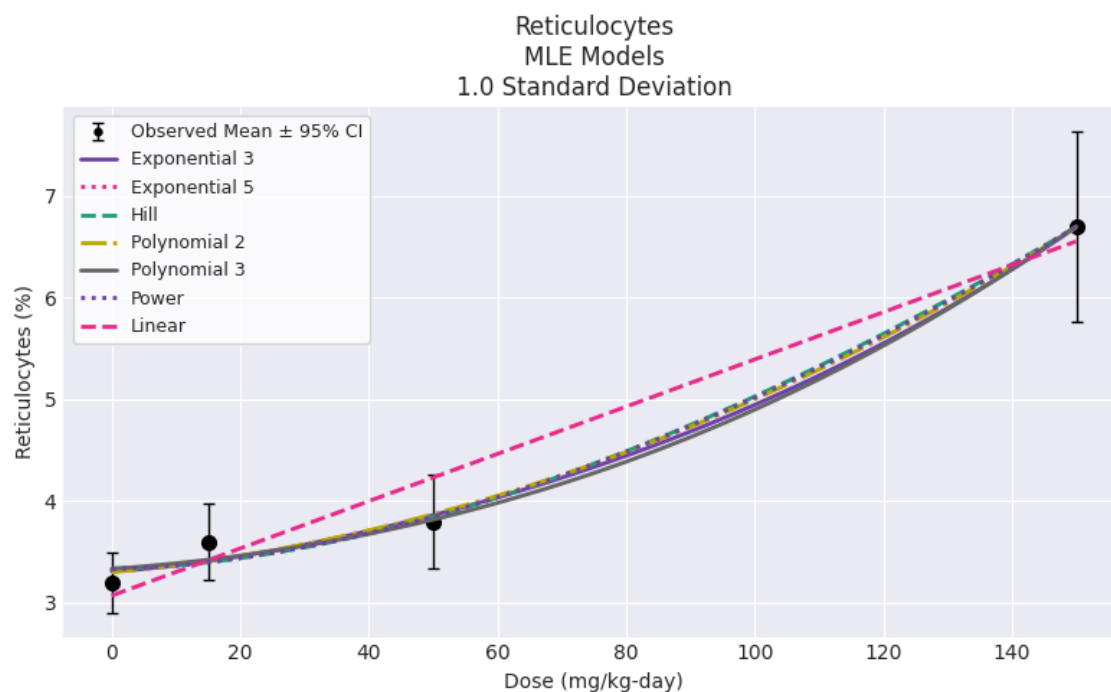
Settings

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	49.821	74.535	142.898	0.355	197.04	-0.473	-0.254	Questionable Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Exponential 5	66.859	74.25	84.004	-	199.168	-0.559	-0.206	Questionable Zero degrees of freedom; saturated model Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Hill	45.761	74.307	142.17	-	199.186	-0.576	-0.19	Questionable Zero degrees of freedom; saturated model Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Polynomial 2	44.908	72.647	92.571	0.367	196.997	-0.428	-0.295	Questionable Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Polynomial 3	44.611	78.185	79.804	0.368	196.993	-0.563	-0.077	Questionable Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)

Power	44.857	74.251	81.255	0.321	197.168	-0.559	-0.206	Questionable Control stdev. fit > 1.5 Constant variance test failed (Test 2 p-value < 0.05)
Linear	36.769	44.717	56.801	0.127	198.309	0.525	-1.718	Questionable 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.

Session for Reticulocytes

Dataset

Name: Reticulocytes

Dose (mg/kg-day)	N	Mean (%)	Std. Dev. (%)
0	18	3.2	0.6
15	16	3.6	0.7
50	17	3.8	0.9
150	15	6.7	1.7

Test 1 Dose Response: 0

Test 2 Homogeneity of Variance: <0.0001

Test 3 Variance Model Selection: 0.7301

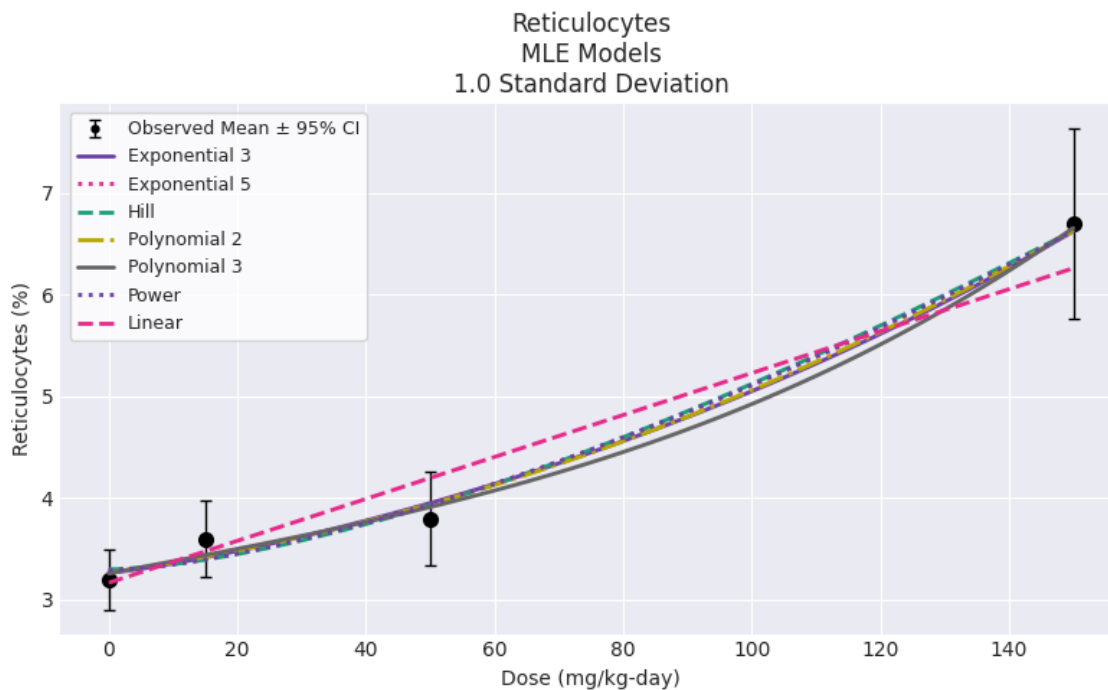
Settings

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

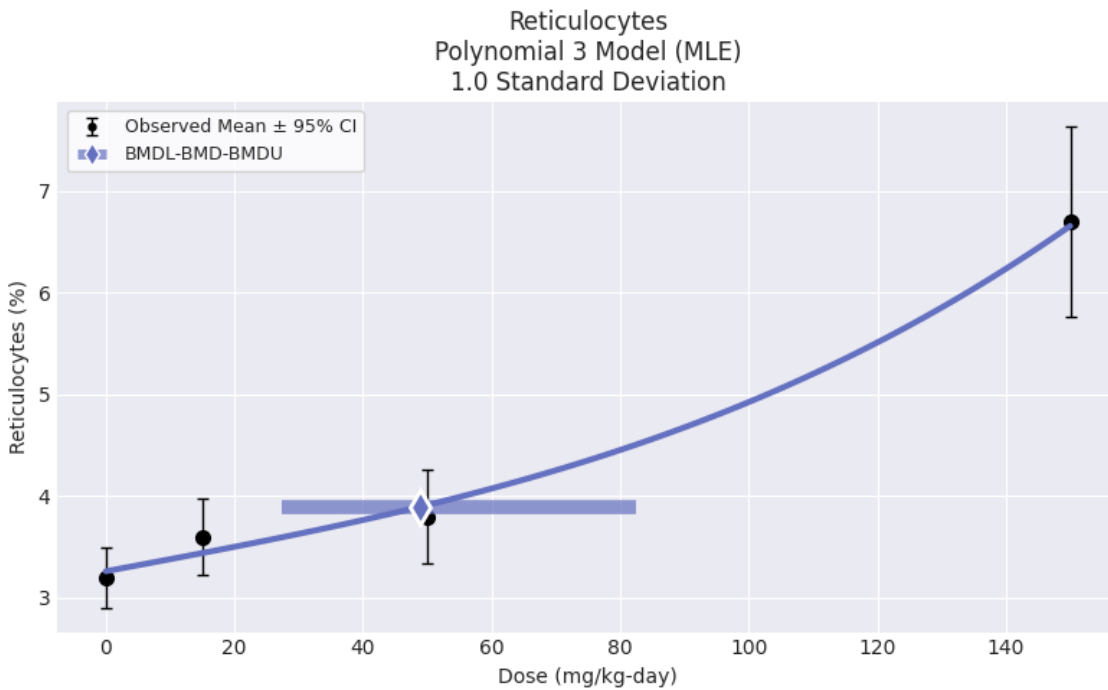
Confidence Level (one sided)				0.95				
Maximum Likelihood Approach								
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Exponential 3	30.385	47.256	82.987	0.425	178.046	-0.434	-0.757	Viable
Exponential 5	42.267	50.044	57.879	-	180.476	-0.598	-0.693	Questionable Zero degrees of freedom; saturated model
Hill	27.082	51.087	83.252	-	180.565	-0.647	-0.649	Questionable Zero degrees of freedom; saturated model
Polynomial 2	26.808	47.949	74.83	0.207	177.927	-0.445	-0.706	Viable
Polynomial 3 ^{ab}	27.446	48.928	82.553	0.552	175.524	-0.41	-0.573	Recommended - Lowest AIC
Power	25.393	50.043	83.21	0.143	178.476	-0.598	-0.693	Viable
Linear	22.008	28.901	39.915	0.118	178.604	0.227	0.711	Viable

^a BMDS recommended best fitting model

^b User selected best fitting model; model selected based on lowest AIC



Selected Model: Polynomial 3



Polynomial 3 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	1.0 Standard Deviation
Distribution	Normal + Nonconstant variance
Modeling Direction	Up ($\uparrow$)
Confidence Level (one sided)	0.95
Modeling Approach	MLE
Degree	3

Parameter Settings:

Parameter	Initial	Min	Max
g	0	0	1000
b1	0	0	18
b2	0	0	1e+06
b3	0	0	1e+06
rho	0	0	18
alpha	0	-18	18

Modeling Summary:

BMD	48.9278
BMDL	27.4462
BMDU	82.5529
AIC	175.524
Log-Likelihood	-83.7618
P-Value	0.552031
Model d.f.	2

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	3.26146	no	0.129338
b1	0.0118337	no	0.00544118
b2	0	yes	Not Reported
b3	4.80316e-07	yes	Not Reported
rho	2.73716	no	0.730539
alpha	0.0158711	no	0.000261178

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	18	3.2	3.26146	-0.410484
15	16	3.6	3.44059	0.932927
50	17	3.8	3.91319	-0.572529
150	15	6.7	6.65759	0.0973757

Dose	N	Sample SD	Model Fitted SD
0	18	0.6	0.635258
15	16	0.7	0.683485
50	17	0.9	0.815136
150	15	1.7	1.68686

Likelihoods:

Model	Log-Likelihood	# Params	AIC
A1	-94.092	5	198.184
A2	-82.8531	8	181.706
A3	-83.1677	6	178.335
fitted	-83.7618	4	175.524
reduced	-128.013	2	260.027

Tests of Mean and Variance Fits:

Name	-2 * Log(Likelihood Ratio)	Test d.f.	P-Value
Test 1	90.3206	6	0
Test 2	22.4778	3	5.18804e-05
Test 3	0.629158	2	0.730096
Test 4	1.1883	2	0.552031

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.

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 27, 2026.

Rao-Scott Transformation¹

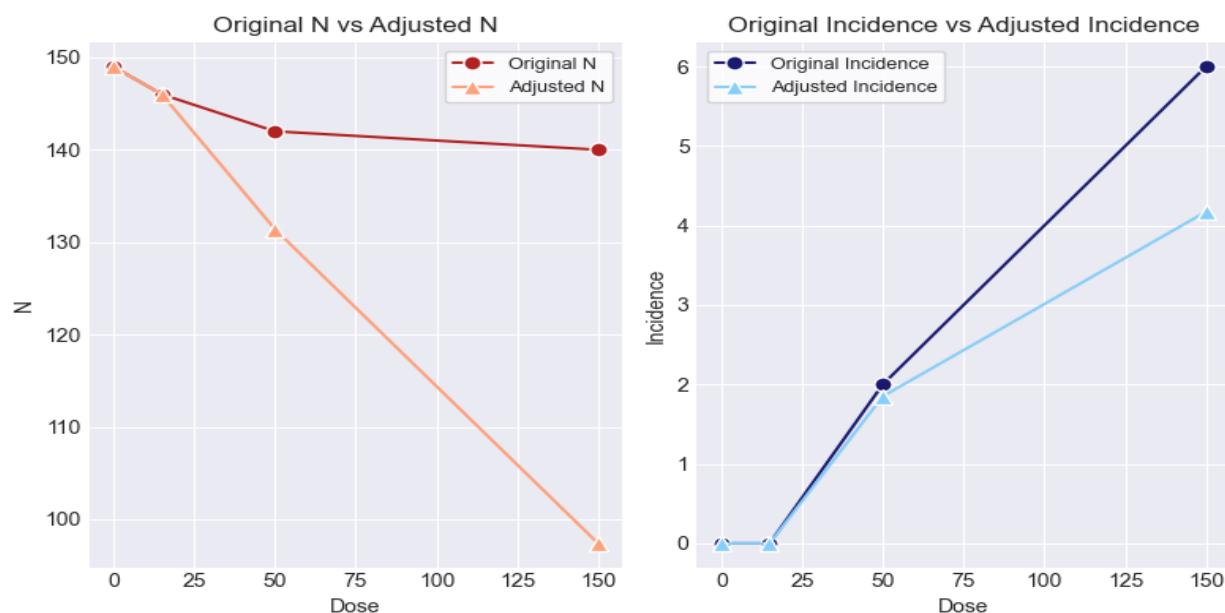
Report generated: 2025-Oct-07 1:55 UTC

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

Summary

Species: Rat

Dose	N	Incidence	Fraction Affected	Design Effect (LS)	Design Effect (OR)	Design Effect (Average)	N (Rao-Scott Transformed)	Incidence (Rao-Scott Transformed)
0	149	0	0	--	--	--	149	0
15	146	0	0	--	--	--	146	0
50	142	2	0.014	1.115	1.046	1.081	131.400	1.851
150	140	6	0.043	1.456	1.419	1.438	97.390	4.174



Rao-Scott Transformation Parameters

Species	Regression Method	A	b	sigma
rabbit	Least Squares	1.0582	0.2397	0.1452
rabbit	Orthogonal	1.1477	0.2739	0.1299

Fox JF, Hogan KA, Davis A. Dose-Response Modeling with Summary Data from Developmental Toxicity Studies. Risk Anal. 2017 May;37(5):905-917. PMID: 27567129. DOI: 10.1111/risa.12667.

¹ Note that the Rao-Scott transformation was manually calculated for the 50 and 150 mg/kg-day dose groups. No transformation was performed for the 0 or 15 mg/kg-day dose groups given that the incidence of delayed ossification was 0 in these dose groups and the design effect would be undefined given division by zero. Hence, for these dose groups, the original, unscaled Ns were used in dose-response modeling.

Rao-Scott Transformation

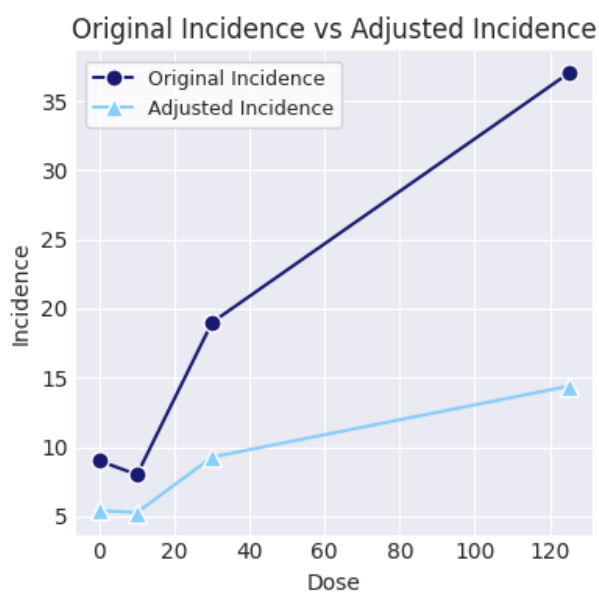
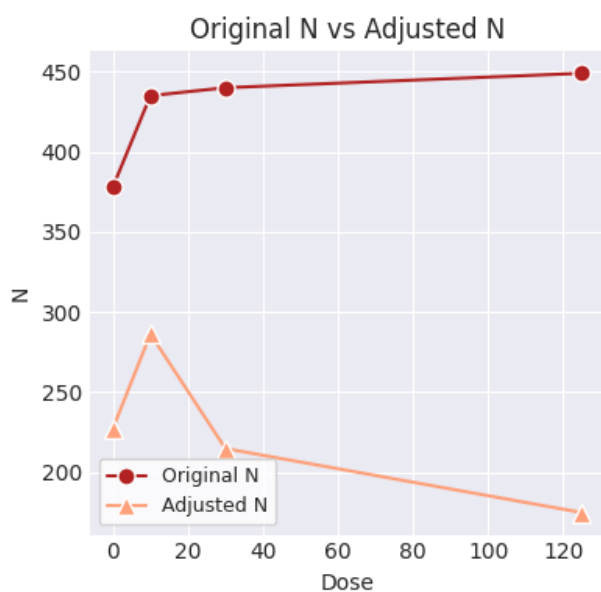
Report generated: 2025-Oct-07 11:10 UTC

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

Summary

Species: Rat

Dose	N	Incidence	Fraction Affected	Design Effect (LS)	Design Effect (OR)	Design Effect (Average)	N (Rao-Scott Transformed)	Incidence (Rao-Scott Transformed)
0	378	9	0.024	1.666	1.662	1.664	227.165	5.409
10	435	8	0.018	1.53	1.511	1.52	286.144	5.262
30	440	19	0.043	2.029	2.07	2.05	214.678	9.27
125	449	37	0.082	2.513	2.628	2.57	174.689	14.395



Rao-Scott Transformation Parameters

Species	Regression Method	A	b	sigma
rat	Least Squares	1.685	0.331	0.125
rat	Orthogonal	1.833	0.369	0.109

Fox JF, Hogan KA, Davis A. Dose-Response Modeling with Summary Data from Developmental Toxicity Studies. Risk Anal. 2017 May;37(5):905-917. PMID: 27567129. DOI: 10.1111/risa.12667.

Liver tumors

NTP 1986

Liver tumors, female mice

1,2-DCP

Report Generated: 2026-Jan-26 16:01 UTC

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

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

Modeling Summary

Datasets

Name: Liver tumors

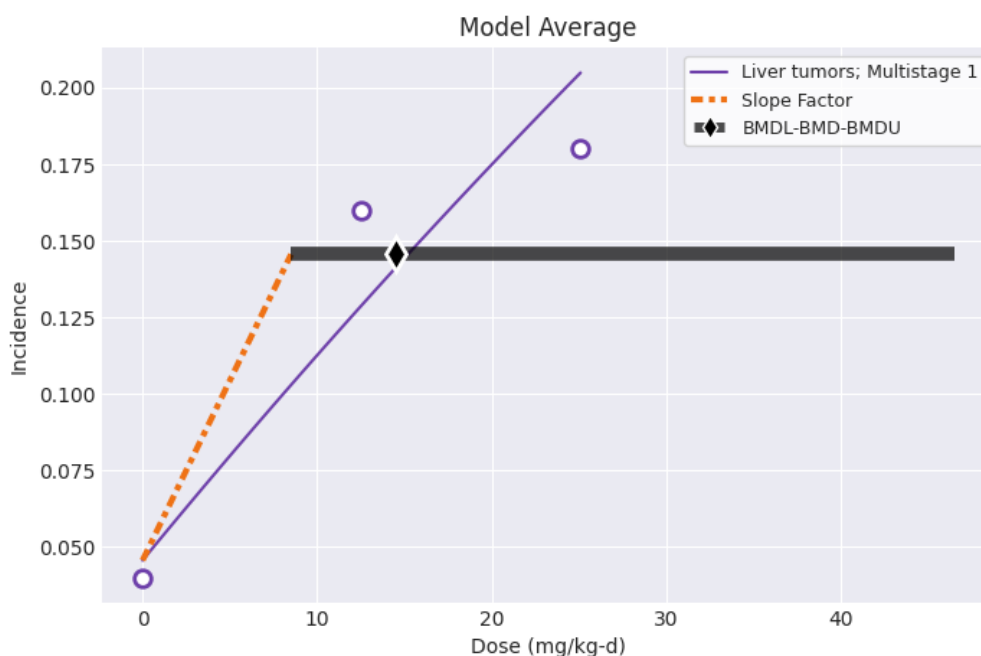
Dose (mg/kg-d)	0	12.5	25.1
Affected / Total (%)	2.0/50.0 (4.0%)	8.0/50.0 (16.0%)	9.0/50.0 (18.0%)

Settings

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

Maximum Likelihood Approach

Dataset: Model	BMDL	BMD	BMDU	CSF	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD
Liver tumors: Multistage 1	8.511	14.477	46.516	0.012	0.414	112.548	-0.19	0.664



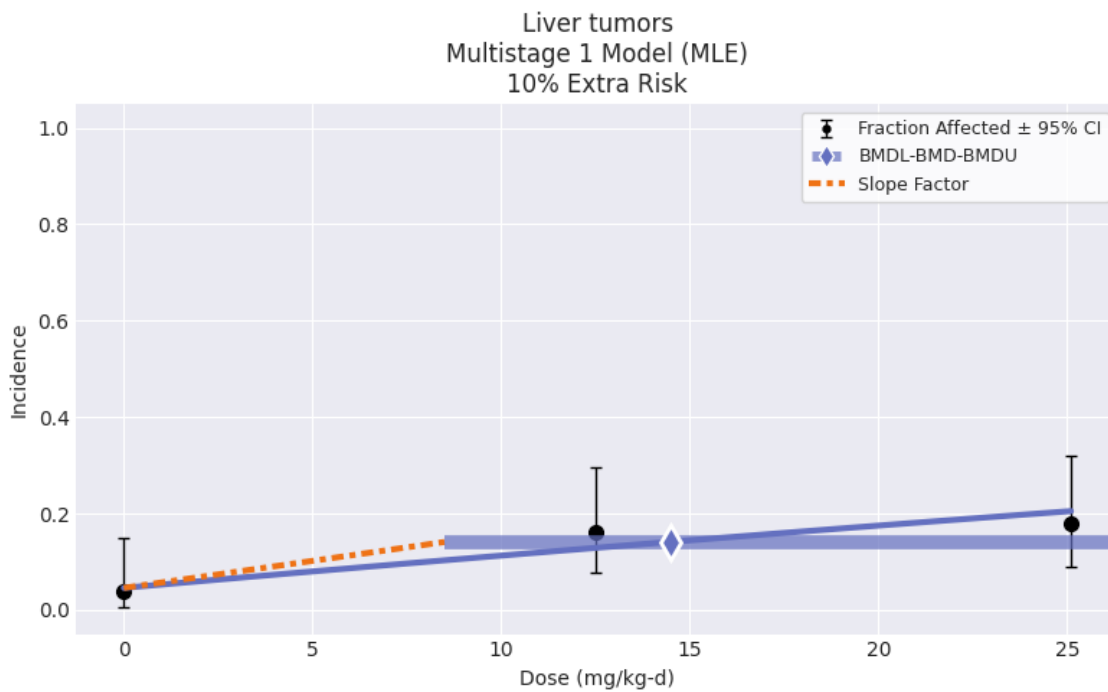
Multitumor MS Combo Model

Version: pybmds 25.1 (bmdscore 25.1)

BMD	14.4773
BMDL	8.51111
BMDU	46.5151
Slope Factor	0.0117494
Combined Log-likelihood	-54.2742
Combined Log-likelihood Constant	-48.8537

Individual Model Results

Liver tumors: Multistage 1



Multistage 1 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	-17	-18	18
b1	0.1	0	10000

Modeling Summary:

BMD	14.4773
BMDL	8.51109
BMDU	46.5158
Slope Factor	0.0117494
AIC	112.548
Log-Likelihood	-54.2742
P-Value	0.414033
Overall d.f.	1
Chi ²	0.66719

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.045592	no	0.0436509
b1	0.00727766	no	0.0624532

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	2.2796	0.045592	-0.189557
12.5	50	8	6.42915	0.128583	0.663657
25.1	50	9	10.2468	0.204936	-0.436827

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-53.9504	3	-	-	-
Fitted model	-54.2742	2	0.647608	1	0.420969
Reduced model	-57.0001	1	6.09946	2	0.0473718

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.

Liver tumors

NTP 1986

Liver tumors, male mice

1,2-DCP

Report Generated: 2026-Jan-26 16:01 UTC

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

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

Modeling Summary

Datasets

Name: Liver tumors

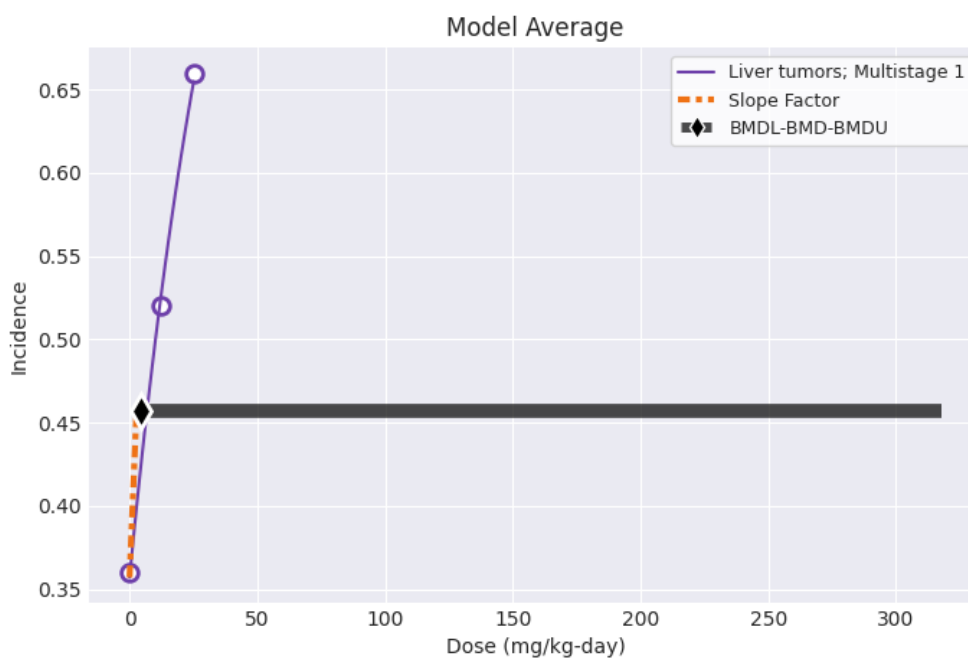
Dose (mg/kg-day)	0	12.5	25.1
Affected / Total (%)	18.0/50.0 (36.0%)	26.0/50.0 (52.0%)	33.0/50.0 (66.0%)

Settings

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

Maximum Likelihood Approach

Dataset: Model	BMDL	BMD	BMDU	CSF	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD
Liver tumors: Multistage 1	2.712	4.253	9.348	0.037	0.883	202.702	0.042	0.042



Multitumor MS Combo Model

Version: pybmds 25.1 (bmdscore 25.1)

BMD	4.25256
BMDL	2.71195
BMDU	317.683
Slope Factor	0.0368738
Combined Log-likelihood	-99.3509
Combined Log-likelihood Constant	-92.8739

Individual Model Results

Liver tumors: Multistage 1



Multistage 1 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	-17	-18	18
b1	0.1	0	10000

Modeling Summary:

BMD	4.25256
BMDL	2.71188
BMDU	9.34802
Slope Factor	0.0368748
AIC	202.702
Log-Likelihood	-99.3509
P-Value	0.882863
Overall d.f.	1
Chi ²	0.0217094

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.35716	no	0.016537
b1	0.0247758	no	0.202117

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	18	17.858	0.35716	0.0419058
12.5	50	26	26.4184	0.528369	-0.11854
25.1	50	33	32.7417	0.654835	0.0768221

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-99.34	3	-	-	-
Fitted model	-99.3509	2	0.0217131	1	0.882853
Reduced model	-103.919	1	9.15741	2	0.0102682

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

U.S. Environmental Protection Agency. (2025). BMDS Online (25.1; pybmbs 25.1; bmdscore 25.1) [Software]. Available from <https://bmdsonline.epa.gov>. Accessed January 26, 2026.

Mammary gland tumors

NTP, 1986

Mammary gland tumors

1,2-DCP

Report Generated: 2026-Jan-26 16:01 UTC

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

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

Modeling Summary

Datasets

Name: Mammary gland tumors

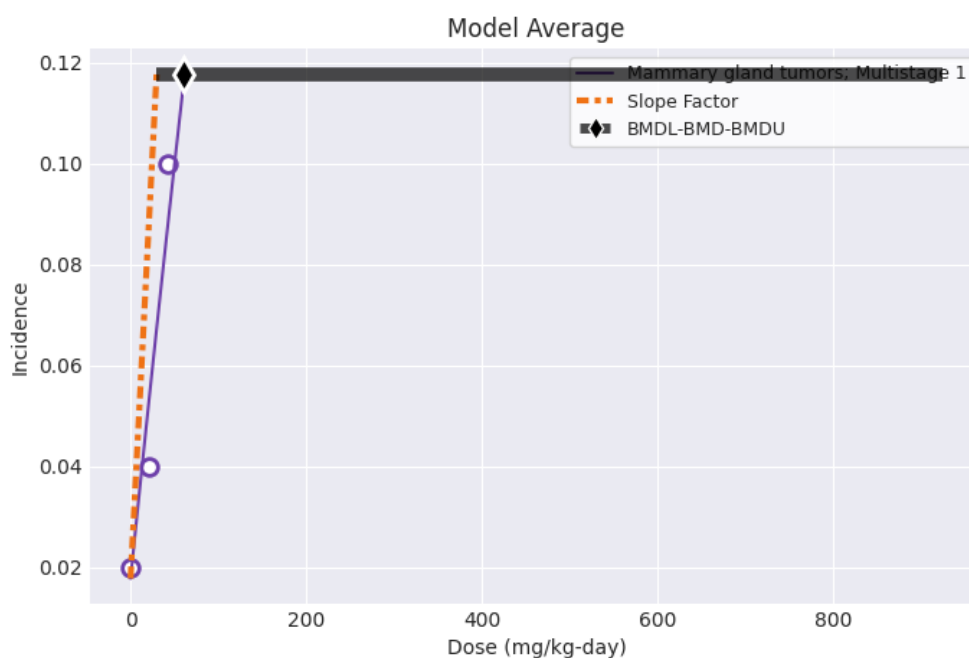
Dose (mg/kg-day)	0	21.4	43
Affected / Total (%)	1.0/50.0 (2.0%)	2.0/50.0 (4.0%)	5.0/50.0 (10.0%)

Settings

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

Maximum Likelihood Approach

Dataset: Model	BMDL	BMD	BMDU	CSF	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD
Mammary gland tumors: Multistage 1	29.452	60.389	-	0.003	0.598	63.399	0.122	0.28



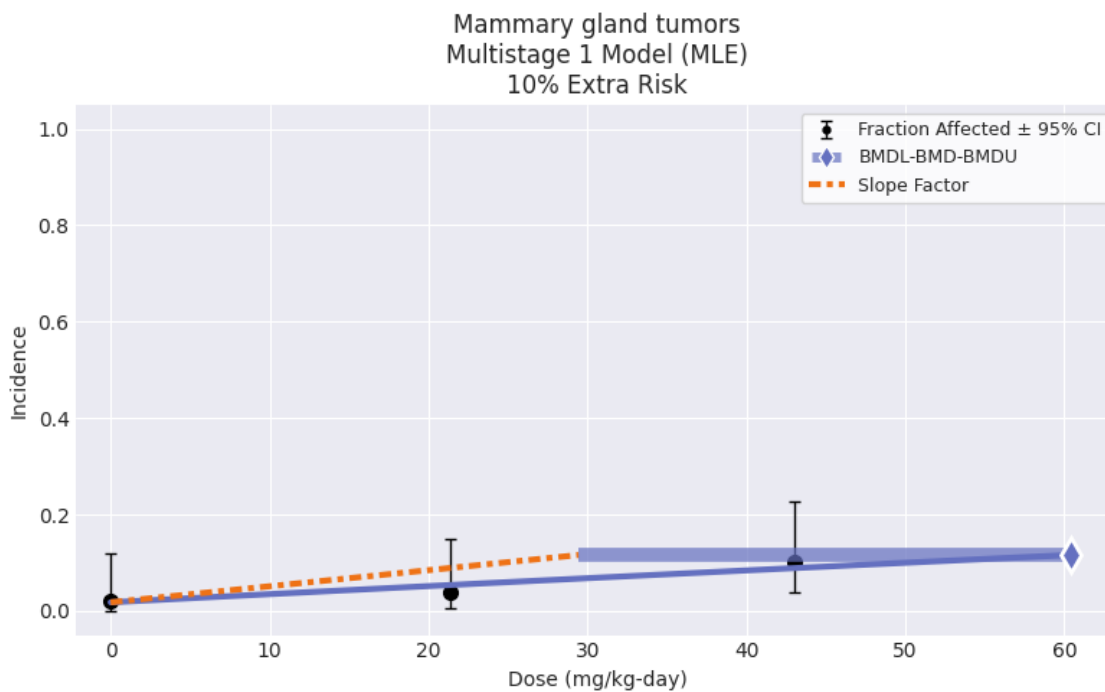
Multitumor MS Combo Model

Version: pybmds 25.1 (bmdscore 25.1)

BMD	60.3894
BMDL	29.5901
BMDU	923.581
Slope Factor	0.0033795
Combined Log-likelihood	-29.6996
Combined Log-likelihood Constant	-25.5891

Individual Model Results

Mammary gland tumors: Multistage 1



Multistage 1 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	-17	-18	18
b1	0.1	0	10000

Modeling Summary:

BMD	60.3894
BMDL	29.4524
BMDU	-9999
Slope Factor	0.00339531
AIC	63.3991
Log-Likelihood	-29.6996
P-Value	0.597507
Overall d.f.	1
Chi ²	0.278772

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0177255	no	0.061783
b1	0.00174469	no	0.0367594

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	1	0.886274	0.0177255	0.121888
21.4	50	2	2.68619	0.0537238	-0.430394
43	50	5	4.43604	0.0887208	0.280494

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-29.5533	3	-	-	-
Fitted model	-29.6996	2	0.292493	1	0.588627
Reduced model	-31.2323	1	3.35802	2	0.186559

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.

Matsumoto 2013, 1,2-DCP

Matsumoto 2013, 1936440

2-year exposure, female rats

Lung

Report Generated: 2026-Jan-26 14:01 UTC

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

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

Modeling Summary

Datasets

Name: Lung tumors, female rats

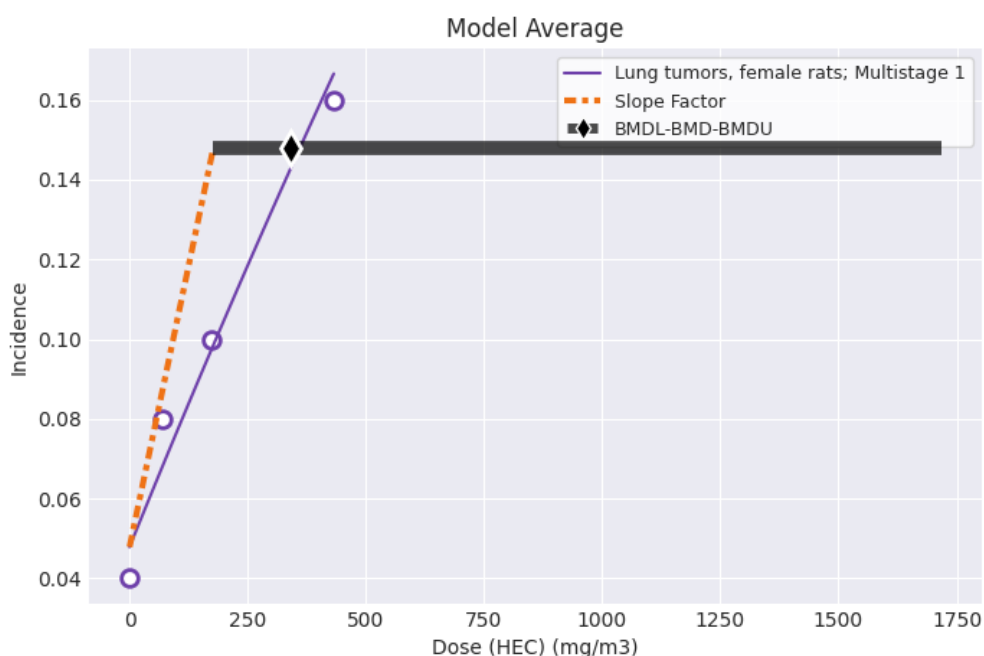
Dose (mg/m3)	0	69.2	173	432
Affected / Total (%)	2.0/50.0 (4.0%)	4.0/50.0 (8.0%)	5.0/50.0 (10.0%)	8.0/50.0 (16.0%)

Settings

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

Maximum Likelihood Approach

Dataset: Model	BMDL	BMD	BMDU	CSF	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD
Lung tumors, female rats: Multistage 1	177.213	341.971	-	<0.001	0.904	125.347	-0.262	-0.124



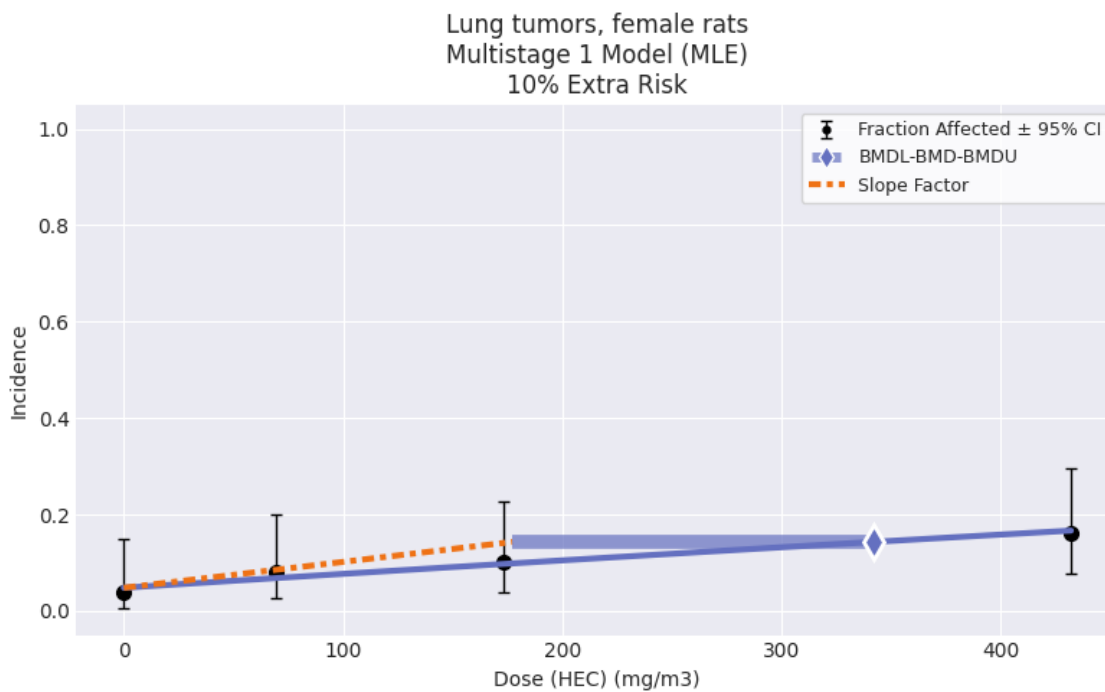
Multitumor MS Combo Model

Version: pybmds 25.1 (bmdscore 25.1)

BMD	341.971
BMDL	177.213
BMDU	1717.44
Slope Factor	0.000564294
Combined Log-likelihood	-60.6734
Combined Log-likelihood Constant	-54.1255

Individual Model Results

Lung tumors, female rats: Multistage 1



Multistage 1 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	-17	-18	18
b1	0.1	0	10000

Modeling Summary:

BMD	341.971
BMDL	177.213
BMDU	-9999
Slope Factor	0.000564293
AIC	125.347
Log-Likelihood	-60.6734
P-Value	0.903976
Overall d.f.	2
Chi ²	0.201904

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0479005	no	0.0345482
b1	0.000308098	no	0.0691964

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	2.39503	0.0479005	-0.261595
69.2	50	4	3.39924	0.0679848	0.33752
173	50	5	4.86598	0.0973196	0.0639466
432	50	8	8.32761	0.166552	-0.124352

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-60.5733	4	-	-	-
Fitted model	-60.6734	2	0.200217	2	0.904739
Reduced model	-62.7912	1	4.4357	3	0.218098

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.

Matsumoto 2013, 1,2-DCP

Matsumoto 2013, 1936440

2-year exposure, male rats

Lung + Spleen

Report Generated: 2026-Jan-26 14:01 UTC

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

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

Modeling Summary

Datasets

Name: Lung tumors, male rats

Dose (mg/m3)	0	77.2	192	482.5
Affected / Total (%)	9.0/50.0 (18.0%)	18.0/50.0 (36.0%)	14.0/50.0 (28.0%)	18.0/50.0 (36.0%)

Name: Spleen tumors, male rats

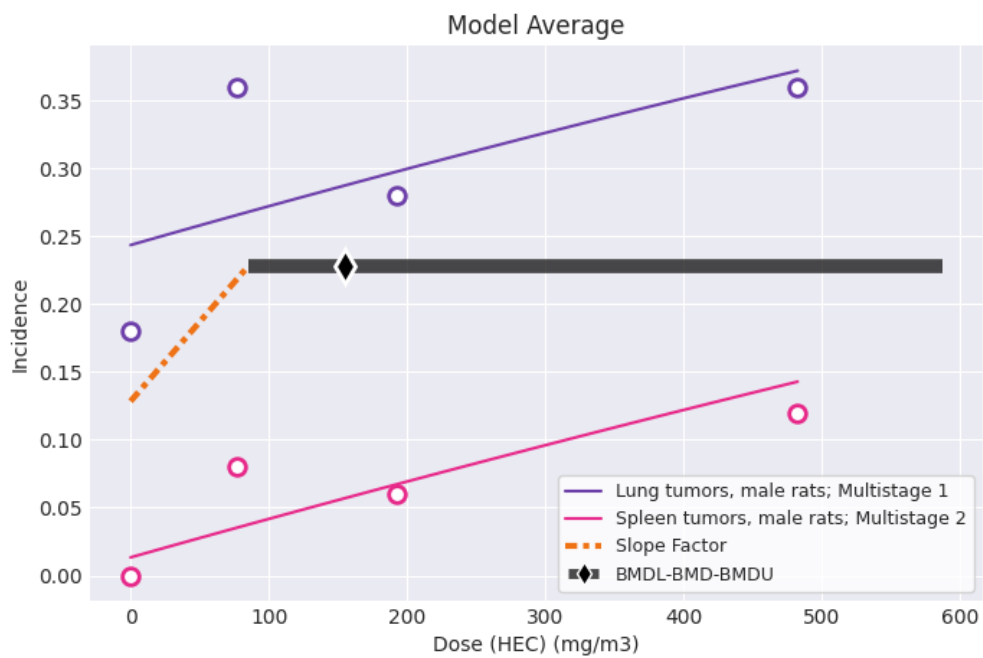
Dose (mg/m3)	0	77.2	192	482.5
Affected / Total (%)	0.0/50.0 (0.0%)	4.0/50.0 (8.0%)	3.0/50.0 (6.0%)	6.0/50.0 (12.0%)

Settings

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

Maximum Likelihood Approach

Dataset: Model	BMDL	BMD	BMDU	CSF	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD
Average	85.422	155.388	587.06	0.001	-	-	-	-
Lung tumors, male rats: Multistage 1	120.547	272.867	-	<0.001	0.176	244.532	-1.049	-0.274
Spleen tumors, male rats: Multistage 2	193.717	360.918	-	<0.001	0.145	95.054	-0.821	-0.464



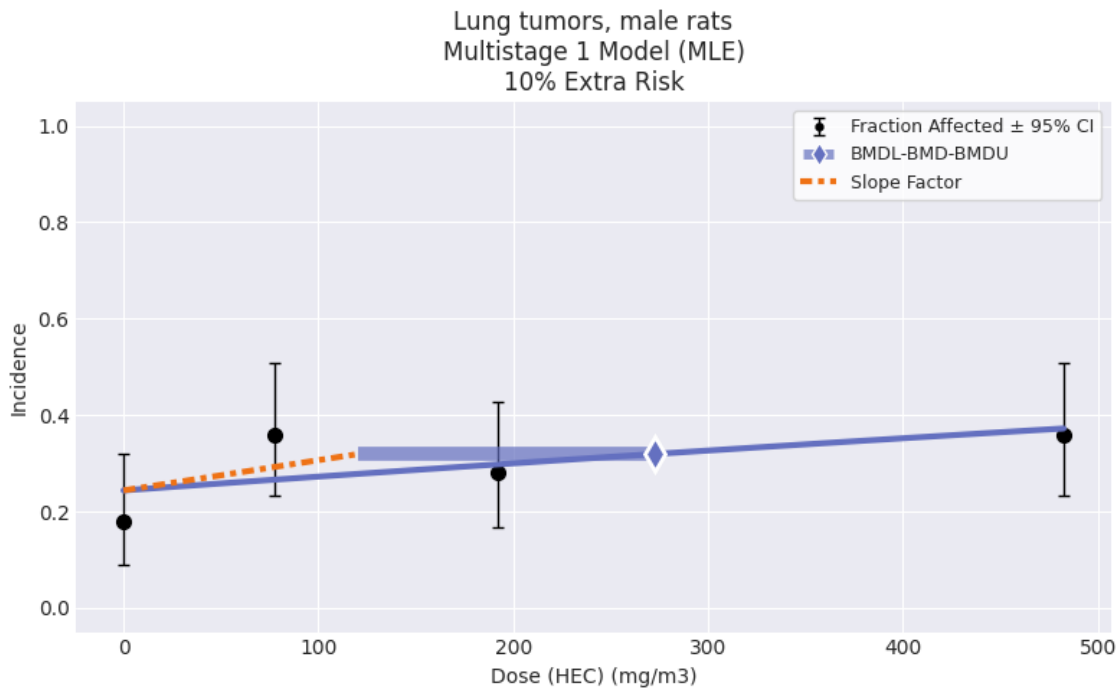
Multitumor MS Combo Model

Version: pybmds 25.1 (bmddscore 25.1)

BMD	155.388
BMDL	85.4217
BMDU	587.06
Slope Factor	0.00117066
Combined Log-likelihood	-165.793
Combined Log-likelihood Constant	-149.069

Individual Model Results

Lung tumors, male rats: Multistage 1



Multistage 1 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	-17	-18	18
b1	0.1	0	10000

Modeling Summary:

BMD	272.867
BMDL	120.547
BMDU	-9999
Slope Factor	0.00082955
AIC	244.532
Log-Likelihood	-120.266
P-Value	0.175893
Overall d.f.	2
Chi ²	3.47576

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.243695	no	0.0154063
b1	0.000386124	no	0.13452

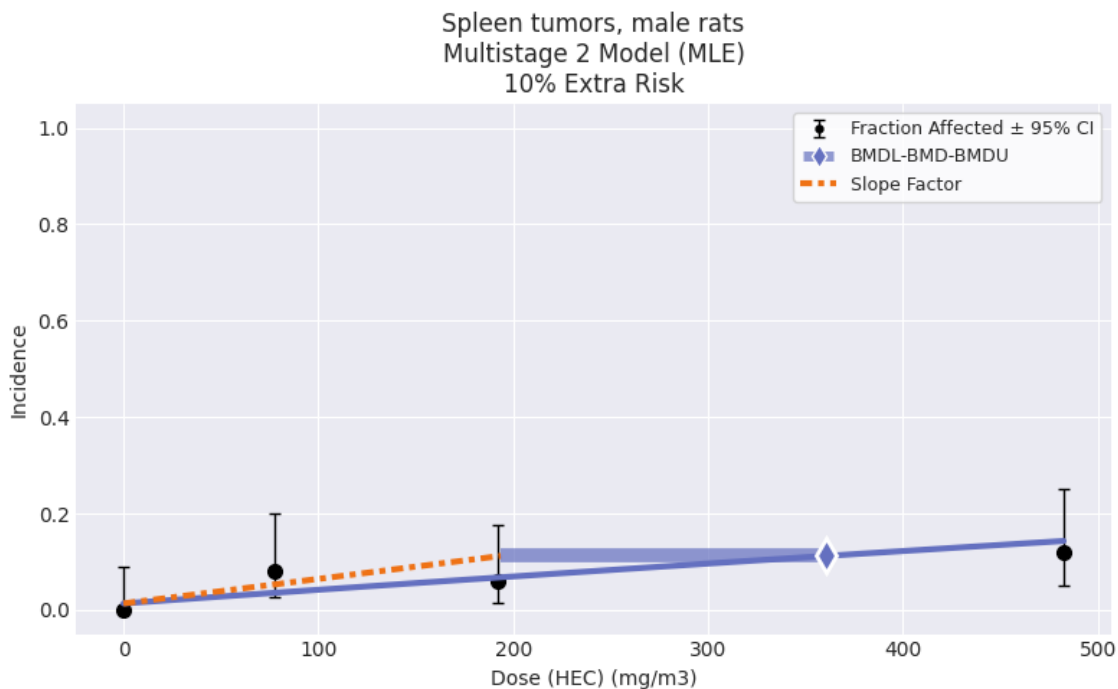
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	9	12.1848	0.243695	-1.04911
77.2	50	18	13.2954	0.265907	1.50592
192	50	14	14.8868	0.297737	-0.274277
482.5	50	18	18.6126	0.372251	-0.17921

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-118.559	4	-	-	-
Fitted model	-120.266	2	3.41333	2	0.18147
Reduced model	-121.314	1	5.50892	3	0.138106

Spleen tumors, male rats: Multistage 2



Multistage 2 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Modeling approach	frequentist_restricted
Degree	2

Parameter Settings:

Parameter	Initial	Min	Max
g	-17	-18	18
b1	0.1	0	10000
b2	0.1	0	10000

Modeling Summary:

BMD	360.918
BMDL	193.717
BMDU	-9999
Slope Factor	0.000516216
AIC	95.0536
Log-Likelihood	-45.5268
P-Value	0.144905
Overall d.f.	2
Chi ²	3.86335

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0133126	no	0.114957
b1	0.000291924	no	0.0715987
b2	0	yes	Not Reported

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	50	0	0.665629	0.0133126	-0.821347
77.2	50	4	1.76502	0.0353004	1.71279
192	50	3	3.35472	0.0670945	-0.200513
482.5	50	6	7.14733	0.142947	-0.463568

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-43.6331	4	-	-	-
Fitted model	-45.5268	2	3.78745	2	0.15051
Reduced model	-48.1018	1	8.93745	3	0.0301342

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.

Matsumoto 2013, 1,2-DCP

Matsumoto 2013, 1936440

2-year exposure, male rats

Lung + Spleen + Harderian gland tumors

Report Generated: 2026-Jan-26 14:01 UTC

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

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

Modeling Summary

Datasets

Name: Lung tumors, male rats

Dose (mg/m3)	0	77.2	192	482.5
Affected / Total (%)	9.0/50.0 (18.0%)	18.0/50.0 (36.0%)	14.0/50.0 (28.0%)	18.0/50.0 (36.0%)

Name: Harderian gland, male rats

Dose (mg/m3)	0	77.2	192	482.5
Affected / Total (%)	1.0/50.0 (2.0%)	2.0/50.0 (4.0%)	3.0/50.0 (6.0%)	6.0/50.0 (12.0%)

Name: Spleen tumors, male rats

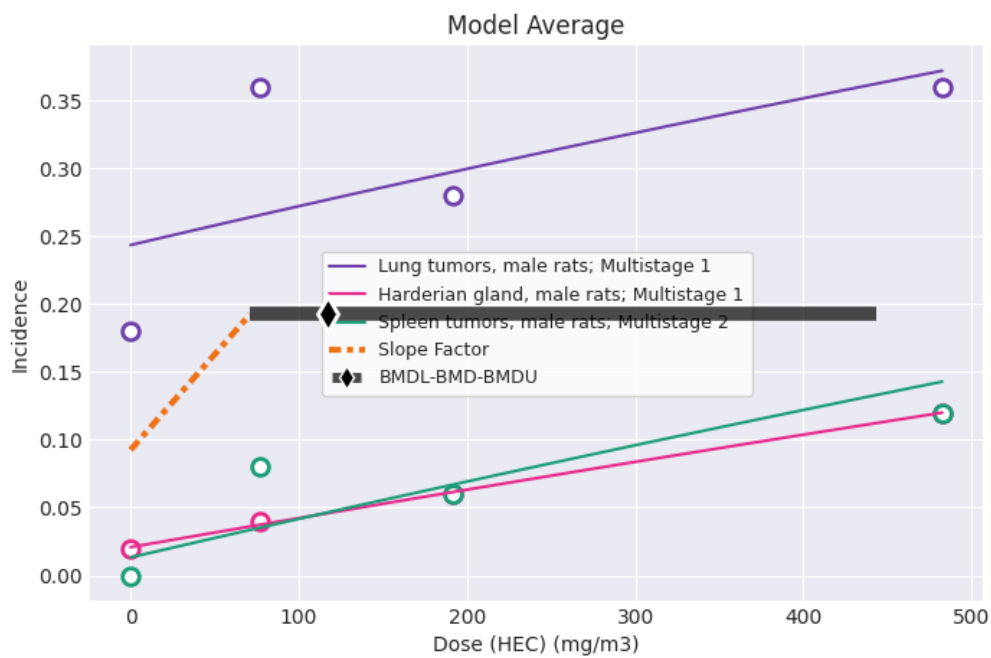
Dose (mg/m3)	0	77.2	192	482.5
Affected / Total (%)	0.0/50.0 (0.0%)	4.0/50.0 (8.0%)	3.0/50.0 (6.0%)	6.0/50.0 (12.0%)

Settings

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

Maximum Likelihood Approach

Dataset: Model	BMDL	BMD	BMDU	CSF	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD
Average	71.003	117.142	443.295	0.001	-	-	-	-
Lung tumors, male rats: Multistage 1	120.547	272.867	-	<0.001	0.176	244.532	-1.049	-0.274
Harderian gland, male rats: Multistage 1	251.121	475.928	-	<0.001	0.993	90	-0.043	-0.001
Spleen tumors, male rats: Multistage 2	193.717	360.918	-	<0.001	0.145	95.054	-0.821	-0.464



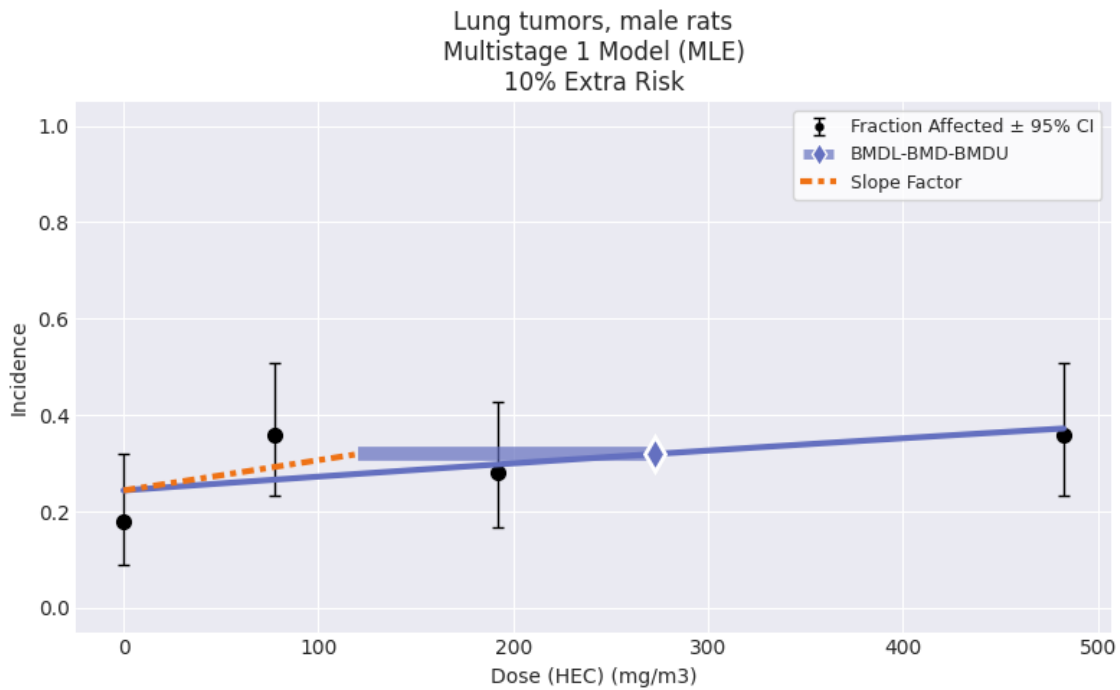
Multitumor MS Combo Model

Version: pybmds 25.1 (bmdscore 25.1)

BMD	117.142
BMDL	71.003
BMDU	443.295
Slope Factor	0.00140839
Combined Log-likelihood	-208.793
Combined Log-likelihood Constant	-186.556

Individual Model Results

Lung tumors, male rats: Multistage 1



Multistage 1 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	-17	-18	18
b1	0.1	0	10000

Modeling Summary:

BMD	272.867
BMDL	120.547
BMDU	-9999
Slope Factor	0.00082955
AIC	244.532
Log-Likelihood	-120.266
P-Value	0.175893
Overall d.f.	2
Chi ²	3.47576

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.243695	no	0.0154063
b1	0.000386124	no	0.13452

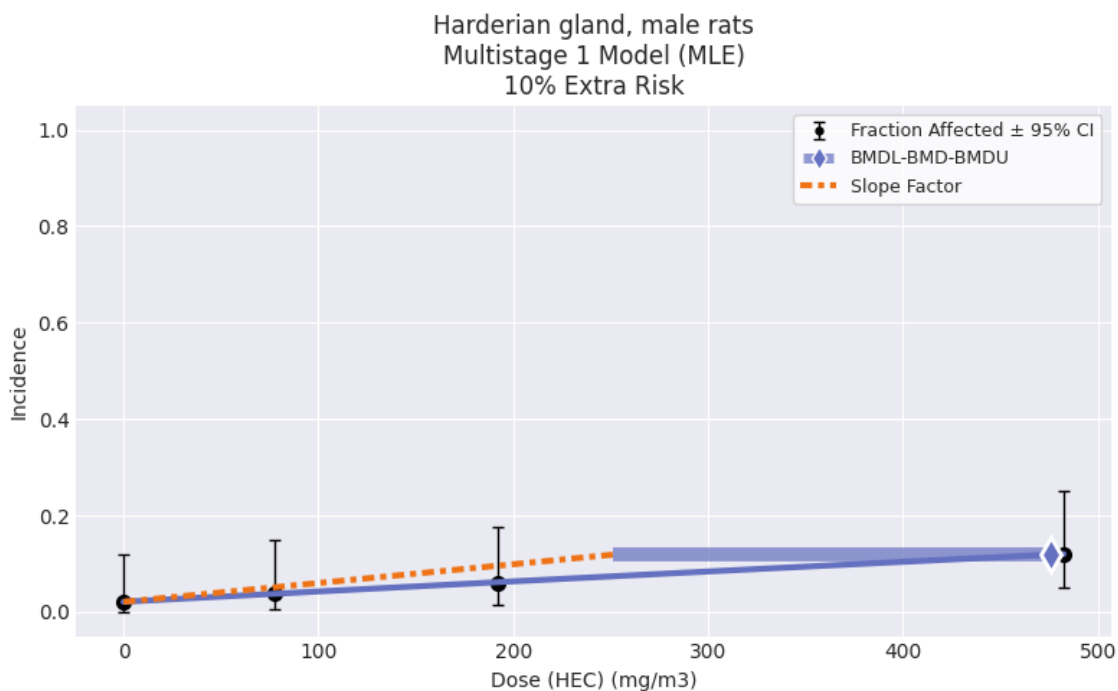
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	9	12.1848	0.243695	-1.04911
77.2	50	18	13.2954	0.265907	1.50592
192	50	14	14.8868	0.297737	-0.274277
482.5	50	18	18.6126	0.372251	-0.17921

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-118.559	4	-	-	-
Fitted model	-120.266	2	3.41333	2	0.18147
Reduced model	-121.314	1	5.50892	3	0.138106

Harderian gland, male rats: Multistage 1



Multistage 1 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	-17	-18	18
b1	0.1	0	10000

Modeling Summary:

BMD	475.928
BMDL	251.121
BMDU	-9999
Slope Factor	0.000398214
AIC	90.0005
Log-Likelihood	-43.0002
P-Value	0.993497
Overall d.f.	2
Chi ²	0.0130482

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0208629	no	0.0526688
b1	0.000221379	no	0.052134

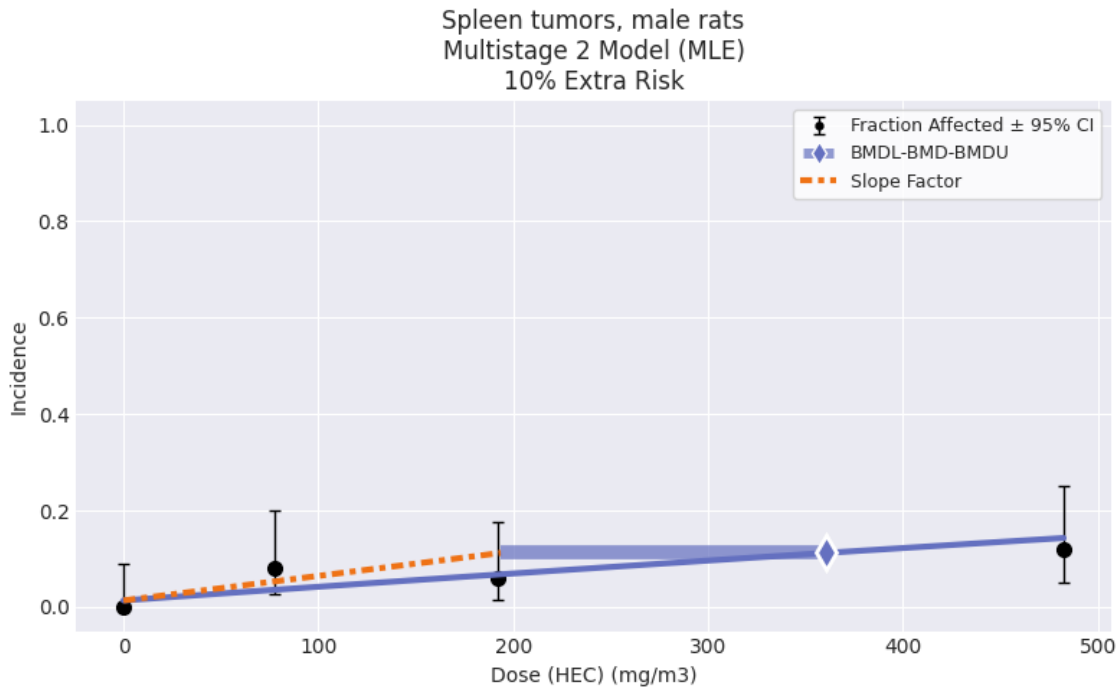
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	1	1.04315	0.0208629	-0.0426925
77.2	50	2	1.87273	0.0374547	0.094791
192	50	3	3.08044	0.0616089	-0.0473144
482.5	50	6	6.00289	0.120058	-0.00125814

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-42.9938	4	-	-	-
Fitted model	-43.0002	2	0.0129026	2	0.993569
Reduced model	-45.3935	1	4.79943	3	0.187087

Spleen tumors, male rats: Multistage 2



Multistage 2 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Modeling approach	frequentist_restricted
Degree	2

Parameter Settings:

Parameter	Initial	Min	Max
g	-17	-18	18
b1	0.1	0	10000
b2	0.1	0	10000

Modeling Summary:

BMD	360.918
BMDL	193.717
BMDU	-9999
Slope Factor	0.000516216
AIC	95.0536
Log-Likelihood	-45.5268
P-Value	0.144905
Overall d.f.	2
Chi ²	3.86335

Model Parameters:

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Variable	Estimate	On Bound	Std Error
g	0.0133126	no	0.114957
b1	0.000291924	no	0.0715987
b2	0	yes	Not Reported

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	50	0	0.665629	0.0133126	-0.821347
77.2	50	4	1.76502	0.0353004	1.71279
192	50	3	3.35472	0.0670945	-0.200513
482.5	50	6	7.14733	0.142947	-0.463568

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-43.6331	4	-	-	-
Fitted model	-45.5268	2	3.78745	2	0.15051
Reduced model	-48.1018	1	8.93745	3	0.0301342

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.

Matsumoto 2023, 1,2-DCP

Matsumoto 2023, 1966440

2-year exposure, male rats

Report Generated: 2026-Jan-26 14:01 UTC

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

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

Session for Submucosal gland respiratory metaplasia, male rats

Dataset

Name: Submucosal gland respiratory metaplasia, male rats

Dose (mg/m3)	N	Incidence
0	50	9
4.73	50	13
11.8	50	12
29.55	50	18

Settings

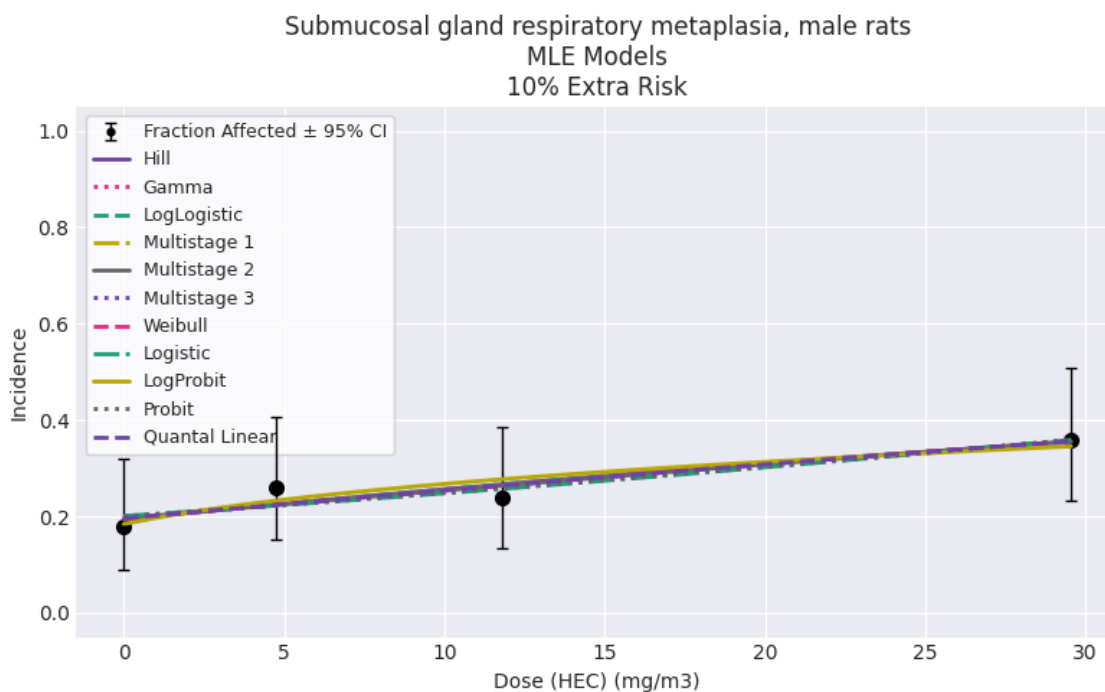
Setting	Value
BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Maximum Multistage Degree	3

Maximum Likelihood Approach

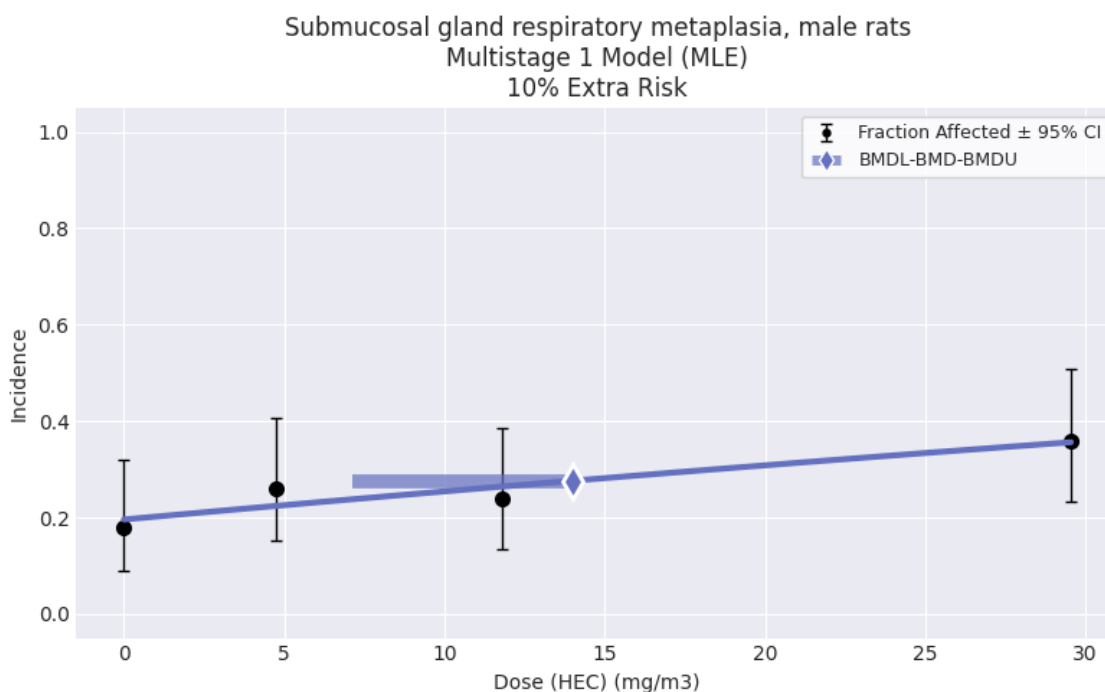
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	6.113	13.193	-	0.738	229.495	-0.249	-0.428	Viable
Gamma	7.149	13.993	-	0.738	229.493	-0.281	-0.387	Viable
LogLogistic	6.113	13.193	-	0.738	229.495	-0.249	-0.428	Viable
Multistage 1 ^{ab}	7.149	13.993	-	0.738	229.493	-0.281	-0.387	Recommended - Lowest AIC
Multistage 2	7.149	14.066	-	0.436	231.493	-0.284	-0.383	Viable
Multistage 3	7.154	15.329	-	0.438	231.486	-0.325	-0.321	Viable
Weibull	7.149	13.993	-	0.738	229.493	-0.281	-0.387	Viable
Logistic	10.216	16.246	-	0.732	229.509	-0.372	-0.28	Viable
LogProbit	0	9.731	-	0.436	231.507	-0.082	-0.589	Unusable BMDL does not exist
Probit	9.84	15.958	-	0.733	229.506	-0.361	-0.293	Viable
Quantal Linear	7.149	13.993	-	0.738	229.493	-0.281	-0.387	Viable

^a BMDS recommended best fitting model

^b User selected best fitting model; Multistage 1 model selected based on lowest AIC



Selected Model: Multistage 1



Multistage 1 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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	13.9931
BMDL	7.14888
BMDU	-9999
AIC	229.493
Log-Likelihood	-112.747
P-Value	0.738278
Overall d.f.	2
Chi ²	0.606869

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.195764	no	0.0167828
b1	0.00752949	no	0.116481

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	9	9.7882	0.195764	-0.280926
4.73	50	13	11.1951	0.223902	0.612317
11.8	50	12	13.2068	0.264136	-0.387118
29.55	50	18	17.8097	0.356195	0.0561898

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-112.447	4	-	-	-
Fitted model	-112.747	2	0.598481	2	0.741381
Reduced model	-114.611	1	4.32791	3	0.228163

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.

Non-cancer liver lesions

NTP 1986

Non-cancer liver lesions

1,2-DCP

Report Generated: 2026-Jan-26 16:01 UTC

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

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

Session for Hepatocytomegaly

Dataset

Name: Hepatocytomegaly

Dose (mg/kg-day)	N	Incidence
0	50	3
89.3	50	5
179	50	15

Settings

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

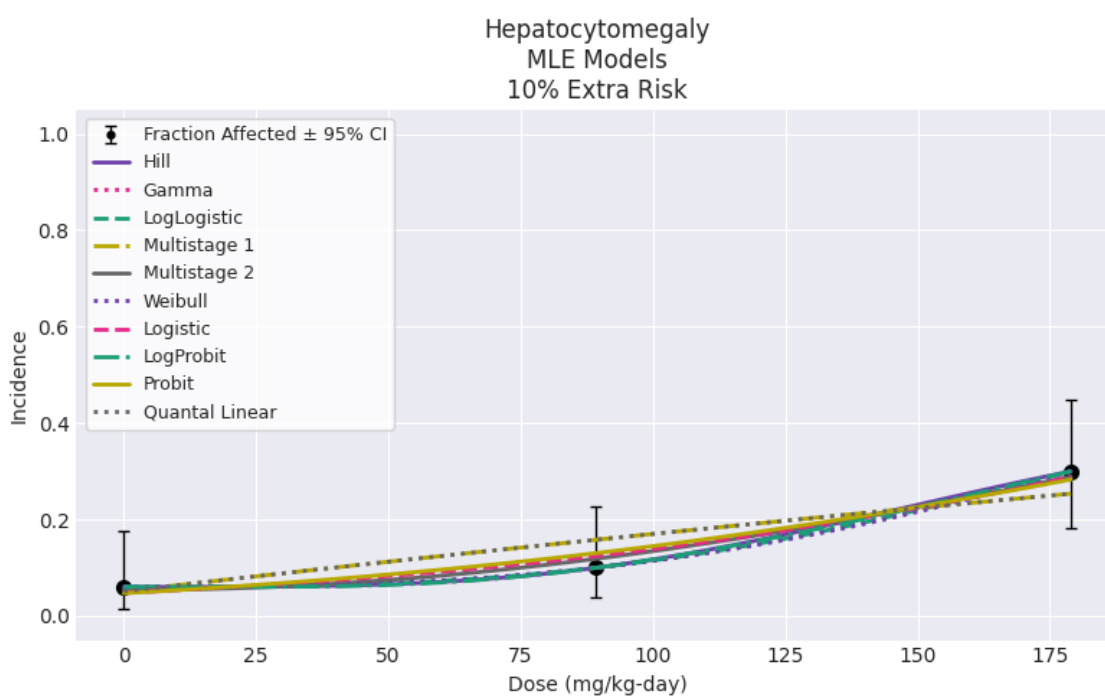
Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	61.88	118.431	176.751	-	124.291	<0.001	-0.	Questionable Zero degrees of freedom; saturated model
Gamma	61.957	121.106	170.955	-	122.291	<0.001	-0.	Questionable Zero degrees of freedom; saturated model
LogLogistic	61.828	121.982	175.617	-	122.291	<0.001	-0.	Questionable Zero degrees of freedom; saturated model
Multistage 1	50.111	78.436	158.76	0.165	122.346	0.301	-1.124	Viable
Multistage 2	59.711	108.733	153.033	0.627	120.534	0.198	-0.407	Viable
Weibull ^{ab}	61.956	123.167	175.899	1.	120.291	<0.001	-0.	Recommended - Lowest AIC
Logistic	82.751	103.099	143.046	0.491	120.77	0.405	-0.523	Viable
LogProbit	63.376	119.073	177.237	-	122.291	-0.	<0.001	Questionable Zero degrees of freedom; saturated model
Probit	77.592	98.301	143.045	0.416	120.968	0.432	-0.636	Viable

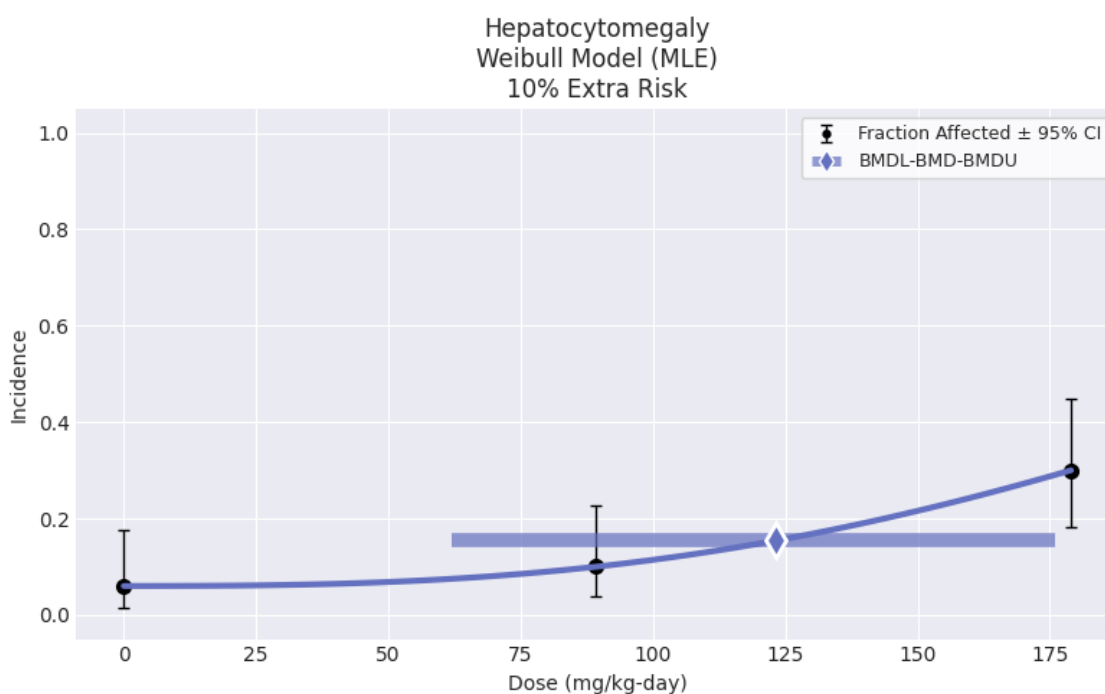
Quantal Linear	50.111	78.436	158.765	0.165	122.346	0.301	-1.124	Viable
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^a BMDS recommended best fitting model

^b User selected best fitting model; model selected based on lowest AIC



Selected Model: Weibull



Weibull Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-18	18
a	1	1	18
b	1e-06	1e-06	100

Modeling Summary:

BMD	123.167
BMDL	61.9561
BMDU	175.899
AIC	120.291
Log-Likelihood	-58.1457
P-Value	1
Overall d.f.	1
Chi ²	3.49833e-13

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.06	no	0.0371479
a	2.75226	no	1.90973
b	1.85822e-07	yes	Not Reported

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	50	3	3	0.06	2.98167e-07
89.3	50	5	5	0.1	-4.62187e-07
179	50	15	15	0.3	2.17513e-07

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-58.1457	3	-	-	-
Fitted model	-58.1457	2	3.41061e-13	1	1
Reduced model	-64.2672	1	12.2429	2	0.00219532

Session for Necrosis

Dataset

Name: Necrosis

Dose (mg/kg-day)	N	Incidence
0	50	2
89.3	50	5
179	50	10

Settings

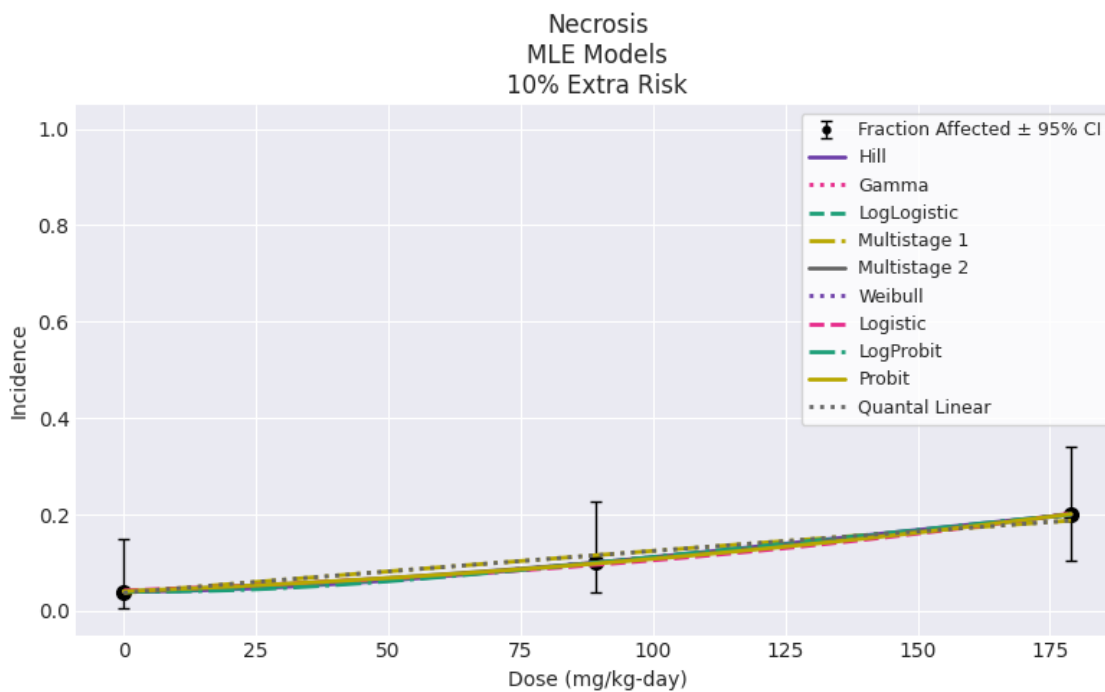
Setting	Value
BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Maximum Multistage Degree	2

Maximum Likelihood Approach

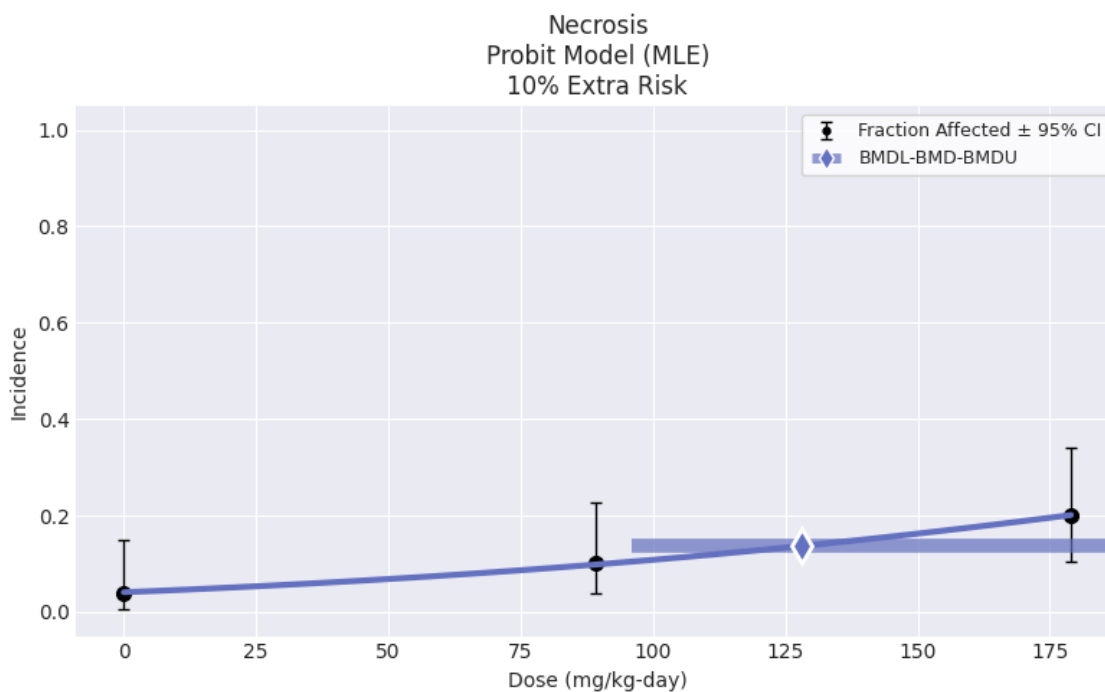
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	0	121.951	290.786	-	107.343	<0.001	-0.	Unusable Zero degrees of freedom; saturated model BMDL does not exist
Gamma	67.055	123.533	283.887	-	105.343	<0.001	-0.	Questionable Zero degrees of freedom; saturated model
LogLogistic	63.301	123.388	289.173	-	105.343	<0.001	<0.001	Questionable Zero degrees of freedom; saturated model
Multistage 1	66.045	111.337	300.807	0.673	103.524	0.094	-0.342	Viable
Multistage 2	67.054	125.242	283.908	-	105.343	<0.001	-0.	Questionable Zero degrees of freedom; saturated model
Weibull	67.055	123.988	283.878	-	105.343	<0.001	-0.	Questionable Zero degrees of freedom; saturated model
Logistic	101.488	131.965	252.537	0.888	103.363	-0.08	0.109	Viable
LogProbit	0	121.744	-	-	105.343	<0.001	-0.	Unusable Zero degrees of freedom; saturated model BMDL does not exist
Probit ^{ab}	96.071	128.074	255.944	0.959	103.346	-0.026	0.04	Recommended - Lowest AIC
Quantal Linear	66.045	111.337	300.771	0.673	103.524	0.094	-0.342	Viable

^a BMDS recommended best fitting model

^b User selected best fitting model; model selected based on lowest AIC



Selected Model: Probit



Probit Model

Version: pybmds 25.1 (bmdscore 25.1)

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	18

Modeling Summary:

BMD	128.074
BMDL	96.0715
BMDU	255.944
AIC	103.346
Log-Likelihood	-49.6728
P-Value	0.959478
Overall d.f.	1
Chi ²	0.00258146

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-1.74218	no	0.273132
b	0.00504979	no	0.00203756

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	2.03695	0.0407389	-0.0264302
89.3	50	5	4.91561	0.0983122	0.0400852
179	50	10	10.0471	0.200942	-0.0166156

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-49.6715	3	-	-	-
Fitted model	-49.6728	2	0.00257774	1	0.959508
Reduced model	-53.0142	1	6.68551	2	0.0353394

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.

Non-cancer liver pathology

NTP, 1986

Non-cancer liver pathology, female rats

1,2-DCP

Report Generated: 2026-Jan-26 16:01 UTC

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

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

Session for Clear cell foci

Dataset

Name: Clear cell foci

Dose (mg/kg-day)	N	Incidence
0	50	3
89.3	50	5
179	50	11

Settings

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

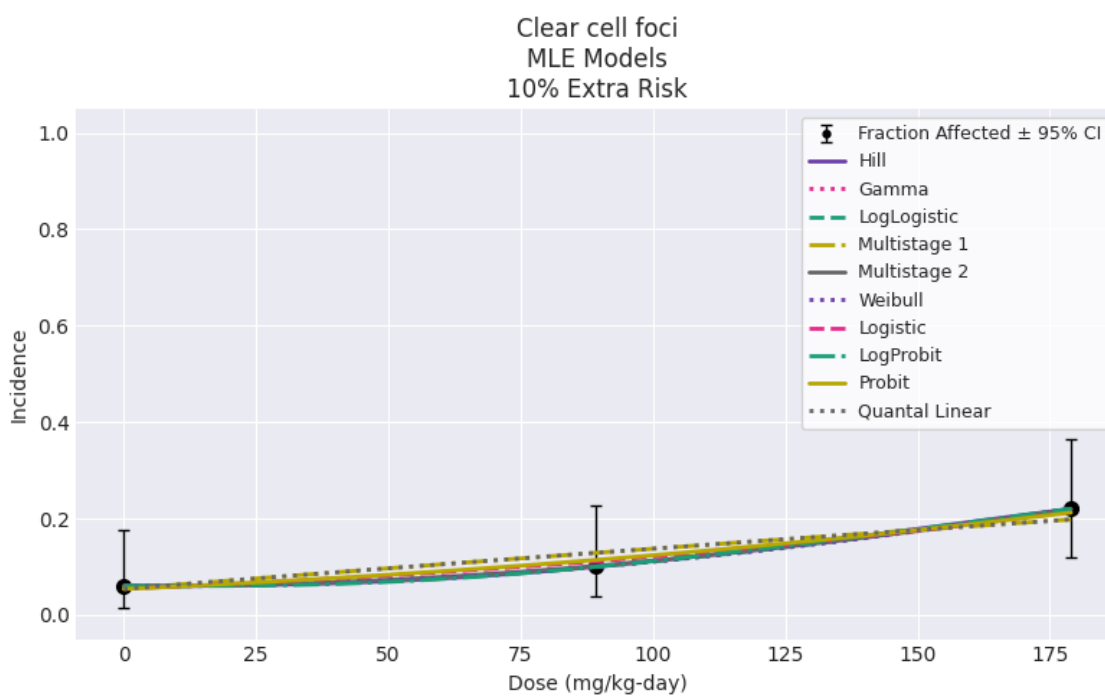
Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	0.007	132.829	300.831	-	115.896	-0.	<0.001	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 Zero degrees of freedom; saturated model BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0
Gamma	69.076	135.08	293.569	-	113.896	-0.	-0.	Questionable Zero degrees of freedom; saturated model
LogLogistic	65.891	135.452	298.683	-	113.896	<0.001	<0.001	Questionable Zero degrees of freedom; saturated model
Multistage 1	65.5	114.228	369.032	0.455	112.475	0.189	-0.607	Viable
Multistage 2 ^{ab}	69.057	134.654	293.939	0.959	111.898	0.024	0.017	Recommended - Lowest AIC
Weibull	69.076	136.255	293.583	-	113.896	-0.	-0.	Questionable Zero degrees of freedom; saturated model

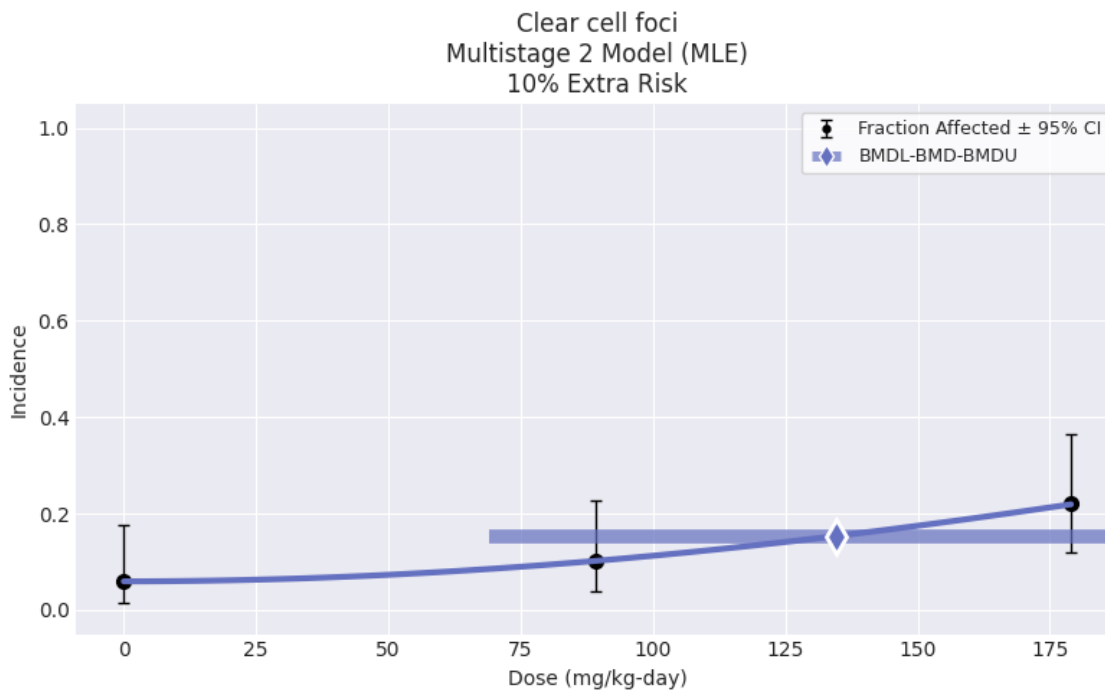
Logistic	96.449	127.919	274.158	0.748	112.	0.175	-0.252	Viable
LogProbit	0.006	133.004	-	-	113.896	<0.001	-0.	Questionable lowest dose/BMDL ratio > 3.0 lowest dose/BMDL ratio > 10.0 Zero degrees of freedom; saturated model BMD/BMDL ratio > 3.0 BMD/BMDL ratio > 20.0
Probit	91.54	124.951	283.361	0.694	112.053	0.197	-0.313	Viable
Quantal Linear	65.5	114.228	368.946	0.455	112.475	0.189	-0.607	Viable

^a BMDS recommended best fitting model

^b User selected best fitting model; model selected based on lowest AIC



Selected Model: Multistage 2



Multistage 2 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Modeling approach	frequentist_restricted
Degree	2

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-18	18
b1	0	0	10000
b2	0	0	10000

Modeling Summary:

BMD	134.654
BMDL	69.0568
BMDU	293.939
AIC	111.898
Log-Likelihood	-53.9492
P-Value	0.959131
Overall d.f.	1
Chi²	0.00262597

Model Parameters:

Variable	Estimate	On Bound	Std Error
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g	0.0592095	no	0.0330295
b1	1.02372e-18	yes	Not Reported
b2	5.81084e-06	no	0.0822255

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	50	3	2.96047	0.0592095	0.0236837
89.3	50	5	5.09048	0.10181	-0.0423157
179	50	11	10.9516	0.219031	0.0165661

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-53.9479	3	-	-	-
Fitted model	-53.9492	2	0.00263285	1	0.959077
Reduced model	-57.0001	1	6.10436	2	0.0472557

Session for Necrosis (combined)

Dataset

Name: Necrosis (combined)

Dose (mg/kg-day)	N	Incidence
0	50	2
89.3	50	1
179	50	12

Settings

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

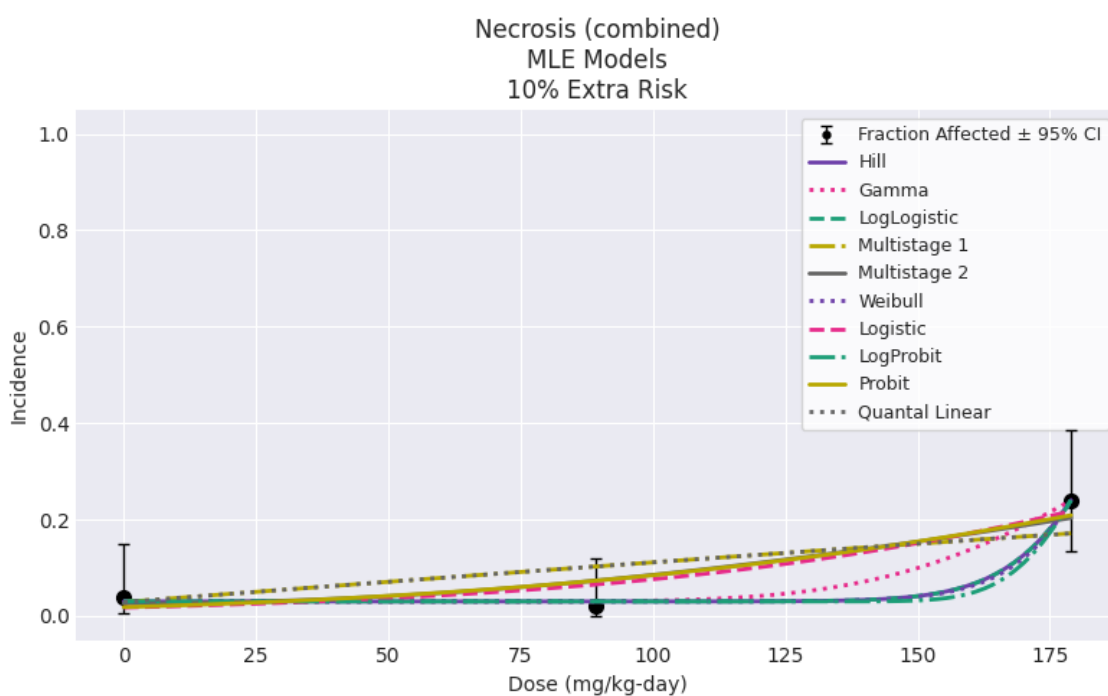
Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD	Recommendation and Notes
Hill	94.983	170.148	178.707	-	88.056	0.415	<0.001	Questionable Zero degrees of freedom; saturated model
Gamma	120.659	157.46	174.12	0.548	86.075	0.422	0.006	Viable
LogLogistic	121.602	170.166	176.975	0.558	86.056	0.415	<0.001	Viable
Multistage 1	71.509	118.686	263.386	0.018	92.792	0.489	-1.924	Questionable Goodness of fit p-value < 0.1
Multistage 2	99.096	129.611	182.316	0.088	89.338	0.63	-1.448	Questionable Goodness of fit p-value < 0.1

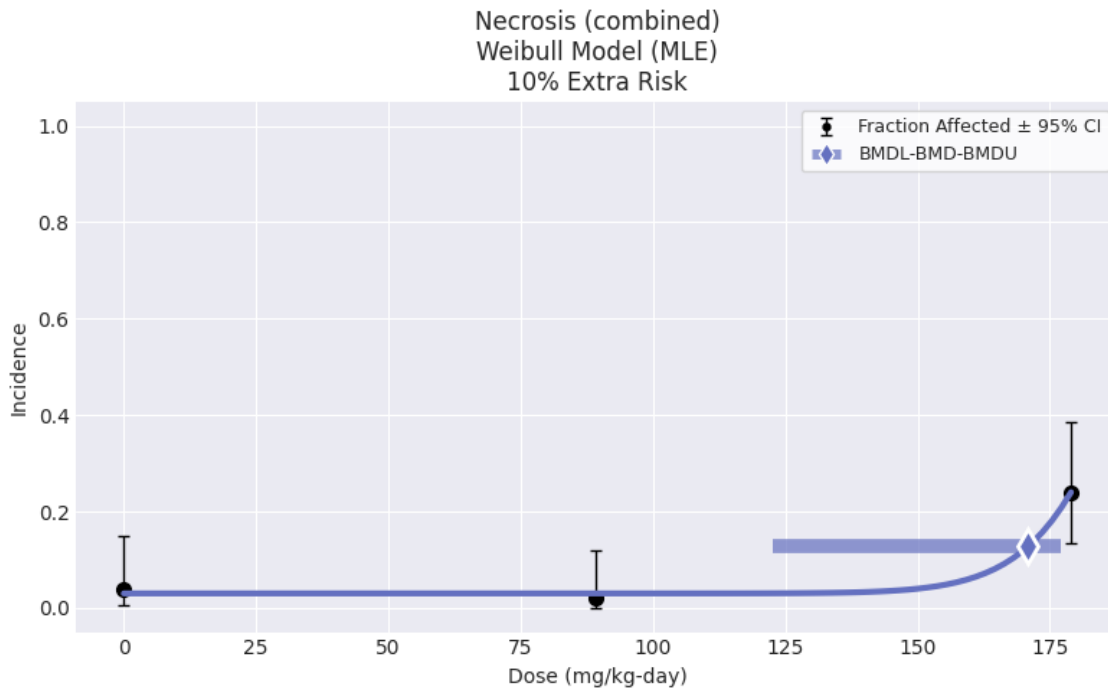
Weibull ^{ab}	122.731	170.842	177.11	0.558	86.056	0.415	<0.001	Recommended - Lowest AIC
Logistic	106.3	130.04	169.495	0.068	89.224	1.228	-1.295	Questionable Goodness of fit p-value < 0.1
LogProbit	118.779	171.625	178.015	-	88.056	0.415	<0.001	Questionable Zero degrees of freedom; saturated model
Probit	100.028	125.567	175.486	0.054	89.854	1.153	-1.443	Questionable Goodness of fit p-value < 0.1
Quantal Linear	71.51	118.686	263.387	0.018	92.792	0.489	-1.924	Questionable Goodness of fit p-value < 0.1

^a BMDS recommended best fitting model

^b User selected best fitting model; model selected based on lowest AIC



Selected Model: Weibull



Weibull Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	0	-18	18
a	1	1	18
b	1e-06	1e-06	100

Modeling Summary:

BMD	170.842
BMDL	122.731
BMDU	177.11
AIC	86.0565
Log-Likelihood	-41.0282
P-Value	0.557718
Overall d.f.	1
Chi ²	0.343671

Model Parameters:

Variable	Estimate	On Bound	Std Error

g	0.0299997	no	0.0366222
a	18	yes	Not Reported
b	6.85481e-42	no	0.0813933

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	50	2	1.49999	0.0299997	0.414526
89.3	50	1	1.50003	0.0300006	-0.414534
179	50	12	12	0.24	4.76718e-06

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-40.8532	3	-	-	-
Fitted model	-41.0282	2	0.350137	1	0.554035
Reduced model	-48.7624	1	15.8186	2	0.000367317

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.

Umeda 2010, 1,2-DCP

Umeda 2010, 866309

2-year exposure, female rats

Report Generated: 2026-Jan-26 14:01 UTC

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

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

Modeling Summary

Datasets

Name: Neoplastic nasal lesions, combined - female rats

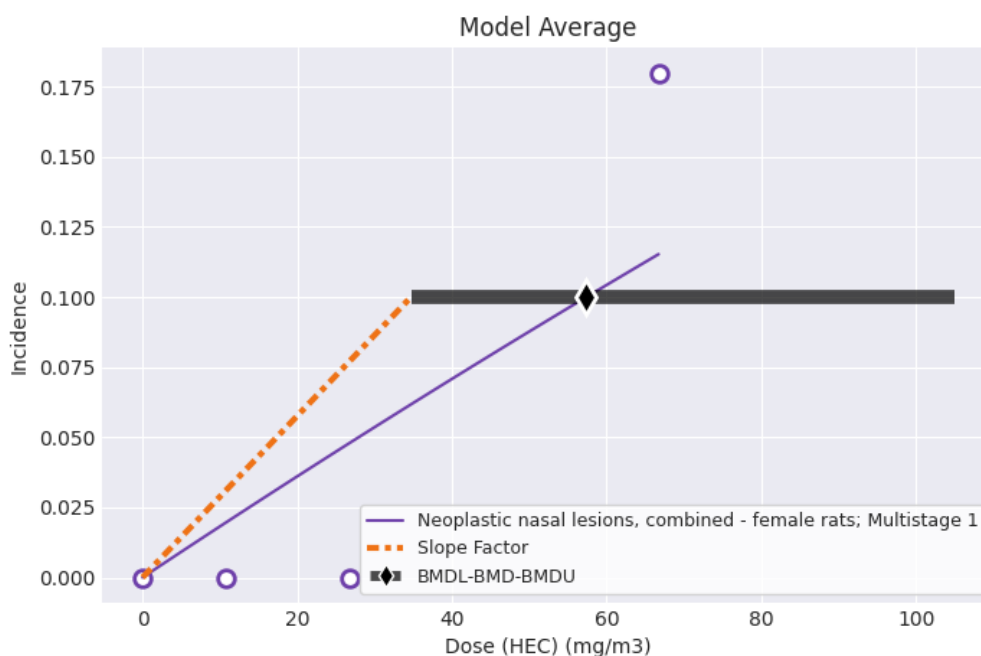
Dose (mg/m3)	0	10.7	26.75	66.71
Affected / Total (%)	0.0/50.0 (0.0%)	0.0/50.0 (0.0%)	0.0/50.0 (0.0%)	9.0/50.0 (18.0%)

Settings

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

Maximum Likelihood Approach

Dataset: Model	BMDL	BMD	BMDU	CSF	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD
Neoplastic nasal lesions, combined - female rats: Multistage 1	34.7	57.383	104.983	0.003	0.135	57.807	-0.001	1.433



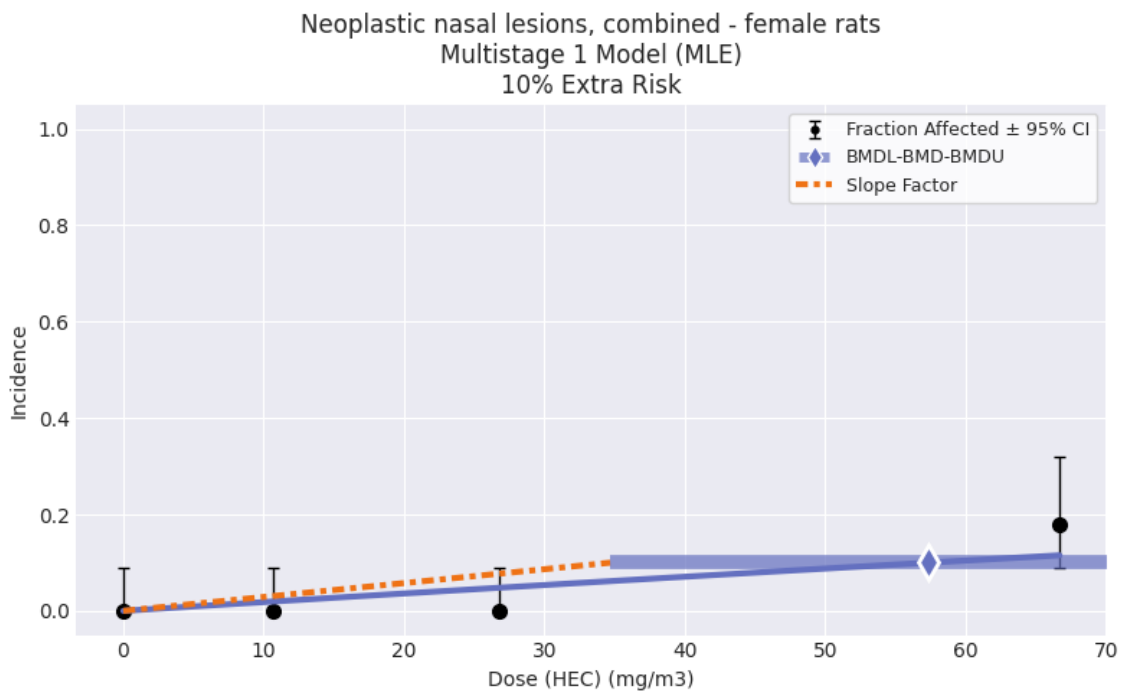
Multitumor MS Combo Model

Version: pybmds 25.1 (bmdscore 25.1)

BMD	57.3826
BMDL	34.7054
BMDU	104.934
Slope Factor	0.0028814
Combined Log-likelihood	-27.9034
Combined Log-likelihood Constant	-21.6417

Individual Model Results

Neoplastic nasal lesions, combined - female rats: Multistage 1



Multistage 1 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	-17	-18	18
b1	0.1	0	10000

Modeling Summary:

BMD	57.3826
BMDL	34.6999
BMDU	104.983
Slope Factor	0.00288185
AIC	57.8068
Log-Likelihood	-27.9034
P-Value	0.134953
Overall d.f.	3
Chi ²	5.56242

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
b1	0.00183611	no	0.0408499

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	50	0	7.61499e-07	1.523e-08	-0.000872639
10.7	50	0	0.972731	0.0194546	-0.996007
26.75	50	0	2.39646	0.0479292	-1.58654
66.71	50	9	5.76411	0.115282	1.43293

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-23.5697	4	-	-	-
Fitted model	-27.9034	1	8.66747	3	0.034055
Reduced model	-36.7042	1	26.2691	3	8.37677e-06

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.

Umeda 2010, 1,2-DCP

Umeda 2010, 866309

2-year exposure, male rats

Report Generated: 2026-Jan-26 14:01 UTC

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

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

Modeling Summary

Datasets

Name: Neoplastic nasal lesions, combined - male rats

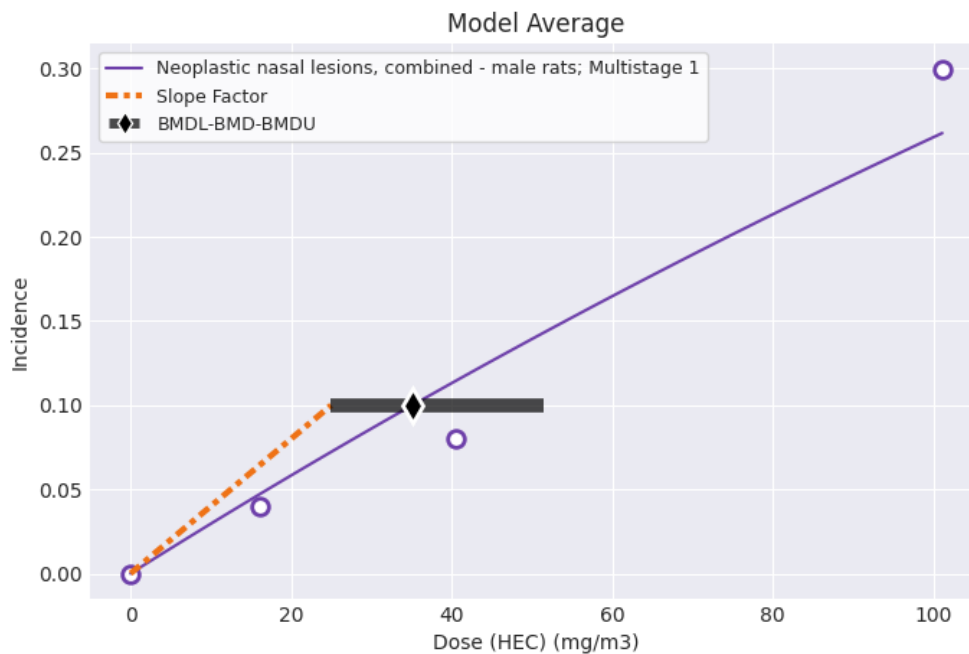
Dose (mg/m3)	0	16.2	40.54	101.1
Affected / Total (%)	0.0/50.0 (0.0%)	2.0/50.0 (4.0%)	4.0/50.0 (8.0%)	15.0/50.0 (30.0%)

Settings

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

Maximum Likelihood Approach

Dataset: Model	BMDL	BMD	BMDU	CSF	P-Value	AIC	Scaled Residual at Control	Scaled Residual near BMD
Neoplastic nasal lesions, combined - male rats: Multistage 1	24.984	35.102	51.468	0.004	0.794	108.841	-0.001	-0.767



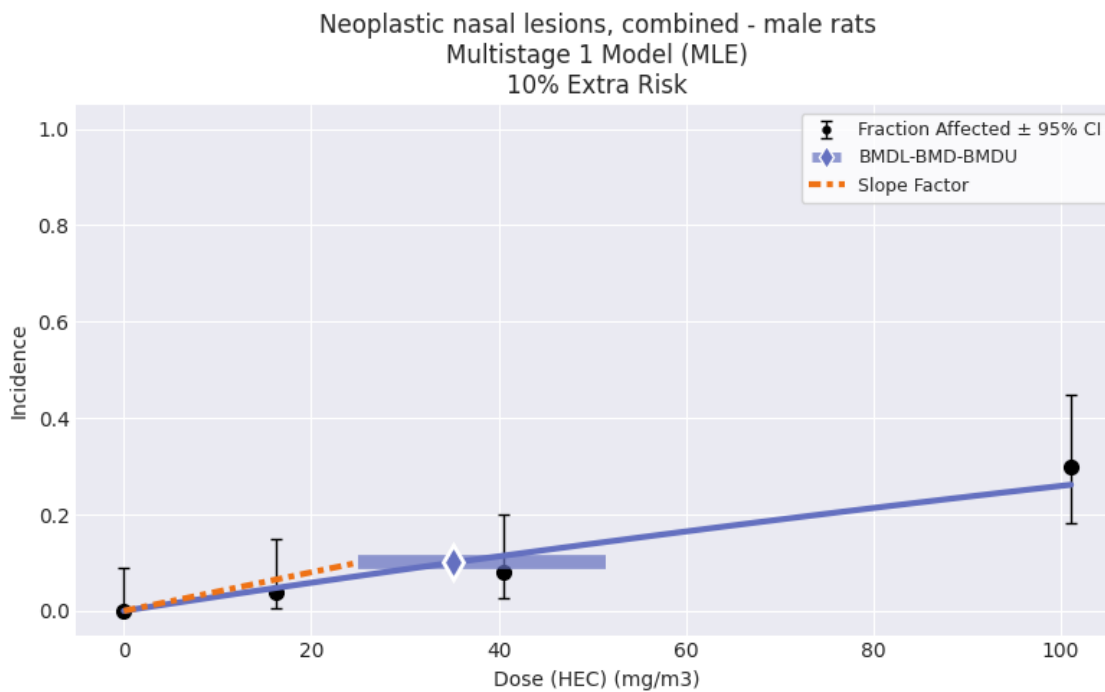
Multitumor MS Combo Model

Version: pybmds 25.1 (bmdscore 25.1)

BMD	35.1021
BMDL	24.9885
BMDU	51.4663
Slope Factor	0.00400184
Combined Log-likelihood	-53.4205
Combined Log-likelihood Constant	-47.9002

Individual Model Results

Neoplastic nasal lesions, combined - male rats: Multistage 1



Multistage 1 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Initial	Min	Max
g	-17	-18	18
b1	0.1	0	10000

Modeling Summary:

BMD	35.1021
BMDL	24.9841
BMDU	51.4676
Slope Factor	0.00400255
AIC	108.841
Log-Likelihood	-53.4205
P-Value	0.794124
Overall d.f.	3
Chi ²	1.02946

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
b1	0.00300154	no	0.0664075

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	50	0	7.61499e-07	1.523e-08	-0.000872639
16.2	50	2	2.37309	0.0474617	-0.248148
40.54	50	4	5.72853	0.114571	-0.767499
101.1	50	15	13.0869	0.261738	0.615488

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-52.8789	4	-	-	-
Fitted model	-53.4205	1	1.08315	3	0.781142
Reduced model	-67.1864	1	28.6151	3	2.69773e-06

Recommended citation

Please adapt as appropriate; the citations below capture the package version and timestamps for easier reproducibility of the analysis.

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 26, 2026.