

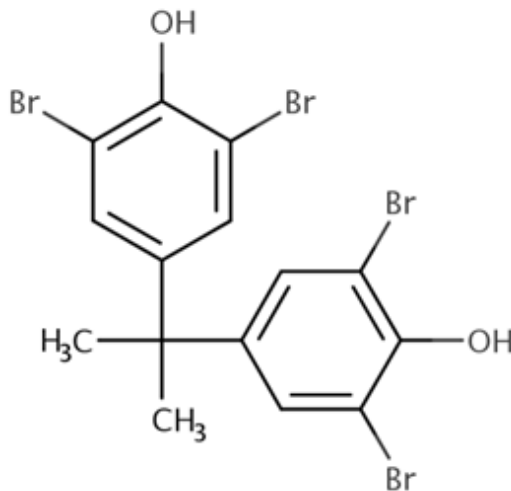


United States
Environmental Protection Agency

June 2026
Office of Chemical Safety and
Pollution Prevention

**Draft Supplemental Information on Benchmark Dose (BMD)
Modeling Results in the Human Health and Environmental
Hazard Assessment for 4,4'-(1-Methylethylidene)bis[2,6-
dibromophenol] (TBBPA)**

CASRN: 79-94-7



June 2026

TABLE OF CONTENTS

1	POLYCYSTIC KIDNEY LESIONS IN MALE RATS	5
1.1	Session for Polycystic Kidney Lesions in Male Rats	5
1.1.1	Dataset	5
1.1.2	Settings	5
1.1.3	Maximum Likelihood Approach	5
1.1.4	Individual Model Results	6
1.1.4.1	Hill Model	6
1.1.4.2	Gamma Model	8
1.1.4.3	LogLogistic Model	10
1.1.4.4	Multistage 1 Model	12
1.1.4.5	Multistage 2 Model	14
1.1.4.6	Multistage 3 Model	16
1.1.4.7	Weibull Model	18
1.1.4.8	Logistic Model	20
1.1.4.9	LogProbit Model	21
1.1.4.10	Probit Model	23
1.1.4.11	Quantal Linear Model	25
1.2	Session for Polycystic Kidney Lesions in Male Rats	26
1.2.1	Dataset	26
1.2.2	Settings	26
1.2.3	Bayesian Summary	27
1.2.4	Individual Model Results	28
1.2.4.1	Hill Model	28
1.2.4.2	Gamma Model	30
1.2.4.3	Logistic Model	31
1.2.4.4	LogLogistic Model	33
1.2.4.5	LogProbit Model	35
1.2.4.6	Multistage 2 Model	36
1.2.4.7	Probit Model	38
1.2.4.8	Quantal Linear Model	40
1.2.4.9	Weibull Model	41
2	UTERINE ATYPICAL ENDOMETRIAL HYPERPLASIA	44
2.1	Session for Uterine Atypical Endometrial Hyperplasia	44
2.1.1	Dataset	44
2.1.2	Settings	44
2.1.3	Maximum Likelihood Approach	44
2.1.4	Individual Model Results	46
2.1.4.1	Hill Model	46
2.1.4.2	Gamma Model	48
2.1.4.3	LogLogistic Model	50
2.1.4.4	Multistage 1 Model	51
2.1.4.5	Multistage 2 Model	53
2.1.4.6	Multistage 3 Model	55
2.1.4.7	Weibull Model	57
2.1.4.8	Logistic Model	59
2.1.4.9	LogProbit Model	60

June 2026

75	2.1.4.10 Probit Model.....	61
76	2.1.4.11 Quantal Linear Model.....	62
77	2.2 Session for Uterine Atypical Endometrial Hyperplasia	64
78	2.2.1 Dataset	64
79	2.2.2 Settings	64
80	2.2.3 Bayesian Summary.....	64
81	2.2.4 Individual Model Results.....	65
82	2.2.4.1 Hill Model.....	65
83	2.2.4.2 Gamma Model.....	67
84	2.2.4.3 Logistic Model	69
85	2.2.4.4 LogLogistic Model	70
86	2.2.4.5 LogProbit Model	72
87	2.2.4.6 Probit Model.....	73
88	2.2.4.7 Quantal Linear Model.....	75
89	2.2.4.8 Weibull Model.....	76
90	2.2.4.9 Multistage 2 Model.....	78
91	3 UTERINE ADENOMA, ADENOCARCINOMA, MMT + ATYPICAL ENDOMETRIAL	
92	HYPERPLASIA.....	80
93	3.1 Session for Uterine Adenoma, Adenocarcinoma, and MMT + Atypical Endometrial	
94	Hyperplasia.....	80
95	3.1.1 Dataset	80
96	3.1.2 Settings	80
97	3.1.3 Maximum Likelihood Approach.....	80
98	3.1.4 Individual Model Results.....	81
99	3.1.4.1 Hill Model.....	81
100	3.1.4.2 Gamma Model.....	83
101	3.1.4.3 LogLogistic Model	85
102	3.1.4.4 Multistage 1 Model.....	86
103	3.1.4.5 Multistage 2 Model.....	88
104	3.1.4.6 Multistage 3 Model.....	90
105	3.1.4.7 Weibull Model.....	92
106	3.1.4.8 Logistic Model	94
107	3.1.4.9 LogProbit Model	95
108	3.1.4.10 Probit Model.....	97
109	3.1.4.11 Quantal Linear Model.....	99
110	3.2 Session for Uterine Adenoma, Adenocarcinoma, and MMT + Atypical Endometrial	
111	Hyperplasia.....	100
112	3.2.1 Dataset	100
113	3.2.2 Settings	100
114	3.2.3 Bayesian Summary.....	101
115	3.2.4 Individual Model Results.....	102
116	3.2.4.1 Hill Model.....	102
117	3.2.4.2 Gamma Model.....	104
118	3.2.4.3 Logistic Model	105
119	3.2.4.4 LogLogistic Model	107
120	3.2.4.5 LogProbit Model	108
121	3.2.4.6 Multistage 2 Model.....	110
122	3.2.4.7 Probit Model.....	112

123 3.2.4.8 Quantal Linear Model..... 113
124 3.2.4.9 Weibull Model..... 115
125 **REFERENCES** **117**

1 POLYCYSTIC KIDNEY LESIONS IN MALE RATS

Increased incidence of polycystic kidney lesions in male rat neonates exposed PND 4–21 ([Fukuda et al., 2004](#)).

Report Generated: 2026-Mar-24 16:03 UTC

BMDS Online Version: U.S. Environmental Protection Agency (2025). BMDS Online 25.1 (pybmds 25.1; bmdscore 25.1). Available from <https://bmdsonline.epa.gov>.

1.1 Session for Polycystic Kidney Lesions in Male Rats

1.1.1 Dataset

Dose (mg/kg-day)	N	Incidence
0	6	0
40	6	0
200	6	2
600	6	6

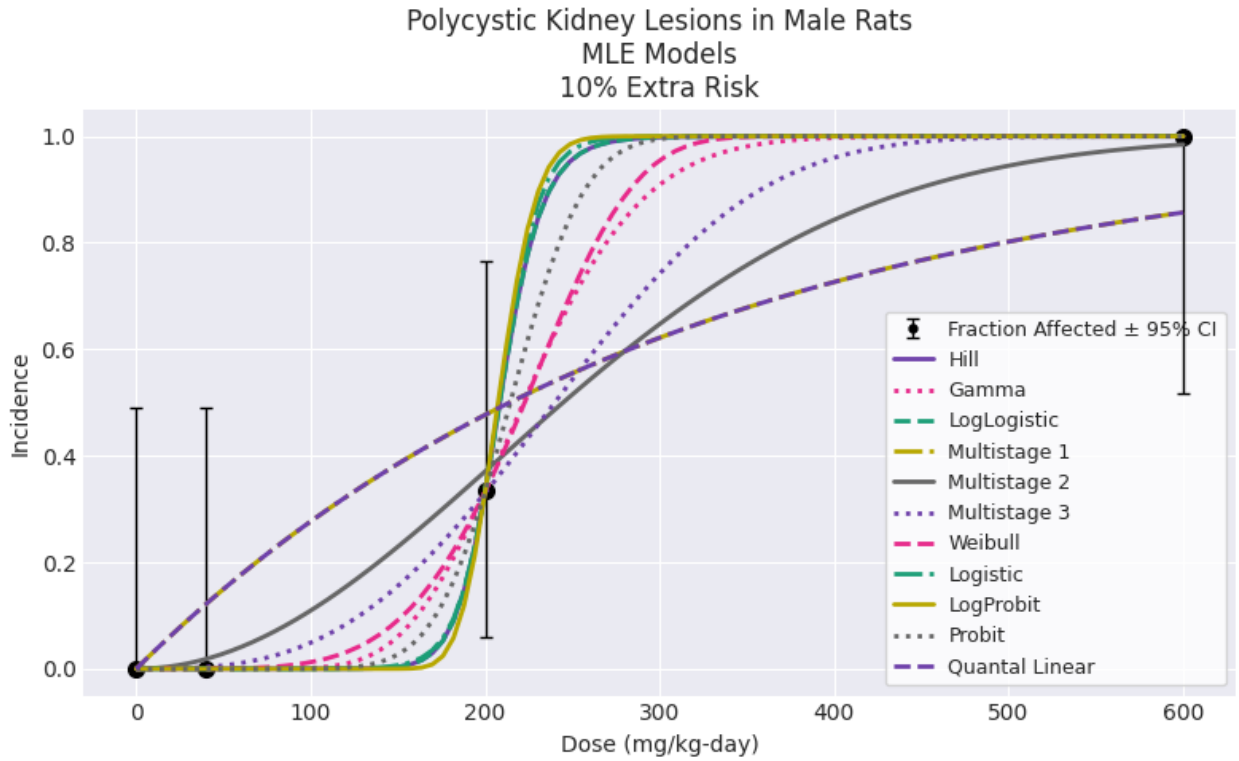
1.1.2 Settings

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

1.1.3 Maximum Likelihood Approach

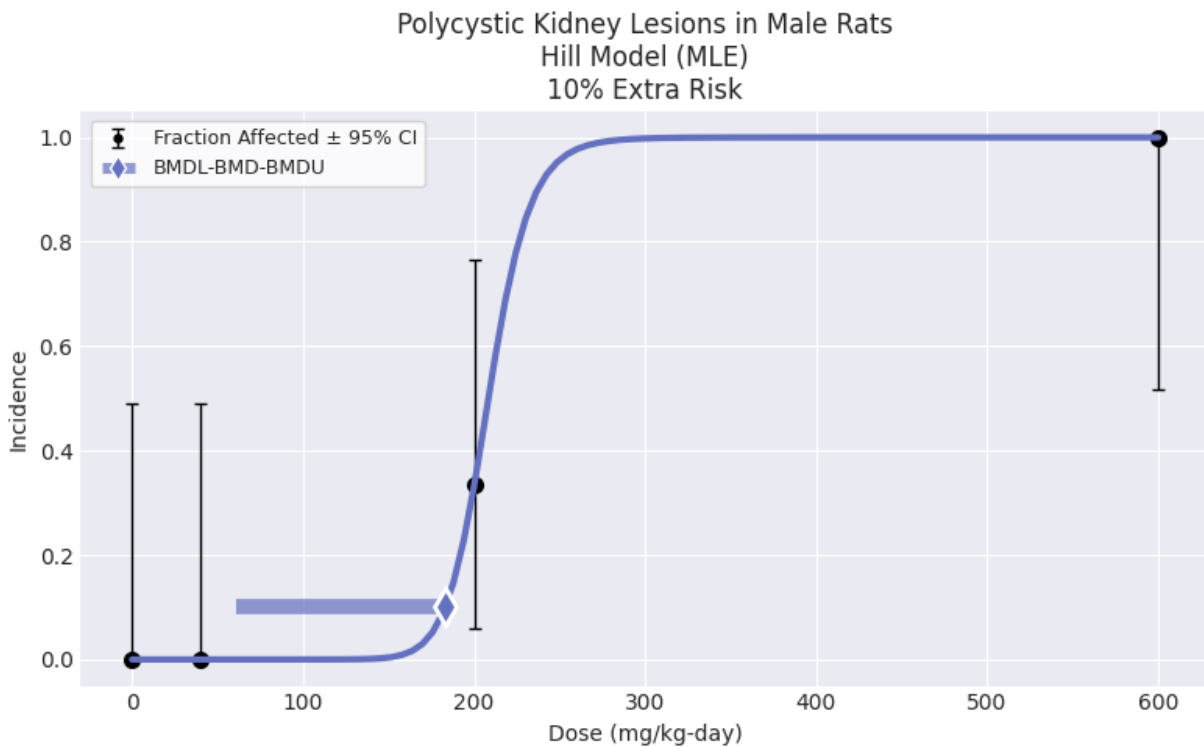
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual Near BMD	Recommendation and Notes
Hill	60.891	183.08	-	1.	11.638	-0.	-0.	Viable BMD/BMDL ratio > 3.0
Gamma	45.37	161.062	204.118	1.	9.638	-0.	-0.	Viable BMD/BMDL ratio > 3.0
LogLogistic	60.891	183.08	-	1.	11.638	-0.	<0.001	Viable BMD/BMDL ratio > 3.0
Multistage 1	17.533	32.517	65.476	0.507	13.555	-0.	-0.911	Viable
Multistage 2	31.931	95.366	146.265	0.97	10.084	-0.	-0.335	Viable
Multistage 3	31.18	128.017	194.625	1.	7.677	-0.	0.013	Viable BMD/BMDL ratio > 3.0
Weibull	0	152.895	206.625	1.	9.64	-0.	0.001	Unusable BMDL does not exist
Logistic	76.111	182.619	204.046	1.	9.638	-0.	<0.001	Viable
LogProbit	58.607	186.284	201.543	1.	11.638	-0.	<0.001	Viable BMD/BMDL ratio > 3.0
Probit	68.922	171.639	204.366	1.	11.638	-0.	<0.001	Viable
Quantal Linear ^a	17.533	32.517	65.475	0.507	13.555	-0.	-0.911	Recommended - Lowest BMDL

^a BMDS recommended best fitting model



1.1.4 Individual Model Results

1.1.4.1 Hill Model



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	183.08
BMDL	60.891
BMDU	-9999
AIC	11.6382
Log-Likelihood	-3.81909
P-Value	1
Overall d.f.	2
Chi ²	3.65523e-07

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
v	1	yes	Not Reported
a	-90.8453	no	5.04264
b	17.0152	no	0.78829

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.

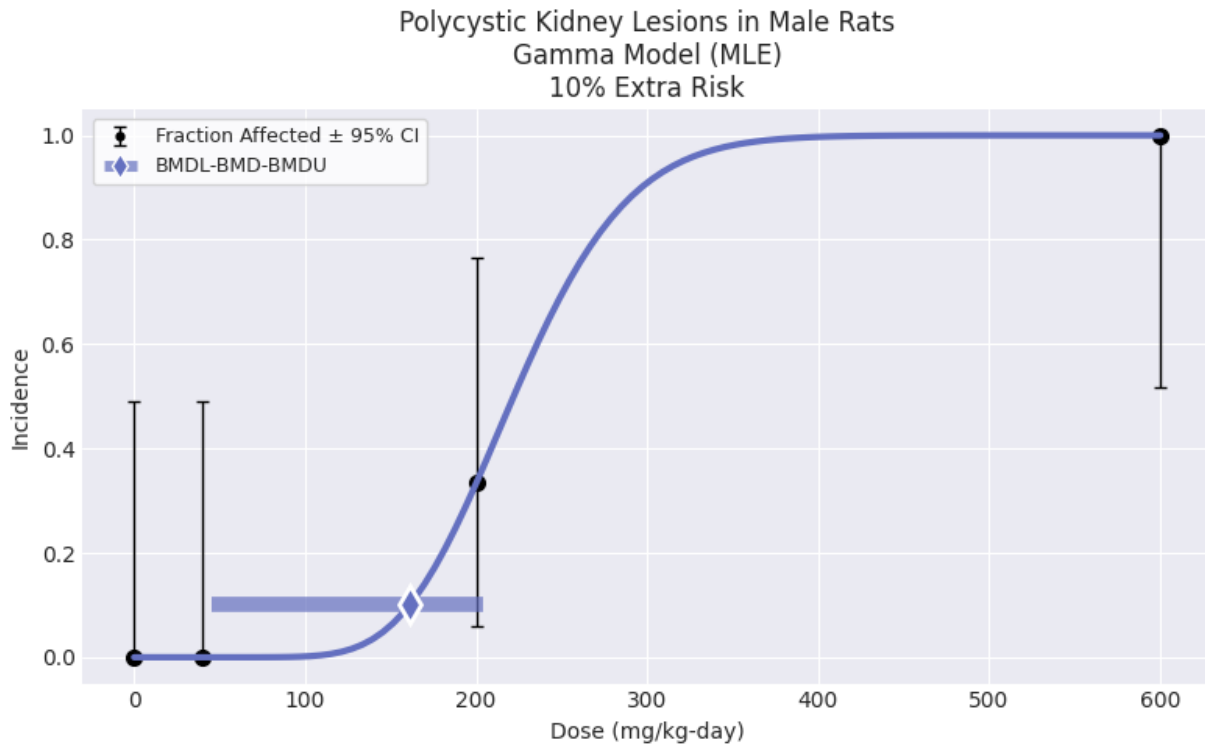
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	9.13799e-08	1.523e-08	-0.000302291
40	6	0	9.13837e-08	1.52306e-08	-0.000302297
200	6	2	2	0.333333	-1.27705e-08
600	6	6	6	1	0.000427504

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-3.81909	2	7.31047e-07	2	1
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

1.1.4.2 Gamma Model



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

June 2026

Modeling Summary:

BMD	161.062
BMDL	45.3695
BMDU	204.118
AIC	9.63817
Log-Likelihood	-3.81909
P-Value	1
Overall d.f.	3
Chi ²	1.86513e-06

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
a	18	yes	Not Reported
b	0.079607	no	0.0103573

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:

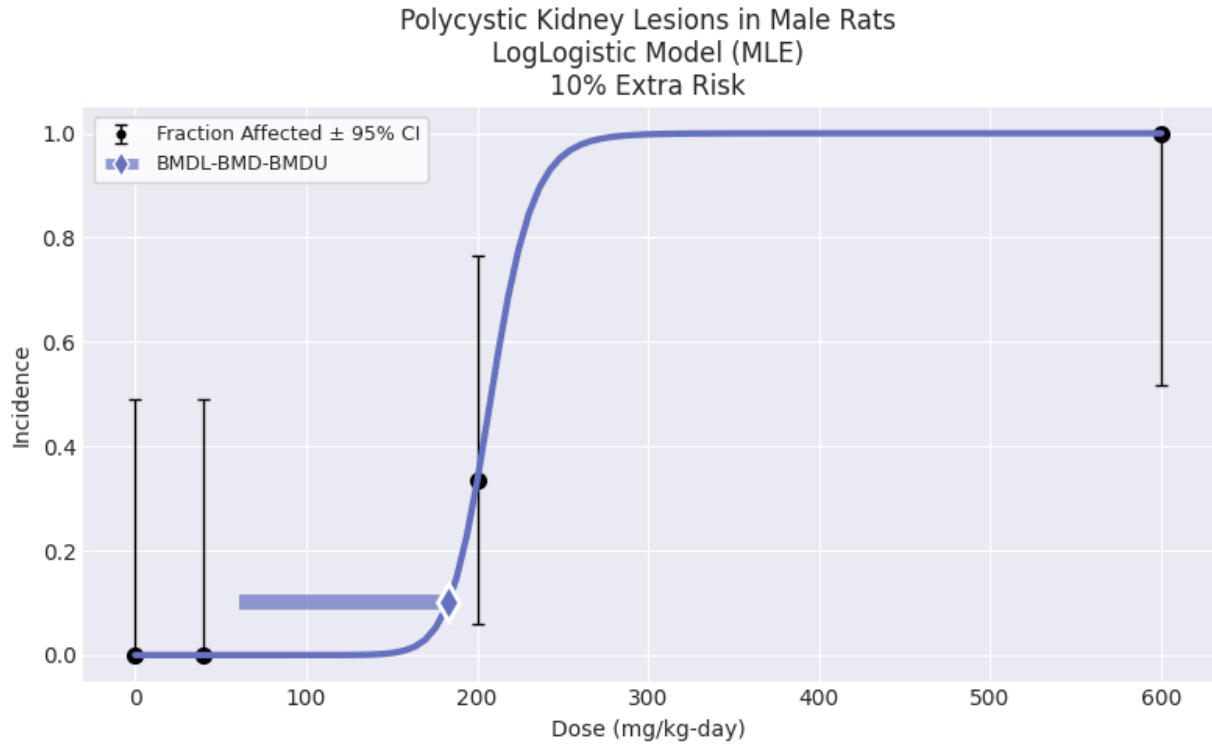
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	9.138e-08	1.523e-08	-0.000302291
40	6	0	1.44093e-07	2.40154e-08	-0.000379595
200	6	2	2.00001	0.333335	-6.53614e-06
600	6	6	6	1	0.00127656

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-3.81909	1	3.73022e-06	3	1
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

282

1.1.4.3 LogLogistic Model



283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305

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	183.08
BMDL	60.891
BMDU	-9999
AIC	11.6382
Log-Likelihood	-3.81909
P-Value	1
Overall d.f.	2
Chi ²	2.74143e-07

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
a	-90.8453	no	5.04264
b	17.0152	no	0.78829

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:

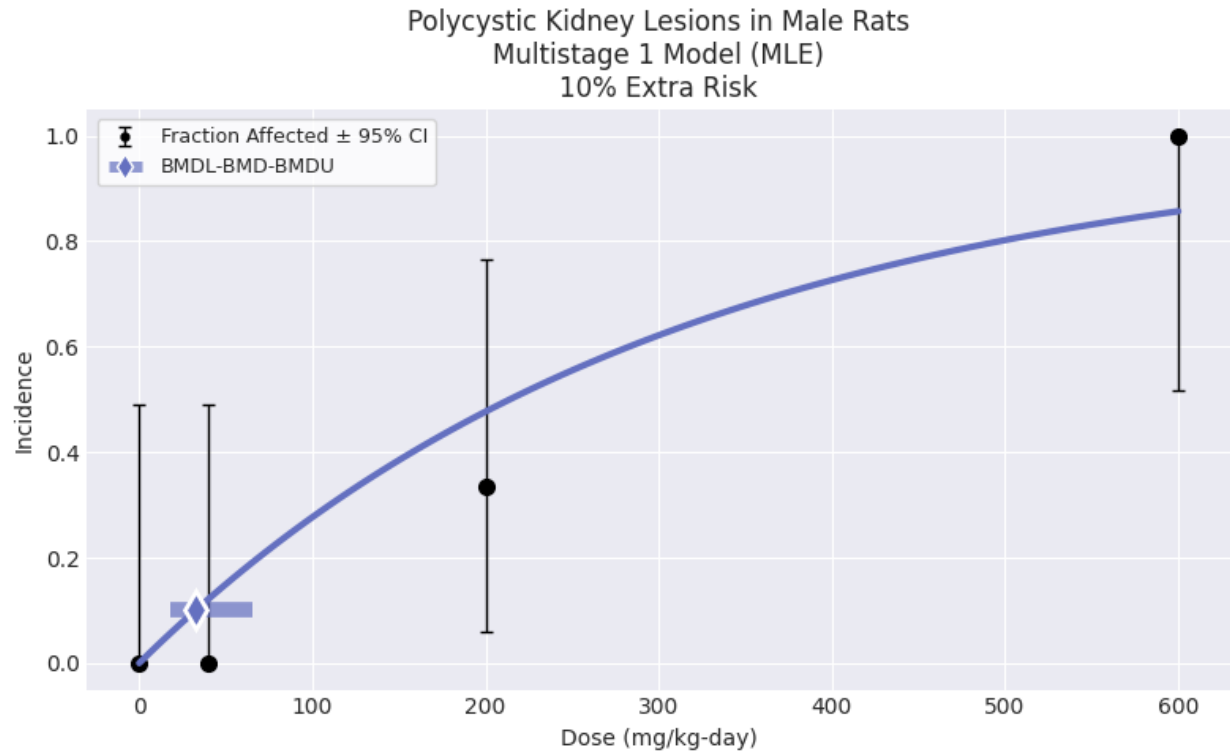
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	9.13799e-08	1.523e-08	-0.000302291
40	6	0	9.13837e-08	1.52306e-08	-0.000302297
200	6	2	2	0.333333	1.01533e-08
600	6	6	6	1	0.000302291

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-3.81909	2	5.48287e-07	2	1
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

349

1.1.4.4 Multistage 1 Model



350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372

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

June 2026

Modeling Summary:

BMD	32.5175
BMDL	17.533
BMDU	65.4765
AIC	13.5546
Log-Likelihood	-5.77728
P-Value	0.507122
Overall d.f.	3
Chi ²	2.3283

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.53298e-08	yes	Not Reported
b1	0.00324012	no	2.15021

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:

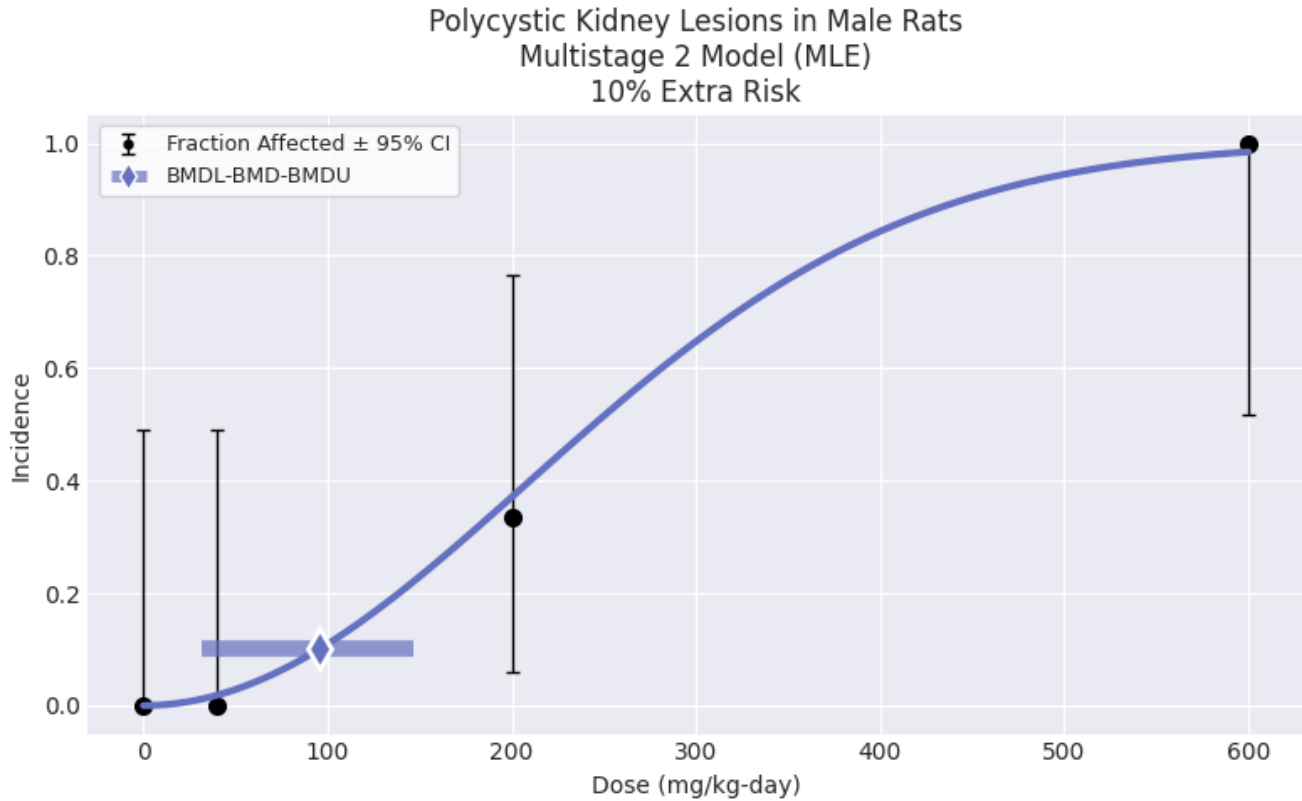
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	9.19787e-08	1.53298e-08	-0.00030328
40	6	0	0.729345	0.121558	-0.911192
200	6	2	2.86153	0.476922	-0.704187
600	6	6	5.14128	0.85688	1.00107

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-5.77728	1	3.91638	3	0.270636
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

415

1.1.4.5 Multistage 2 Model



416

417

418

419

420

421

422

423

424

425

426

427

428

429

430

431

432

433

434

435

436

437

438

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

PUBLIC RELEASE DRAFT
June 2026

Modeling Summary:

BMD	95.3661
BMDL	31.931
BMDU	146.265
AIC	10.0841
Log-Likelihood	-4.04206
P-Value	0.97044
Overall d.f.	3
Chi ²	0.242573

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
b1	0	yes	Not Reported
b2	1.15848e-05	no	2.18972

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:

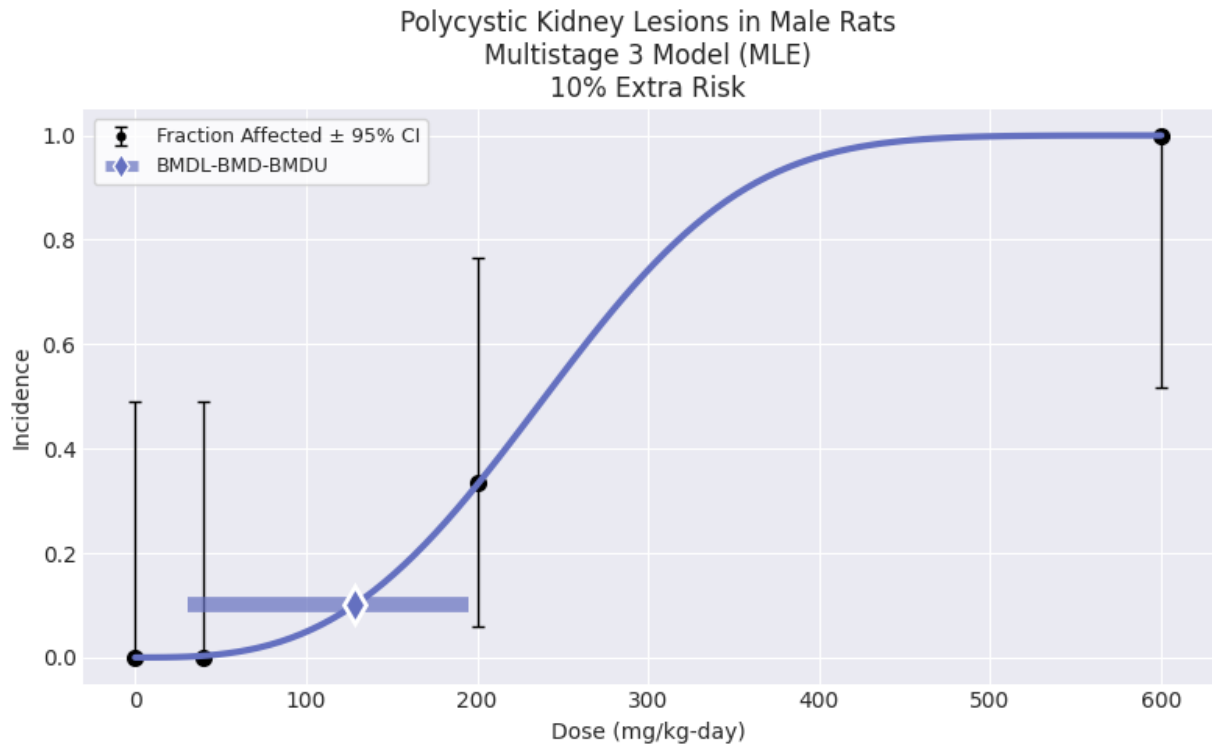
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	9.13799e-08	1.523e-08	-0.000302291
40	6	0	0.11019	0.018365	-0.33504
200	6	2	2.22513	0.370855	-0.190274
600	6	6	5.90734	0.984556	0.306785

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-4.04206	1	0.445957	3	0.930594
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

482

1.1.4.6 Multistage 3 Model



483

484

485

486

487

488

489

490

491

492

493

494

495

496

497

498

499

500

501

502

503

504

505

506

507

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	128.017
BMDL	31.1801
BMDU	194.625
AIC	7.67714
Log-Likelihood	-3.83857
P-Value	0.999952
Overall d.f.	4
Chi ²	0.0195983

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
b1	2.45406e-19	yes	Not Reported
b2	6.40413e-23	yes	Not Reported
b3	5.02203e-08	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:

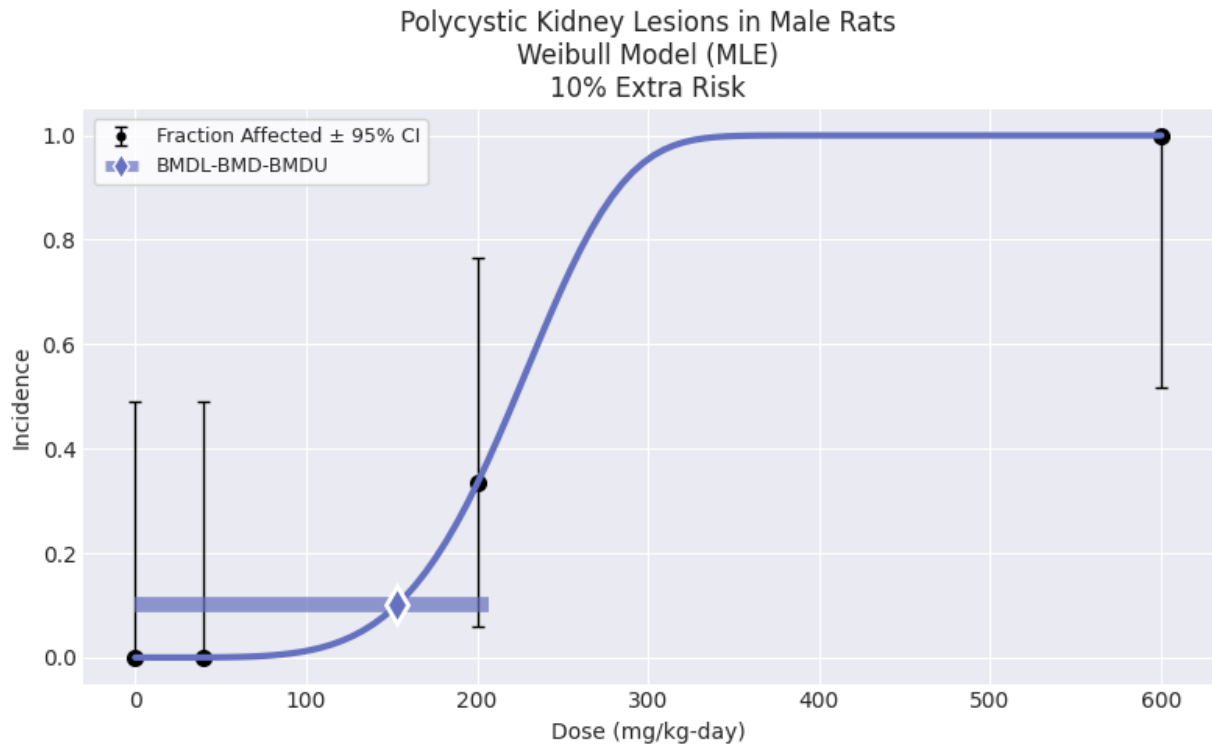
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	9.13799e-08	1.523e-08	-0.000302291
40	6	0	0.0192537	0.00320895	-0.138981
200	6	2	1.98516	0.33086	0.0128747
600	6	6	5.99988	0.999981	0.0108033

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-3.83857	0	0.0389685	4	0.999813
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

552

1.1.4.7 Weibull Model



553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575

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

PUBLIC RELEASE DRAFT
June 2026

Modeling Summary:

BMD	152.895
BMDL	0
BMDU	206.625
AIC	9.63969
Log-Likelihood	-3.81985
P-Value	0.999994
Overall d.f.	3
Chi ²	0.000761992

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
a	5.01436	no	0.647595
b	1.17312e-12	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:

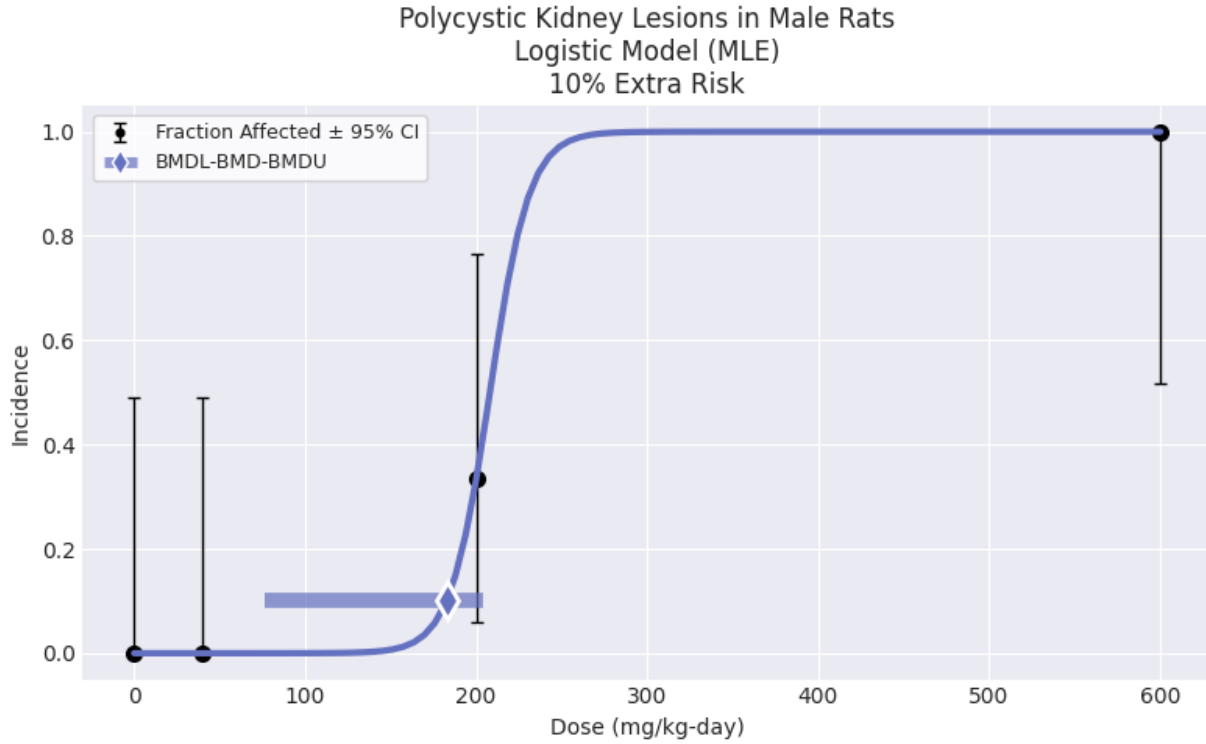
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	9.13799e-08	1.523e-08	-0.000302291
40	6	0	0.000760024	0.000126671	-0.0275703
200	6	2	1.99846	0.333077	0.00133425
600	6	6	6	1	0

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-3.81985	1	0.00152211	3	0.999984
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

619

1.1.4.8 Logistic Model



620

621

622

Logistic Model

623

624

625

Version: pybmds 25.1 (bmdscore 25.1)

626

627

Input Summary:

628

629

630

631

632

633

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

634

Parameter Settings:

635

636

637

638

639

640

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

641

642

Modeling Summary:

643

644

645

646

647

648

649

650

651

652

BMD	182.619
BMDL	76.1108
BMDU	204.046
AIC	9.63818
Log-Likelihood	-3.81909
P-Value	1
Overall d.f.	3
Chi ²	3.0028e-06

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-18	yes	Not Reported
b	0.0865343	no	0.00433013

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.

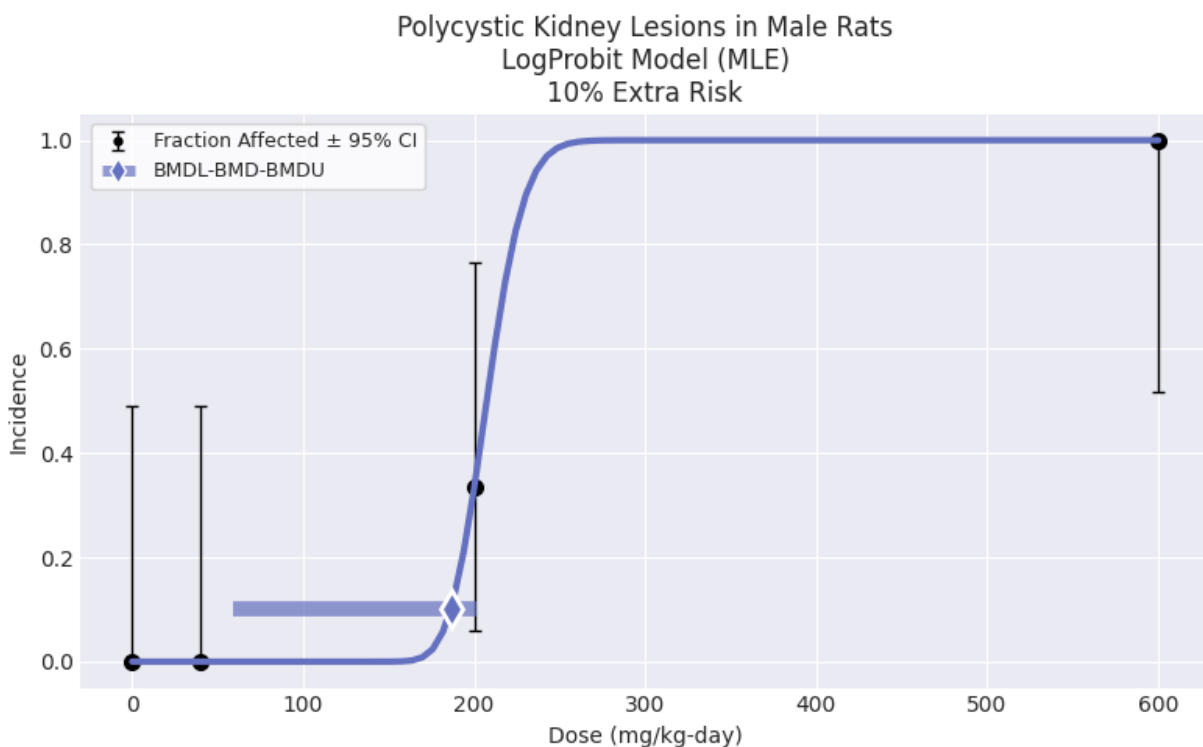
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	9.13799e-08	1.523e-08	-0.000302291
40	6	0	2.91142e-06	4.85236e-07	-0.00170629
200	6	2	2	0.333333	4.94837e-07
600	6	6	6	1	1.03238e-07

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-3.81909	1	6.0056e-06	3	1
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

1.1.4.9 LogProbit Model



LogProbit 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
g	0	-18	18
a	0	-18	18
b	0.0001	0.0001	18

Modeling Summary:

BMD	186.284
BMDL	58.6066
BMDU	201.543
AIC	11.6382
Log-Likelihood	-3.81909
P-Value	1
Overall d.f.	2
Chi ²	1.8276e-07

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.523e-08	yes	Not Reported
a	-63.8817	no	5627.77
b	11.9757	no	1062.18

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.

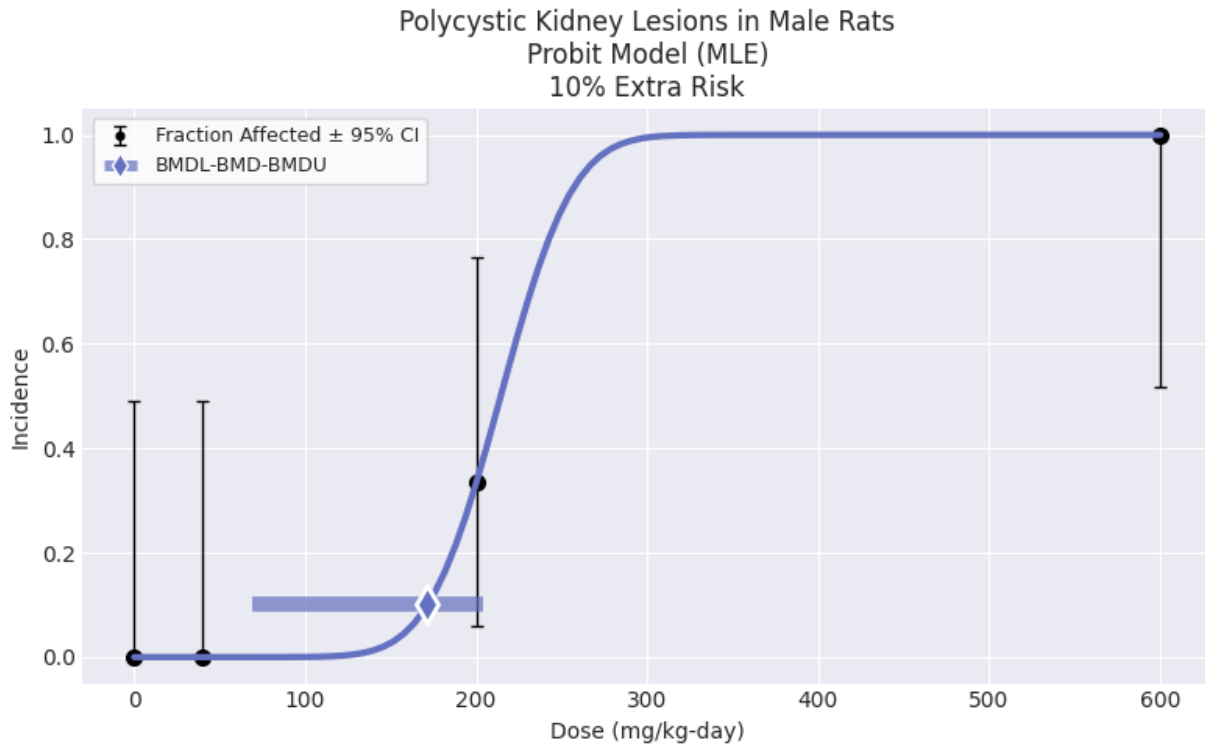
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	9.13799e-08	1.523e-08	-0.000302291
40	6	0	9.13799e-08	1.523e-08	-0.000302291
200	6	2	2	0.333333	1.12718e-08
600	6	6	6	1	0

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-3.81909	2	3.6552e-07	2	1
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

1.1.4.10 Probit Model



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

June 2026

Modeling Summary:

BMD	171.639
BMDL	68.9218
BMDU	204.366
AIC	11.6382
Log-Likelihood	-3.81909
P-Value	1
Overall d.f.	2
Chi ²	5.06914e-07

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-6.43073	no	0.52929
b	0.03	no	1.29926e-07

Goodness of Fit:

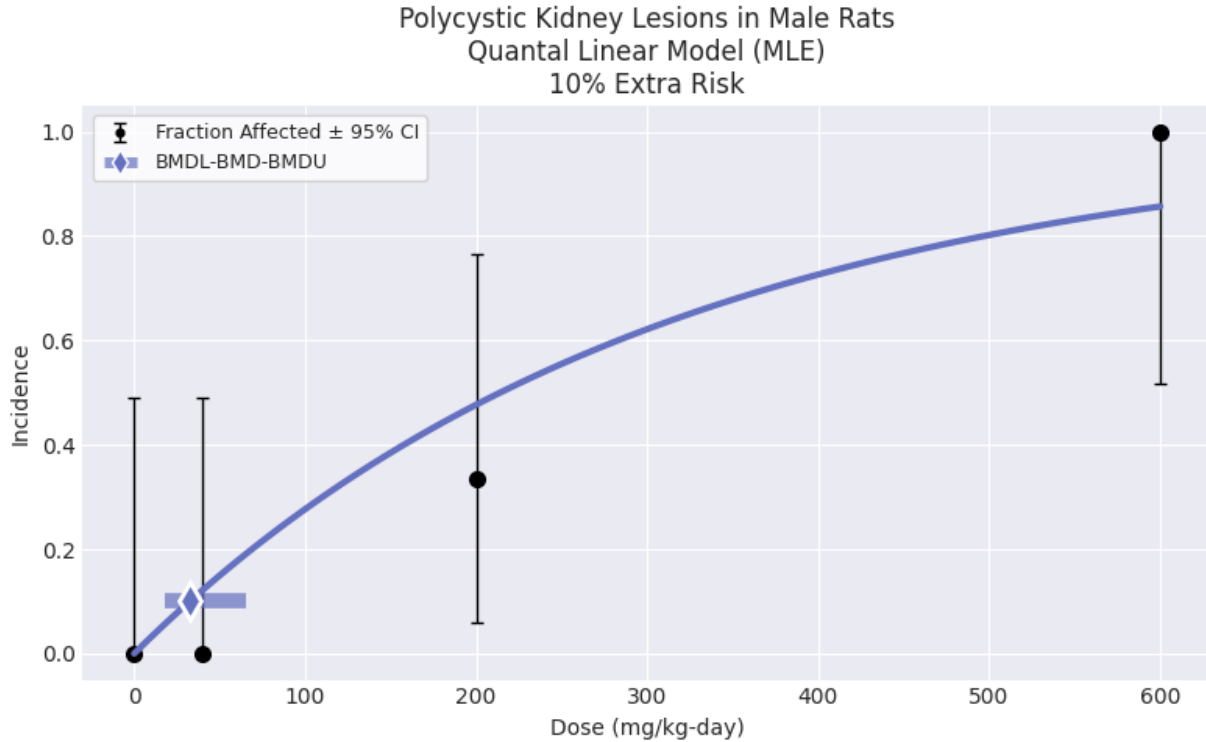
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	3.80983e-10	6.34971e-11	-1.95188e-05
40	6	0	5.06531e-07	8.44219e-08	-0.00071171
200	6	2	2	0.333333	1.45068e-06
600	6	6	6	1	0

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-3.81909	2	1.01306e-06	2	0.999999
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

812

1.1.4.11 Quantal Linear Model



813

814

815

Quantal Linear Model

816

817

818

Version: pybmds 25.1 (bmdscore 25.1)

819

820

Input Summary:

821

822

823

824

825

826

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

827

Parameter Settings:

828

829

830

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

833

834

835

Modeling Summary:

836

837

838

839

840

841

842

843

844

845

BMD	32.5175
BMDL	17.533
BMDU	65.4752
AIC	13.5546
Log-Likelihood	-5.77728
P-Value	0.507122
Overall d.f.	3
Chi ²	2.3283

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	1.53298e-08	yes	Not Reported
b	0.00324012	no	0.00128562

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	6	0	9.19787e-08	1.53298e-08	-0.00030328
40	6	0	0.729345	0.121558	-0.911192
200	6	2	2.86153	0.476922	-0.704187
600	6	6	5.14128	0.85688	1.00107

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-5.77728	1	3.91638	3	0.270636
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

1.2 Session for Polycystic Kidney Lesions in Male Rats

1.2.1 Dataset

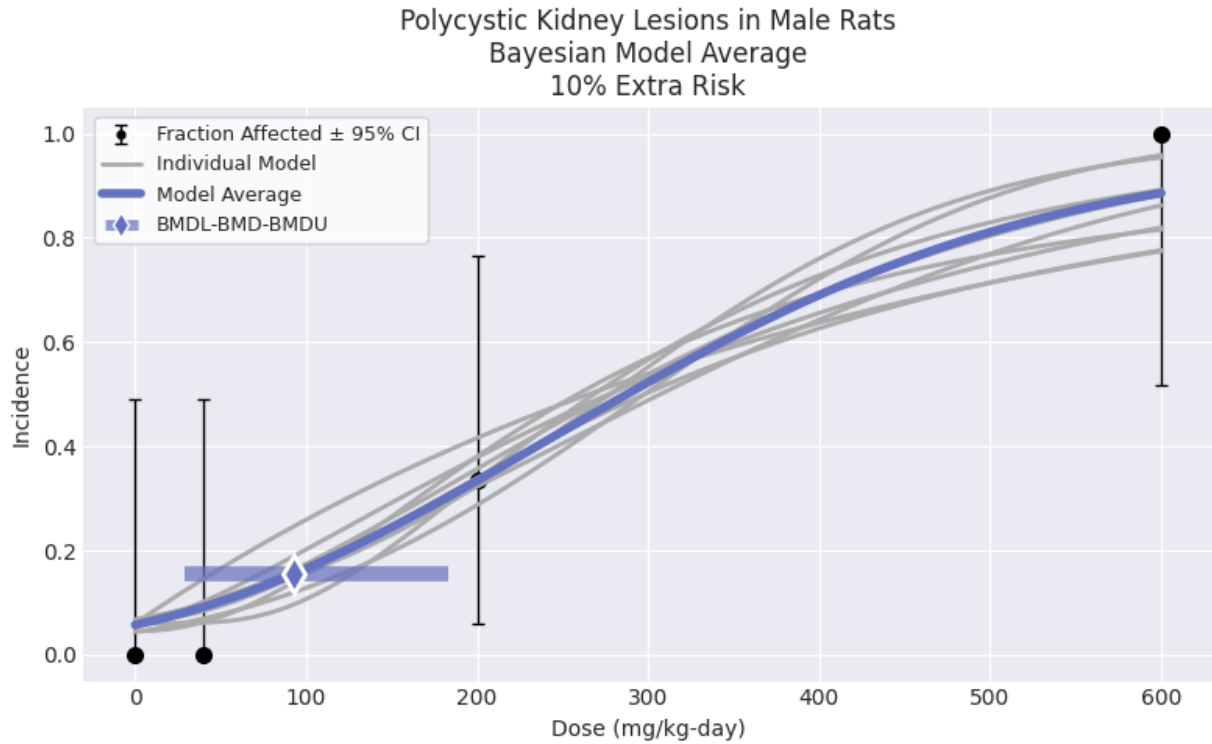
Dose (mg/kg-day)	N	Incidence
0	6	0
40	6	0
200	6	2
600	6	6

1.2.2 Settings

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

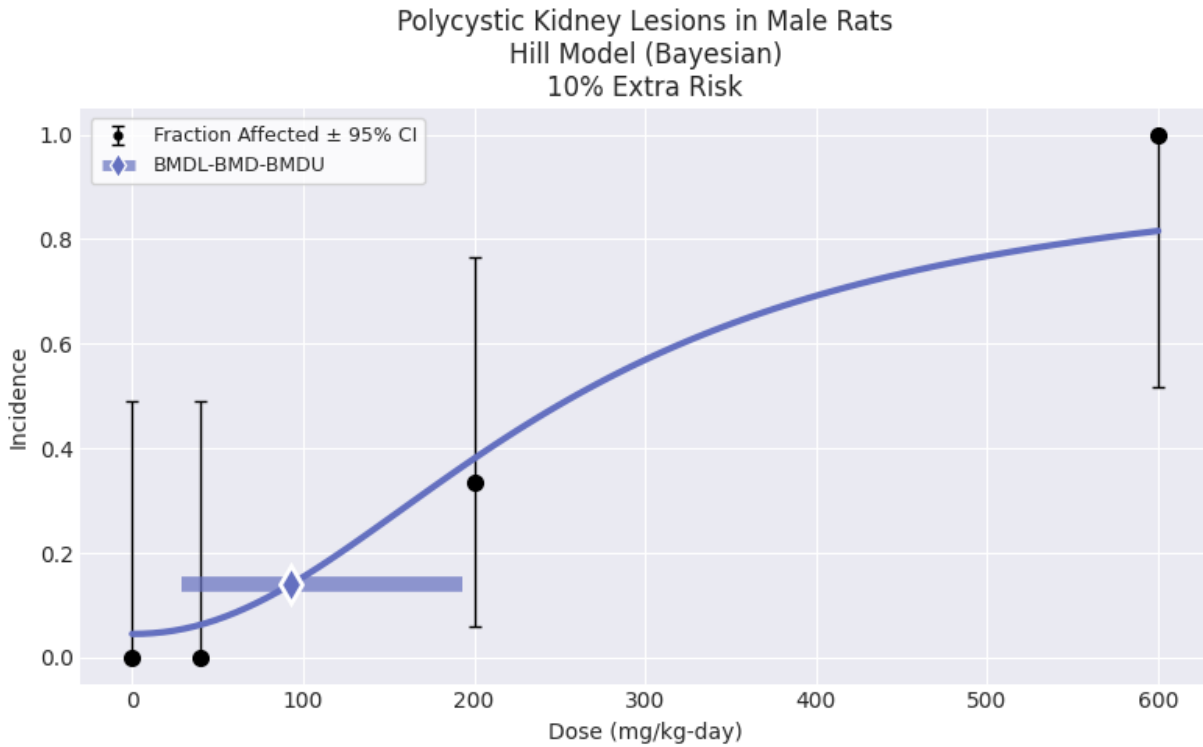
1.2.3 Bayesian Summary

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	28.843	93.203	193.073	-18.153	-0.532	-0.633
Gamma	0.111	0.041	25.591	72.737	157.546	-7.048	-0.62	-0.825
Logistic	0.111	0.147	56.054	102.82	181.244	-7.13	-0.661	-0.798
LogLogistic	0.111	0.043	28.693	97.924	217.567	-13.017	-0.643	-0.741
LogProbit	0.111	0.071	51.999	126.408	242.842	-11.573	-0.623	-0.004
Multistage 2	0.111	0.211	29.733	88.709	159.371	-12.26	-0.632	-0.812
Probit	0.111	0.249	59.161	109.055	193.703	-4.423	-0.523	-0.669
Quantal Linear	0.111	0.124	23.268	44.288	97.447	-5.621	-0.619	-1.01
Weibull	0.111	0.085	24.091	87.267	197.922	-13.075	-0.616	-0.764
Model Average	-	-	28.832	93.195	182.968	-	-	-



1.2.4 Individual Model Results

1.2.4.1 Hill Model



Hill Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	-1	2	-40	40
v	Normal	0	3	-40	40
a	Normal	-3	3.3	-40	40
b	Lognormal	0.693147	0.5	0	40

Modeling Summary:

BMD	93.2031
BMDL	28.8433
BMDU	193.073
AIC	36.9264
Log-Likelihood	-14.4632
P-Value	0.333846
Overall d.f.	1.9192
Chi ²	2.09462

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0450718	no	0.0723509
v	0.940489	no	0.0644542
a	-11.6992	no	4.51093
b	2.11043	no	0.789204

Goodness of Fit:

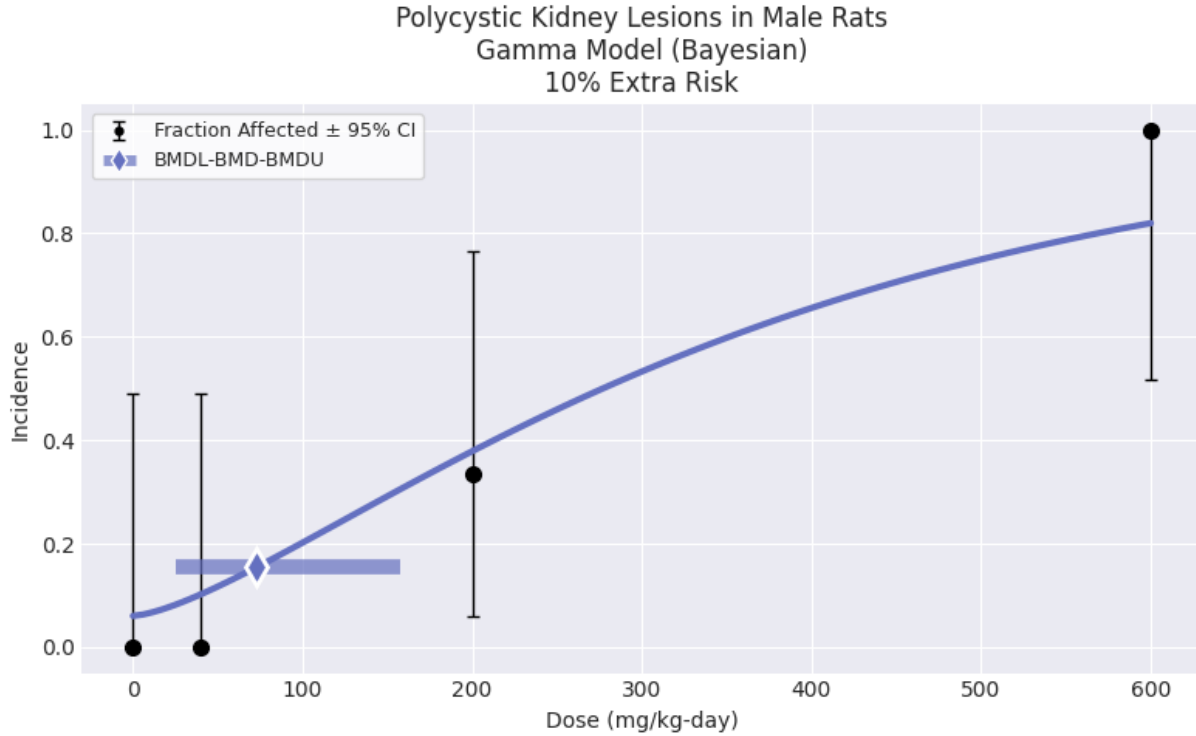
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	0.270431	0.0450718	-0.532161
40	6	0	0.375882	0.062647	-0.633248
200	6	2	2.28283	0.380471	-0.237823
600	6	6	4.89539	0.815898	1.16356

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-14.4632	4	21.2882	0	0
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

954

1.2.4.2 Gamma Model



Gamma Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-18	18
a	Lognormal	0.693147	0.424264	0.2	20
b	Lognormal	0	1	0	10000

Modeling Summary:

BMD	72.7374
BMDL	25.5906
BMDU	157.546
AIC	28.9019
Log-Likelihood	-11.451
P-Value	0.335584
Overall d.f.	2.20723
Chi ²	2.43689

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0602412	no	0.0656031
a	1.48203	no	0.534721
b	0.00390997	no	0.00221445

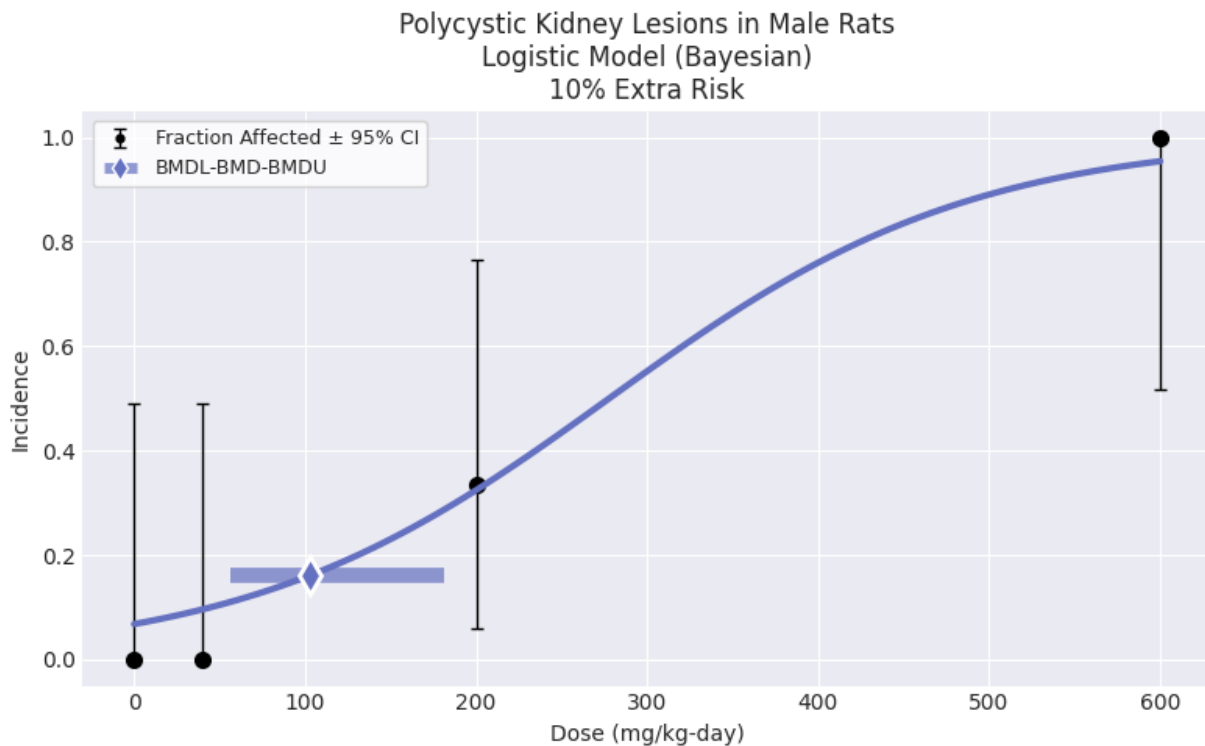
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	0.361447	0.0602412	-0.620175
40	6	0	0.611843	0.101974	-0.825421
200	6	2	2.2725	0.37875	-0.229339
600	6	6	4.91914	0.819857	1.1482

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-11.451	3	15.2637	1	9.34942e-05
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

1.2.4.3 Logistic Model



June 2026

Logistic Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
a	Normal	0	2	-20	20
b	Lognormal	0	2	0	40

Modeling Summary:

BMD	102.82
BMDL	56.0543
BMDU	181.244
AIC	26.6377
Log-Likelihood	-11.3188
P-Value	0.548481
Overall d.f.	2.1788
Chi ²	1.36209

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-2.62076	no	0.884046
b	0.00943587	no	0.00398459

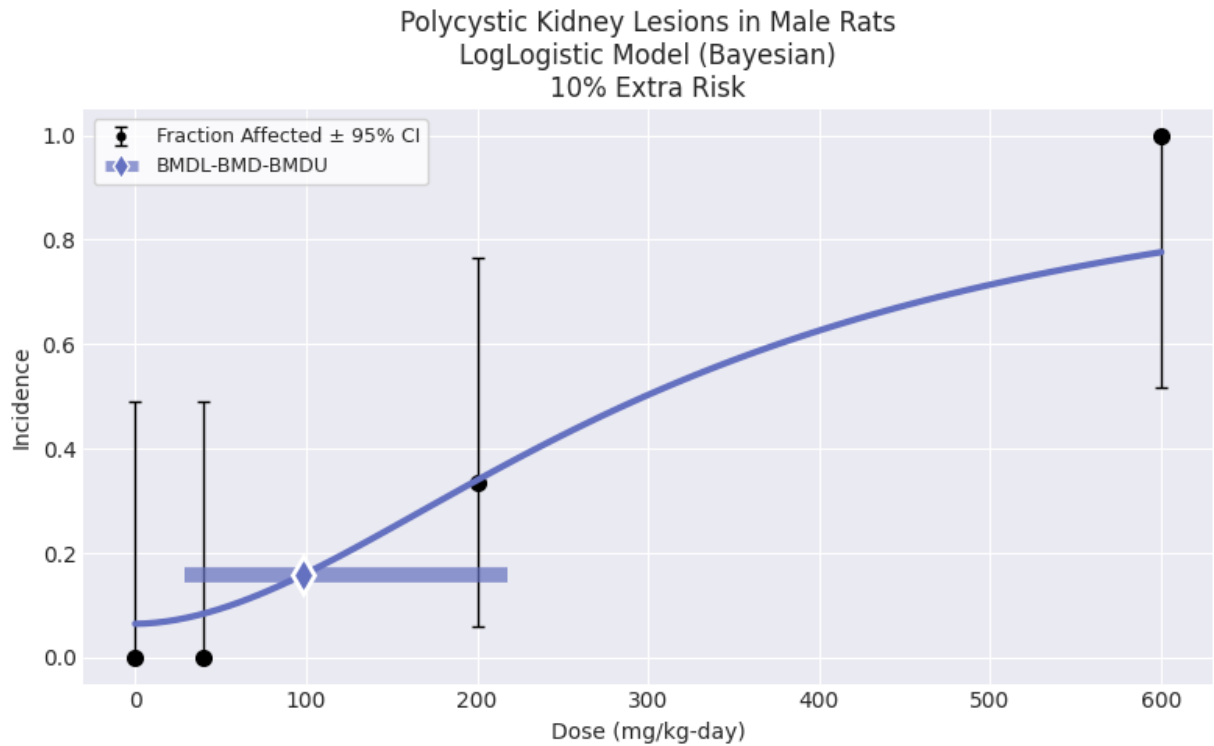
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	0.406886	0.0678143	-0.660671
40	6	0	0.575561	0.0959269	-0.797892
200	6	2	1.94645	0.324408	0.0466971
600	6	6	5.72629	0.954382	0.535528

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-11.3188	2	14.9995	2	0.000553215
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

1.2.4.4 LogLogistic Model



LogLogistic Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
a	Normal	0	1	-40	40
b	Lognormal	0.693147	0.5	0	20

Modeling Summary:

BMD	97.9245
BMDL	28.6934
BMDU	217.567
AIC	28.4263
Log-Likelihood	-11.2132
P-Value	0.291936
Overall d.f.	2.17686
Chi ²	2.69147

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0644261	no	0.0659172
a	-10.6823	no	3.87553
b	1.85095	no	0.644843

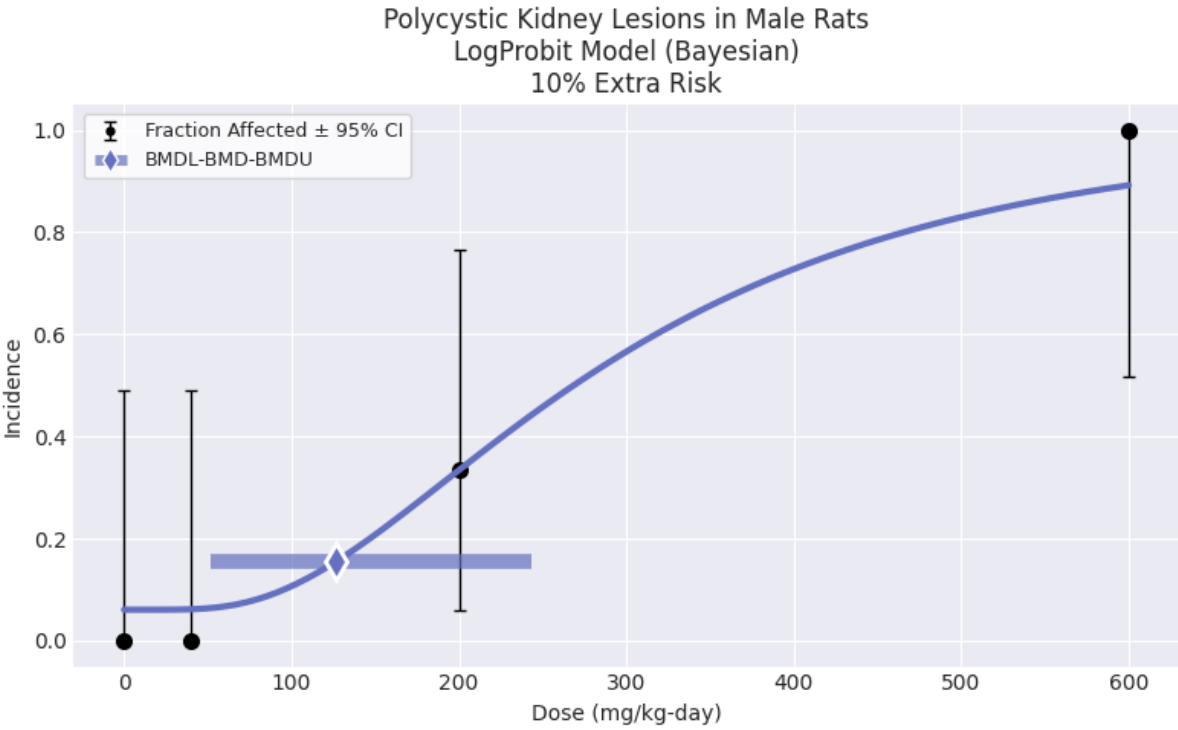
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	0.386557	0.0644261	-0.642788
40	6	0	0.503016	0.083836	-0.740976
200	6	2	2.03762	0.339604	-0.0324334
600	6	6	4.65827	0.776378	1.31461

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-11.2132	3	14.7882	1	0.000120287
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

1.2.4.5 LogProbit Model



LogProbit Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
a	Normal	0	1	-40	40
b	Lognormal	0.693147	0.5	0	20

Modeling Summary:

BMD	126.408
BMDL	51.9988
BMDU	242.842
AIC	26.4925
Log-Likelihood	-10.2463
P-Value	0.431368
Overall d.f.	1.83748
Chi ²	1.50722

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0606788	no	0.065707
a	-8.99492	no	3.1672
b	1.59383	no	0.53829

Goodness of Fit:

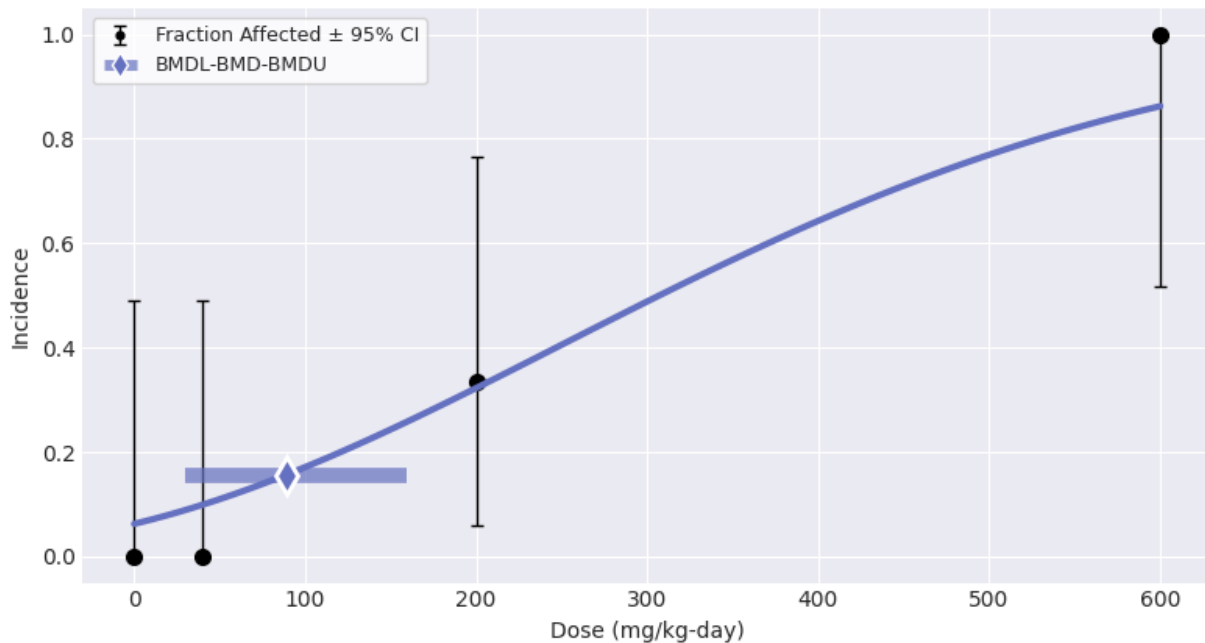
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	0.364073	0.0606788	-0.622568
40	6	0	0.369248	0.0615413	-0.627265
200	6	2	2.00445	0.334074	-0.00384858
600	6	6	5.35224	0.892041	0.852145

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-10.2463	3	12.8543	1	0.000336698
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

1.2.4.6 Multistage 2 Model

Polycystic Kidney Lesions in Male Rats
Multistage 2 Model (Bayesian)
10% Extra Risk



June 2026

Multistage 2 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
b1	Lognormal	0	1	0	1e+06
b2	Lognormal	0	1	0	1e+06

Modeling Summary:

BMD	88.7086
BMDL	29.7326
BMDU	159.371
AIC	26.0922
Log-Likelihood	-10.0461
P-Value	0.365601
Overall d.f.	2.00551
Chi ²	2.01891

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0624453	no	0.0652889
b1	0.000838658	no	0.582471
b2	3.93487e-06	no	1.27804

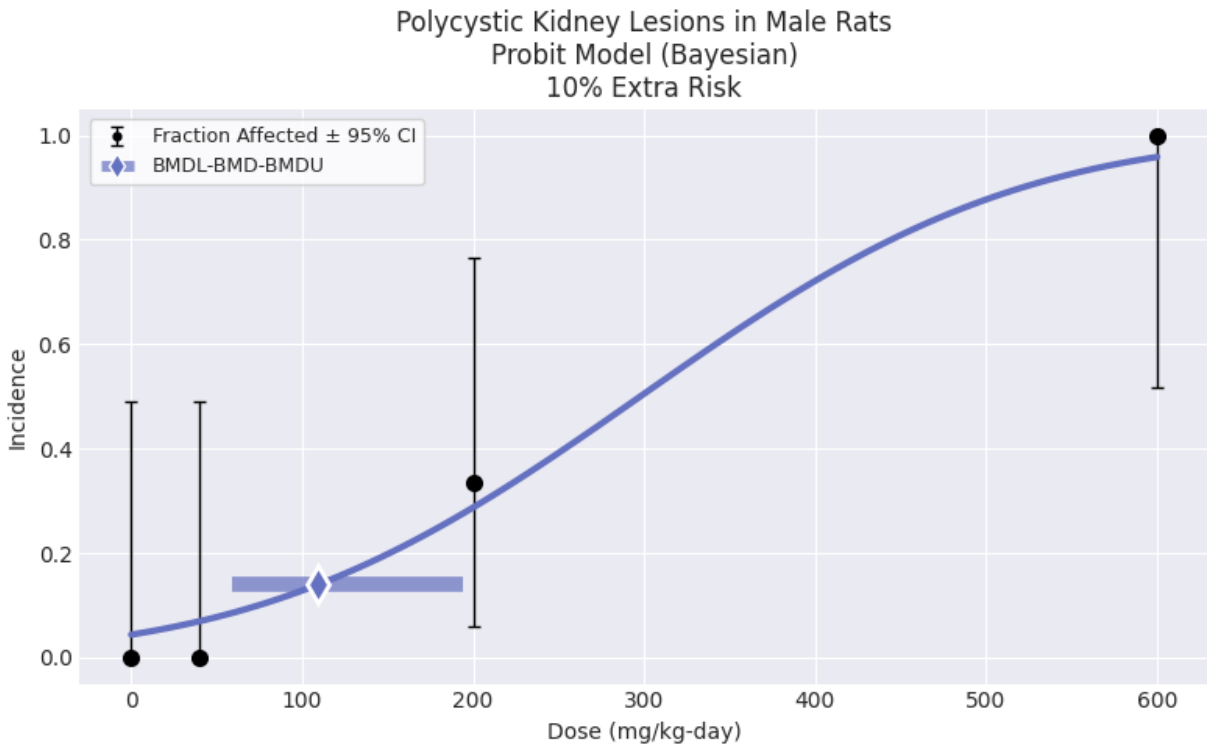
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	0.374672	0.0624453	-0.63216
40	6	0	0.594391	0.0990651	-0.812249
200	6	2	1.93606	0.322677	0.0558362
600	6	6	5.17508	0.862513	0.977965

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-10.0461	3	12.454	1	0.000417101
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

1.2.4.7 Probit Model



Probit Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
a	Normal	0	2	-20	20
b	Lognormal	0	1	0	40

June 2026

Modeling Summary:

BMD	109.055
BMDL	59.1614
BMDU	193.703
AIC	23.4011
Log-Likelihood	-9.70055
P-Value	0.655901
Overall d.f.	2.26654
Chi ²	1.04193

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-1.70983	no	0.555514
b	0.00574286	no	0.00217601

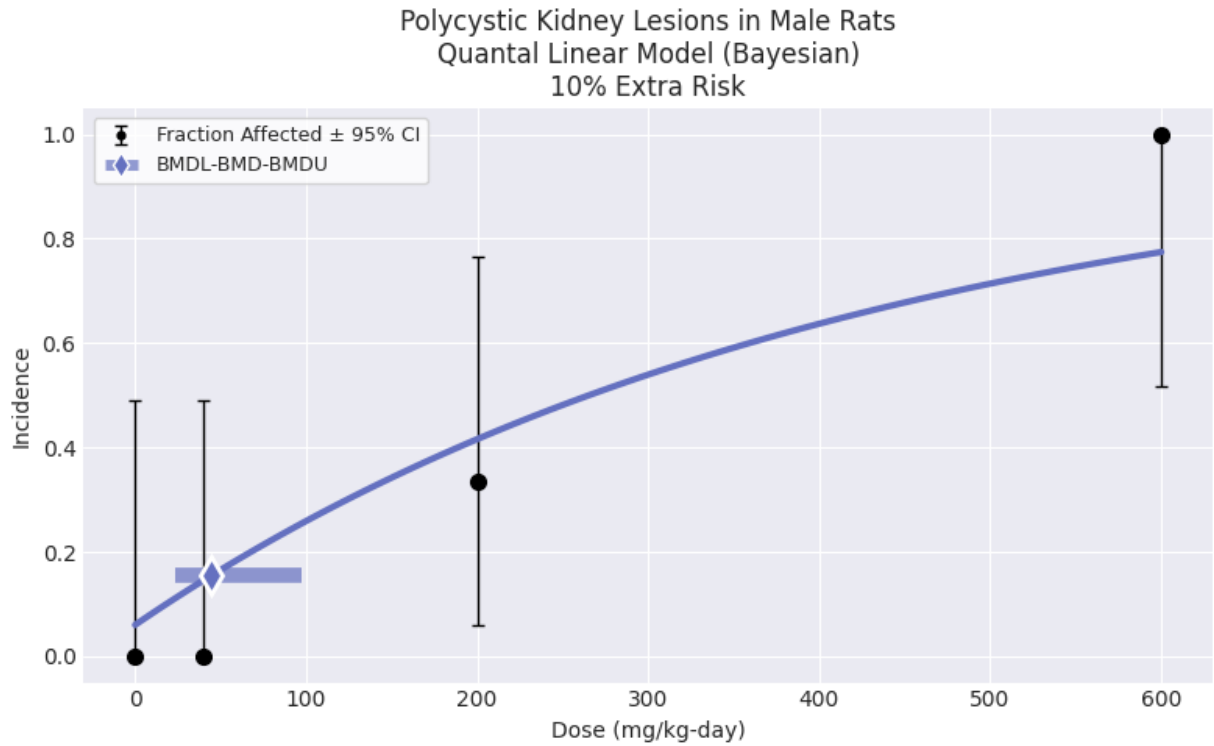
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	0.261894	0.0436489	-0.523304
40	6	0	0.41653	0.0694216	-0.669032
200	6	2	1.72387	0.287312	0.249119
600	6	6	5.75225	0.958708	0.50835

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-9.70055	2	11.7629	2	0.0027907
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

1.2.4.8 Quantal Linear Model



Quantal Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
b	Lognormal	0	1	0	18

Modeling Summary:

BMD	44.2875
BMDL	23.2683
BMDU	97.447
AIC	25.2978
Log-Likelihood	-10.6489
P-Value	0.254936
Overall d.f.	2.43475
Chi ²	3.31994

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0600762	no	0.0656568
b	0.00237901	no	0.00100458

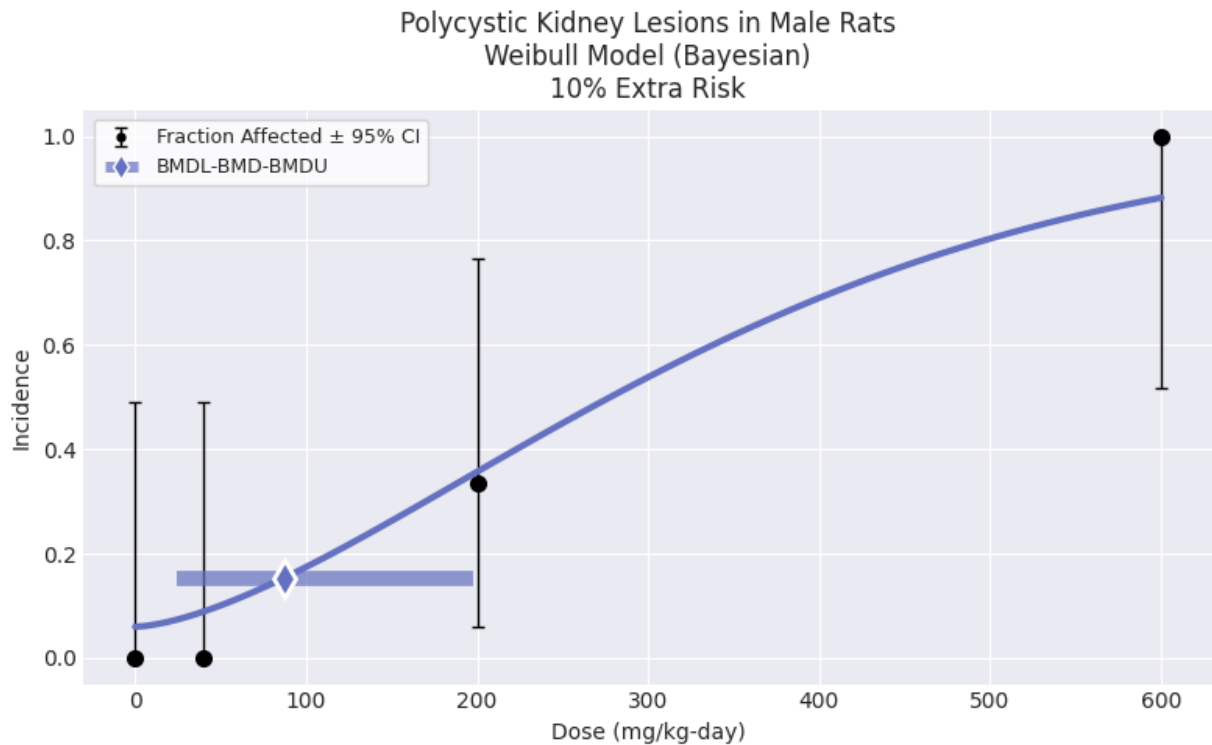
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	0.360457	0.0600762	-0.619271
40	6	0	0.872375	0.145396	-1.01034
200	6	2	2.49566	0.415944	-0.410551
600	6	6	4.6469	0.774484	1.32178

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-10.6489	2	13.6596	2	0.00108108
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

1.2.4.9 Weibull Model



June 2026

Weibull Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
a	Lognormal	0.424264	0.5	0	40
b	Lognormal	0	1.5	0	10000

Modeling Summary:

BMD	87.2674
BMDL	24.0913
BMDU	197.922
AIC	27.8092
Log-Likelihood	-10.9046
P-Value	0.365002
Overall d.f.	1.79981
Chi ²	1.77909

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.059518	no	0.065387
a	1.54652	no	0.542212
b	0.000104981	no	1.1422

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	6	0	0.357108	0.059518	-0.616204
40	6	0	0.532255	0.0887092	-0.764243
200	6	2	2.14076	0.356794	-0.119959
600	6	6	5.29339	0.882232	0.894946

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-3.81909	4	-	-	-
Fitted model	-10.9046	3	14.1711	1	0.000166919
Reduced model	-15.2763	1	22.9145	3	4.20743e-05

2 UTERINE ATYPICAL ENDOMETRIAL HYPERPLASIA

Uterine atypical endometrial hyperplasia incidence in TBBPA-exposed females Wistar Han rats ([NTP, 2014](#)).

Report Generated: 2026-Mar-24 16:03 UTC

BMDs Online Version: U.S. Environmental Protection Agency (2025). BMDs Online 25.1 (pybmds 25.1; bmdscore 25.1). Available from <https://bmdsonline.epa.gov>.

2.1 Session for Uterine Atypical Endometrial Hyperplasia

2.1.1 Dataset

Dose (mg/kg-day)	N	Incidence
0	50	2
178.6	50	13
357	50	11
714	50	13

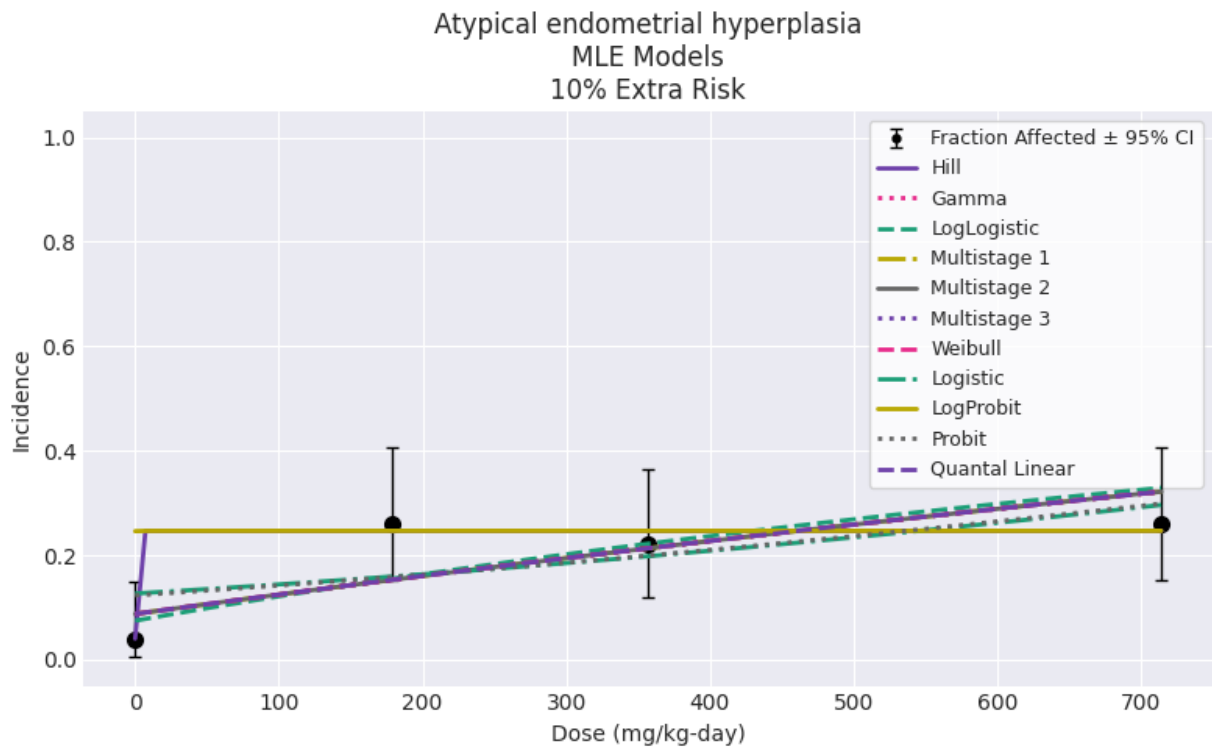
2.1.2 Settings

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

2.1.3 Maximum Likelihood Approach

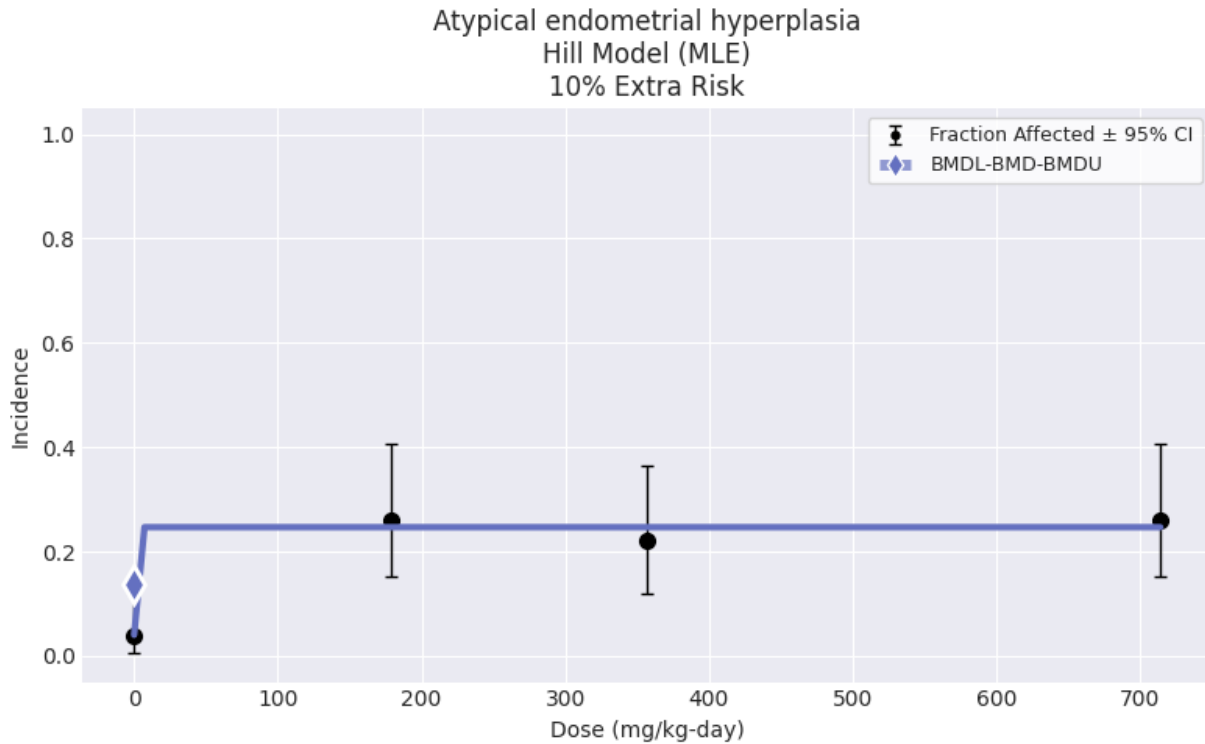
Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual Near BMD	Recommendation and Notes
Hill	0	<0.001	-	0.592	190.387	<0.001	<0.001	Unusable lowest dose/BMD ratio > 3.0 lowest dose/BMD ratio > 10.0 BMDL does not exist
Gamma	153.323	253.688	708.835	0.034	194.57	-1.188	2.109	Questionable Residual near BMD > 2.0 Goodness of fit p-value < 0.1
LogLogistic	122.225	209.236	587.952	0.045	193.901	-0.928	2.06	Questionable Residual near BMD > 2.0 Goodness of fit p-value < 0.1
Multistage 1	153.321	253.688	708.962	0.034	194.57	-1.188	2.109	Questionable Residual near BMD > 2.0 Goodness of fit p-value < 0.1
Multistage 2	153.323	253.688	708.966	0.034	194.57	-1.188	2.109	Questionable Residual near BMD > 2.0 Goodness of fit p-value < 0.1
Multistage 3	153.323	253.688	709.01	0.034	194.57	-1.188	2.109	Questionable Residual near BMD > 2.0 Goodness of fit p-value < 0.1
Weibull	153.323	253.688	708.835	0.034	194.57	-1.188	2.109	Questionable Residual near BMD > 2.0 Goodness of fit p-value < 0.1
Logistic	294.48	422.035	1243.687	0.022	196.343	-1.842	0.389	Questionable Goodness of fit p-value < 0.1

LogProbit	-	0	-	0.866	188.387	<0.001	-	Unusable Did not successfully execute.
Probit	277.257	402.121	1167.217	0.023	196.165	-1.787	0.366	Questionable Goodness of fit p-value < 0.1
Quantal Linear	153.323	253.688	708.835	0.034	194.57	-1.188	2.109	Questionable Residual near BMD > 2.0 Goodness of fit p-value < 0.1



2.1.4 Individual Model Results

2.1.4.1 Hill Model



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

June 2026

Modeling Summary:

BMD	9.43309e-06
BMDL	0
BMDU	-9999
AIC	190.387
Log-Likelihood	-92.1937
P-Value	0.592141
Overall d.f.	1
Chi ²	0.287013

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.04	no	0.0450697
v	0.215278	no	0.0155799
a	11.4291	no	6.61788e-05
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.

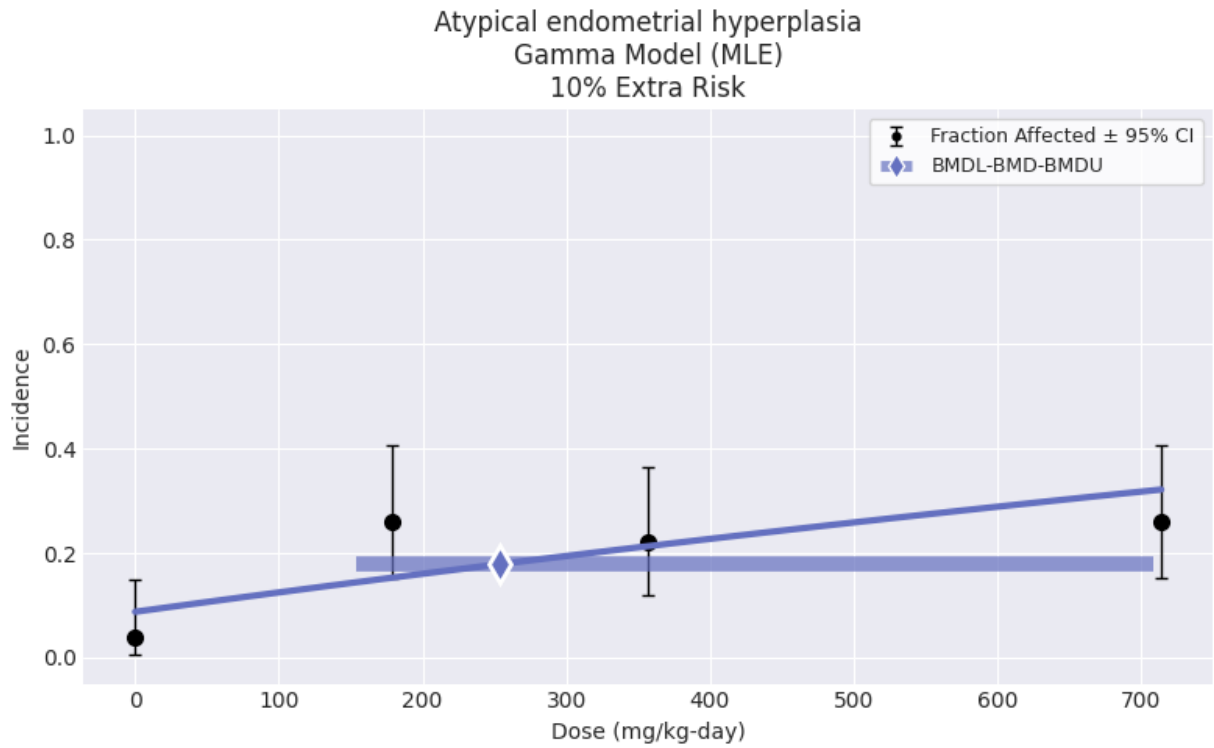
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	2	0.04	3.53116e-08
178.6	50	13	12.3333	0.246667	0.218713
357	50	11	12.3333	0.246667	-0.437426
714	50	13	12.3333	0.246667	0.218713

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-92.1937	3	0.290836	1	0.589685
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.1.4.2 Gamma Model



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	253.688
BMDL	153.323
BMDU	708.835
AIC	194.57
Log-Likelihood	-95.285
P-Value	0.0343179
Overall d.f.	2
Chi ²	6.74418

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0874737	no	0.0340276
a	1	yes	Not Reported
b	0.000415316	no	0.000165018

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.

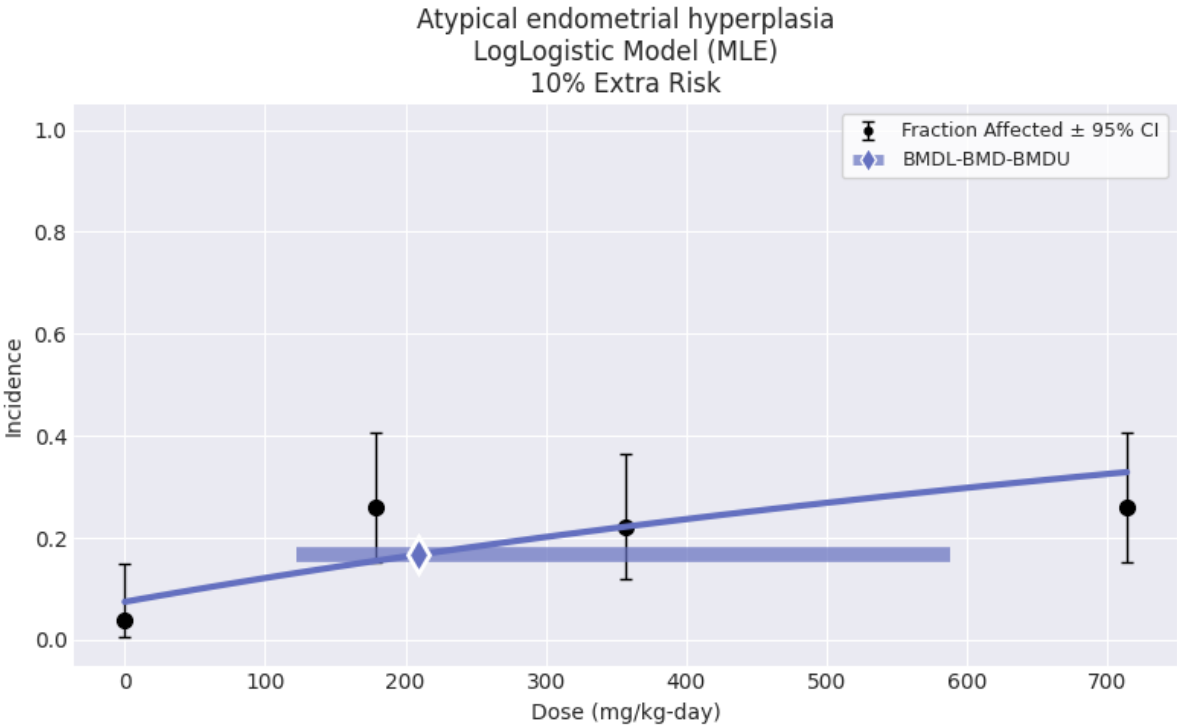
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	4.37369	0.0874737	-1.18817
178.6	50	13	7.63557	0.152711	2.10905
357	50	11	10.661	0.21322	0.117055
714	50	13	16.0819	0.321638	-0.93308

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-95.285	2	6.47336	2	0.0392941
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.1.4.3 LogLogistic Model



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	209.236
BMDL	122.225
BMDU	587.952
AIC	193.901
Log-Likelihood	-94.9506
P-Value	0.0454079
Overall d.f.	2
Chi ²	6.18414

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0744702	no	0.0395363
a	-7.54069	no	0.417575
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.

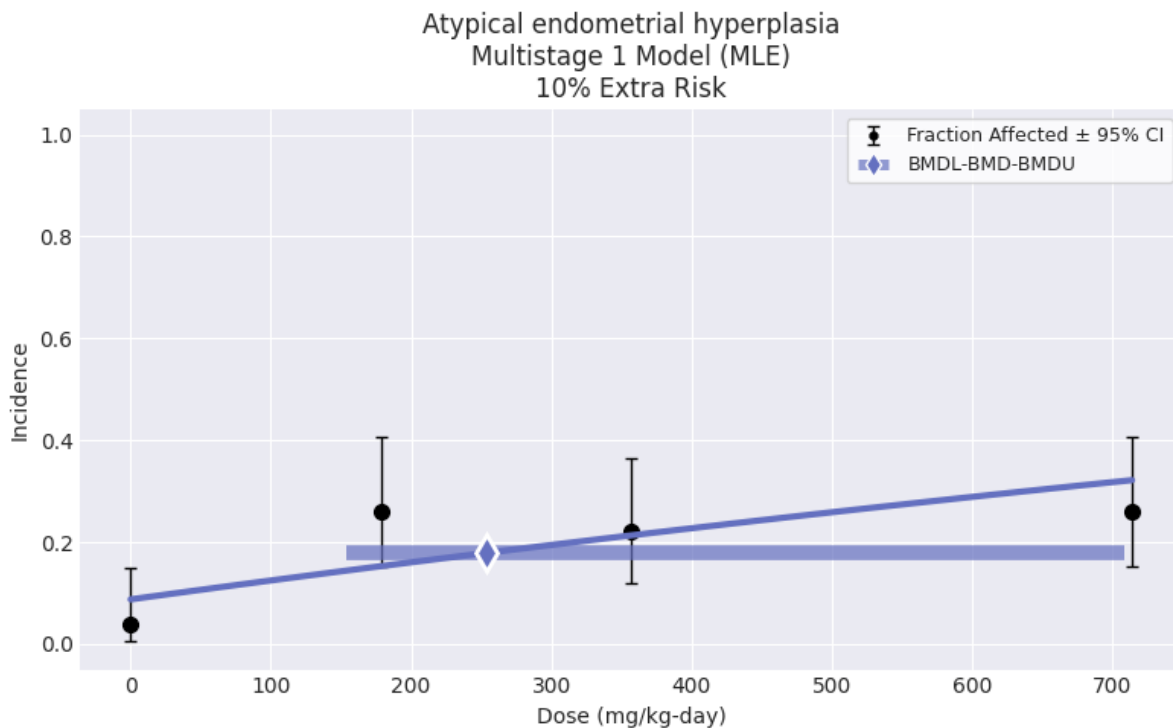
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	3.72351	0.0744702	-0.928416
178.6	50	13	7.73228	0.154646	2.06039
357	50	11	11.0984	0.221968	-0.0334889
714	50	13	16.4458	0.328916	-1.03723

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-94.9506	2	5.80464	2	0.0548958
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.1.4.4 Multistage 1 Model



June 2026

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	253.688
BMDL	153.321
BMDU	708.962
AIC	194.57
Log-Likelihood	-95.285
P-Value	0.0343179
Overall d.f.	2
Chi ²	6.74418

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0874738	no	0.0340289
b1	0.000415316	no	0.117259

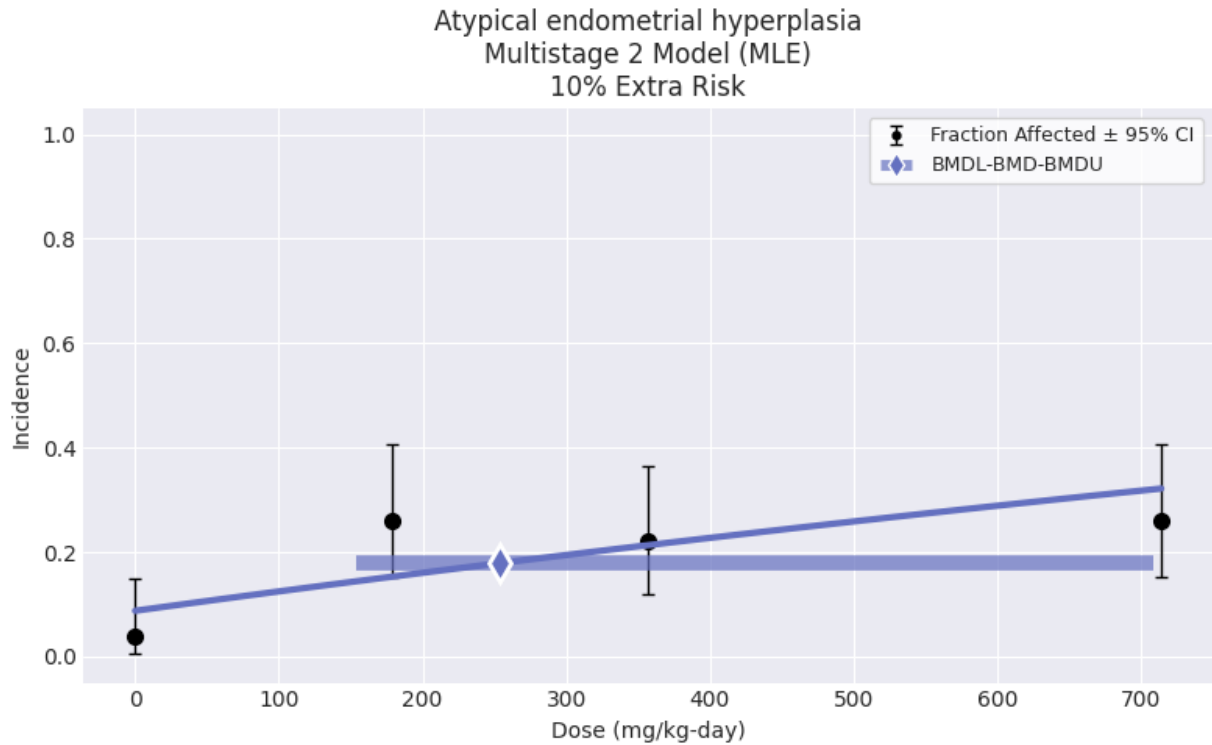
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	4.37369	0.0874738	-1.18817
178.6	50	13	7.63557	0.152711	2.10905
357	50	11	10.661	0.21322	0.117055
714	50	13	16.0819	0.321638	-0.93308

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-95.285	2	6.47336	2	0.0392941
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.1.4.5 Multistage 2 Model



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

June 2026

Modeling Summary:

BMD	253.688
BMDL	153.323
BMDU	708.966
AIC	194.57
Log-Likelihood	-95.285
P-Value	0.0343179
Overall d.f.	2
Chi ²	6.74418

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0874737	no	0.0340273
b1	0.000415316	no	0.117256
b2	1.27705e-21	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.

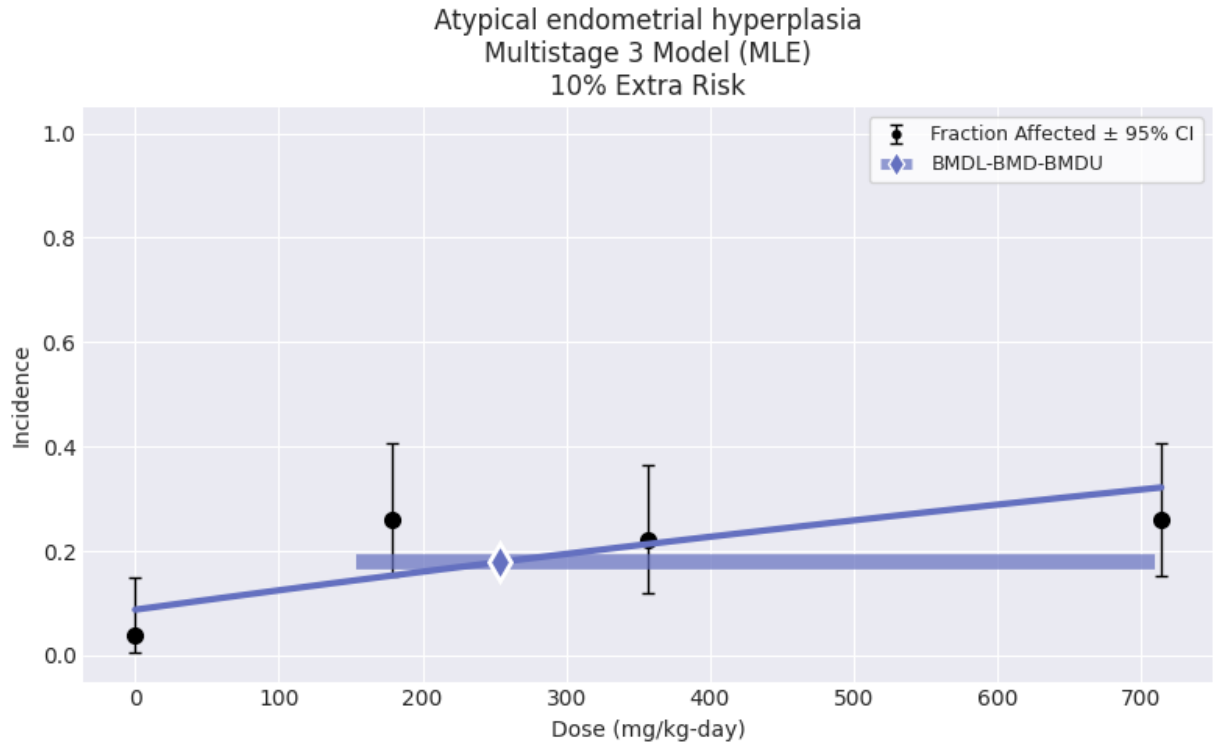
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	4.37369	0.0874737	-1.18817
178.6	50	13	7.63557	0.152711	2.10905
357	50	11	10.661	0.21322	0.117055
714	50	13	16.0819	0.321638	-0.93308

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-95.285	2	6.47336	2	0.0392941
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.1.4.6 Multistage 3 Model



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

June 2026

Modeling Summary:

BMD	253.688
BMDL	153.323
BMDU	709.01
AIC	194.57
Log-Likelihood	-95.285
P-Value	0.0343179
Overall d.f.	2
Chi ²	6.74418

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0874738	no	0.0340242
b1	0.000415316	no	0.117244
b2	0	yes	Not Reported
b3	7.09032e-26	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:

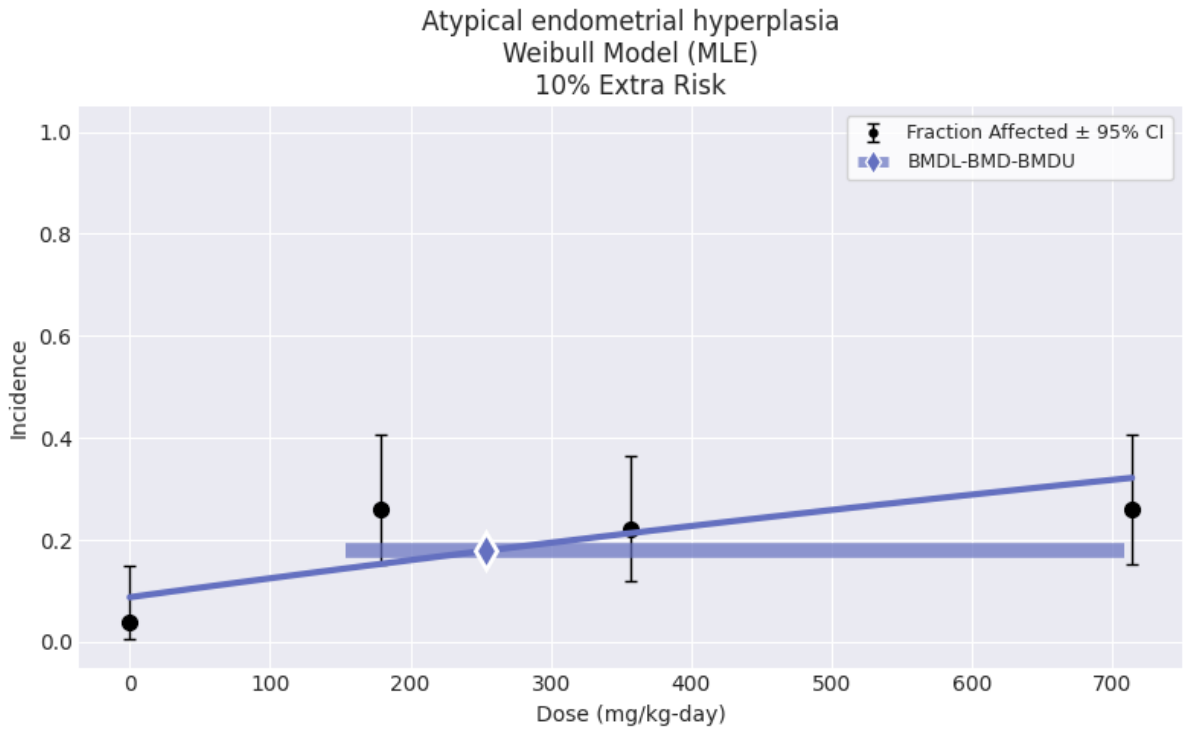
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	4.37369	0.0874738	-1.18817
178.6	50	13	7.63557	0.152711	2.10905
357	50	11	10.661	0.21322	0.117055
714	50	13	16.0819	0.321638	-0.93308

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-95.285	2	6.47336	2	0.0392941
Reduced model	-98.6785	1	13.2603	3	0.00410613

1873

2.1.4.7 Weibull Model



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	253.688
BMDL	153.323
BMDU	708.835
AIC	194.57
Log-Likelihood	-95.285
P-Value	0.0343179
Overall d.f.	2
Chi²	6.74418

PUBLIC RELEASE DRAFT
June 2026

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0874737	no	0.0340225
a	1	yes	Not Reported
b	0.000415316	no	0.117796

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:

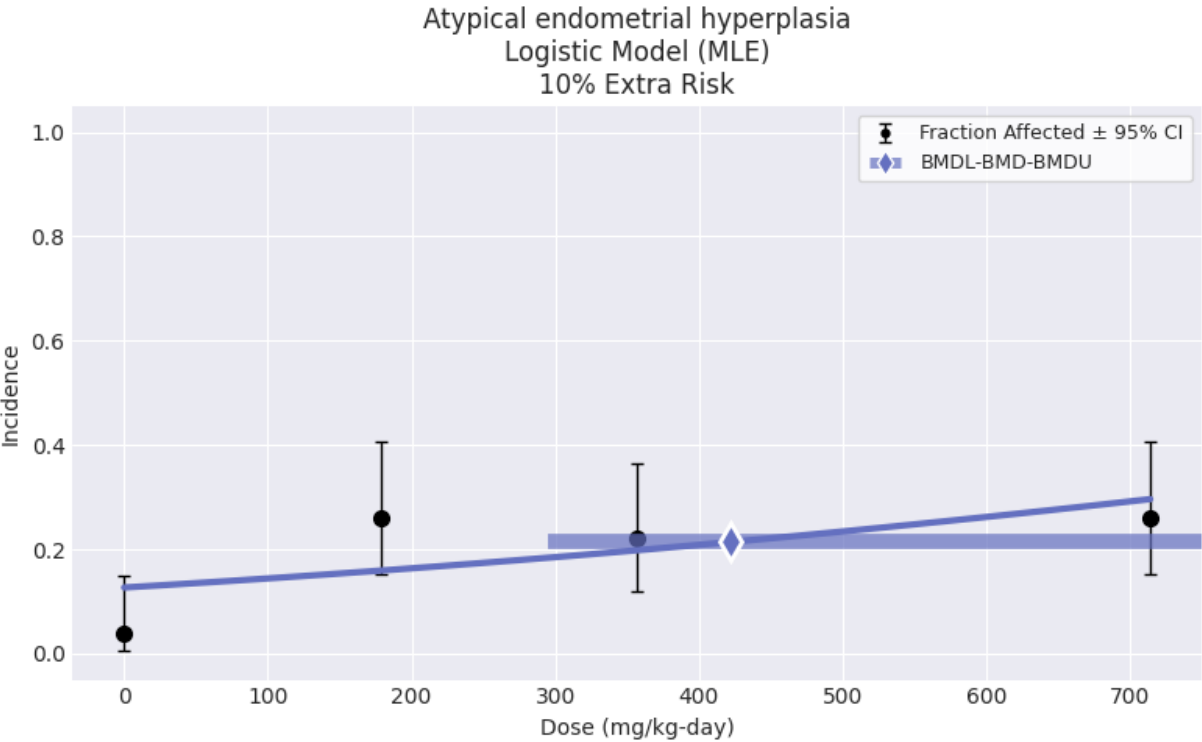
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	4.37369	0.0874737	-1.18817
178.6	50	13	7.63557	0.152711	2.10905
357	50	11	10.661	0.21322	0.117055
714	50	13	16.0819	0.321638	-0.93308

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-95.285	2	6.47336	2	0.0392941
Reduced model	-98.6785	1	13.2603	3	0.00410613

1940

2.1.4.8 Logistic Model



Logistic 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	100

Modeling Summary:

BMD	422.035
BMDL	294.48
BMDU	1243.69
AIC	196.343
Log-Likelihood	-96.1713
P-Value	0.0217194
Overall d.f.	2
Chi²	7.6591

June 2026

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-1.93133	no	0.309217
b	0.00149279	no	0.000668712

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	6.33018	0.126604	-1.84159
178.6	50	13	7.9565	0.15913	1.94988
357	50	11	9.90349	0.19807	0.38909
714	50	13	14.8098	0.296197	-0.560582

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-96.1713	2	8.24593	2	0.0161964
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.1.4.9 LogProbit Model**LogProbit Model**

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

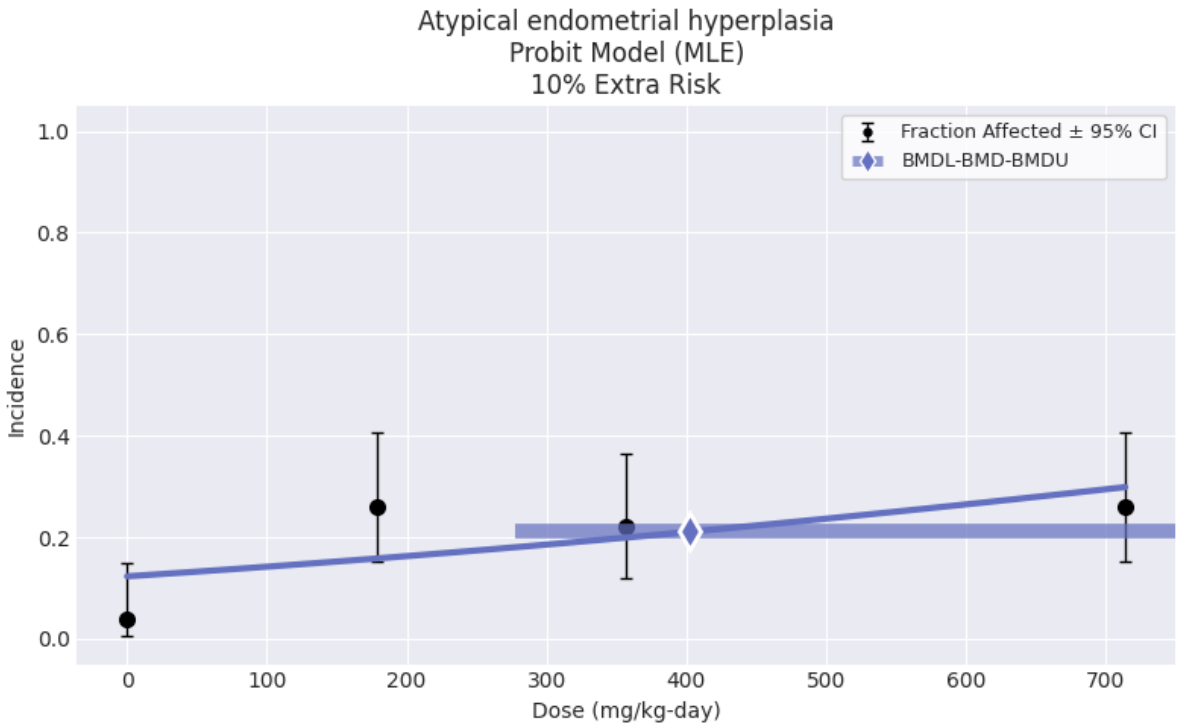
Parameter Settings:

Parameter	Initial	Min	Max
g	0	-18	18
a	0	-18	18
b	0.0001	0.0001	18

Model has not successfully executed; no results available.

2025

2.1.4.10 Probit Model



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	402.121
BMDL	277.257
BMDU	1167.22
AIC	196.165
Log-Likelihood	-96.0823
P-Value	0.0225992
Overall d.f.	2
Chi ²	7.57968

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-1.16021	no	0.172234
b	0.000885701	no	0.000390474

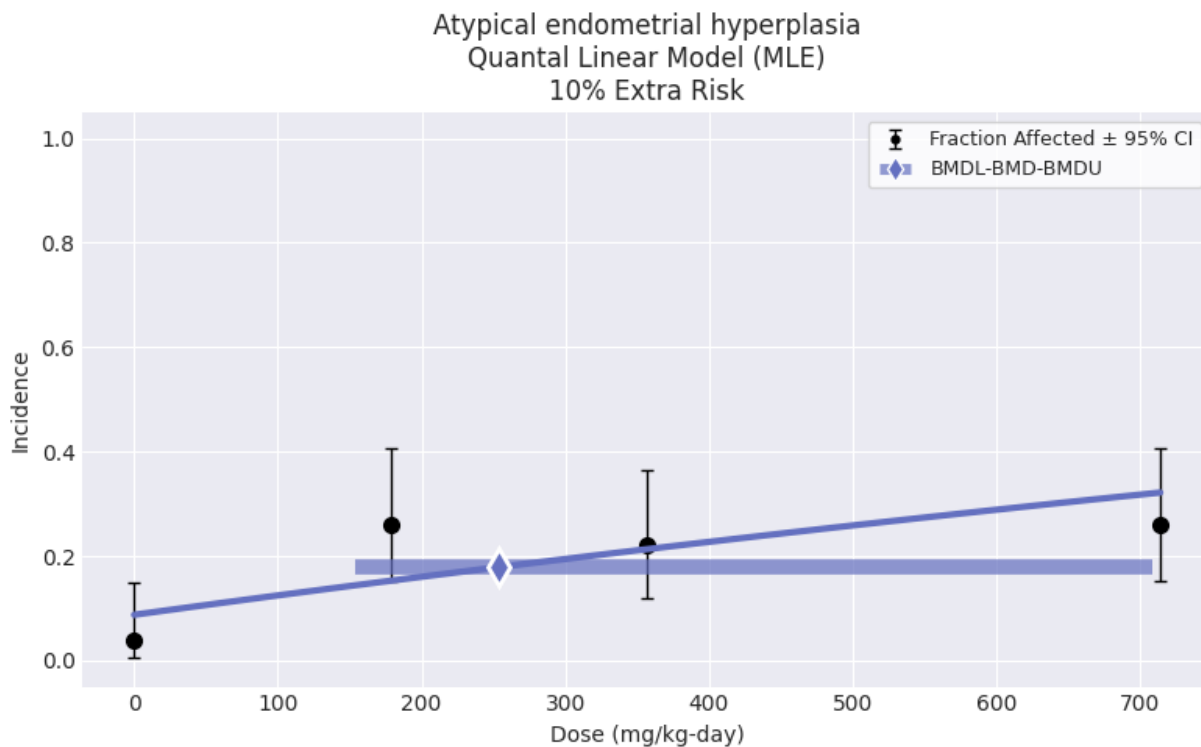
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	6.14907	0.122981	-1.78666
178.6	50	13	7.90829	0.158166	1.97337
357	50	11	9.96651	0.19933	0.365854
714	50	13	14.9406	0.298812	-0.599561

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-96.0823	2	8.06801	2	0.0177033
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.1.4.11 Quantal Linear Model



June 2026

Quantal Linear 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
g	0	-18	18
b	0	0	100

Modeling Summary:

BMD	253.688
BMDL	153.323
BMDU	708.835
AIC	194.57
Log-Likelihood	-95.285
P-Value	0.0343179
Overall d.f.	2
Chi ²	6.74418

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0874738	no	0.0340227
b	0.000415316	no	0.000164988

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	4.37369	0.0874738	-1.18817
178.6	50	13	7.63557	0.152711	2.10905
357	50	11	10.661	0.21322	0.117055
714	50	13	16.0819	0.321638	-0.93308

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-95.285	2	6.47336	2	0.0392941
Reduced model	-98.6785	1	13.2603	3	0.00410613

June 2026

2.2 Session for Uterine Atypical Endometrial Hyperplasia

2.2.1 Dataset

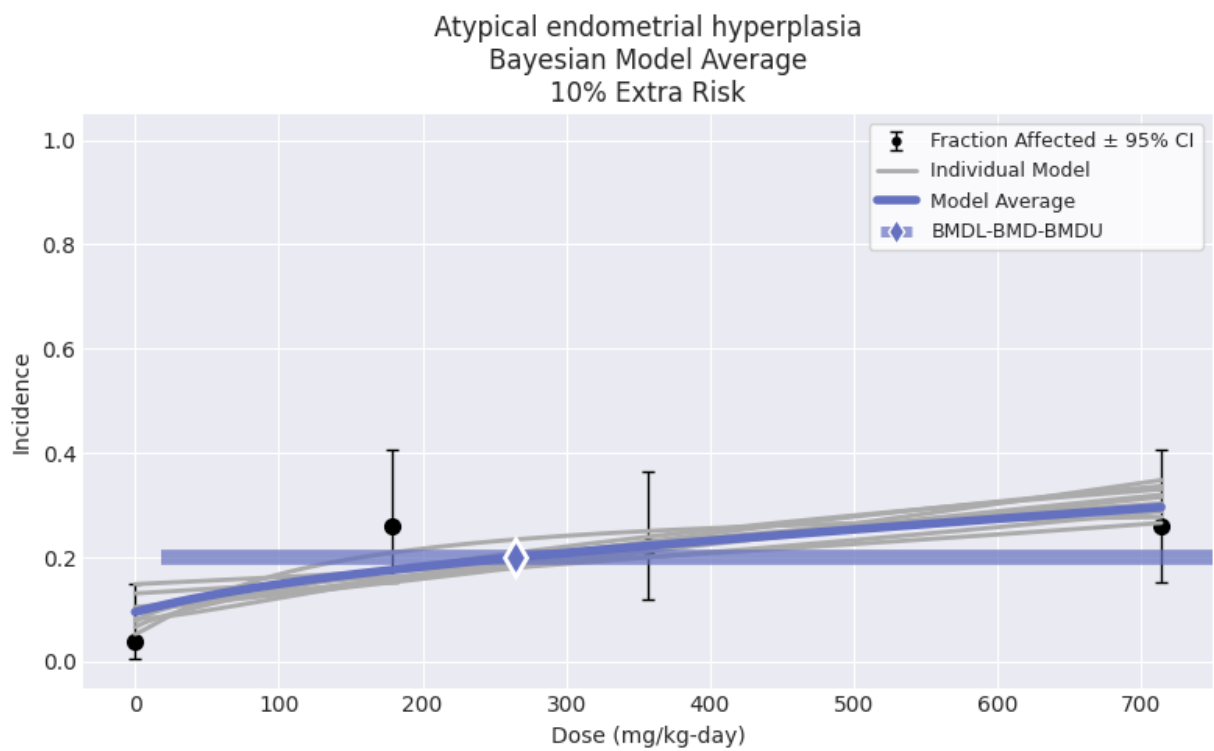
Dose (mg/kg-day)	N	Incidence
0	50	2
178.6	50	13
357	50	11
714	50	13

2.2.2 Settings

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

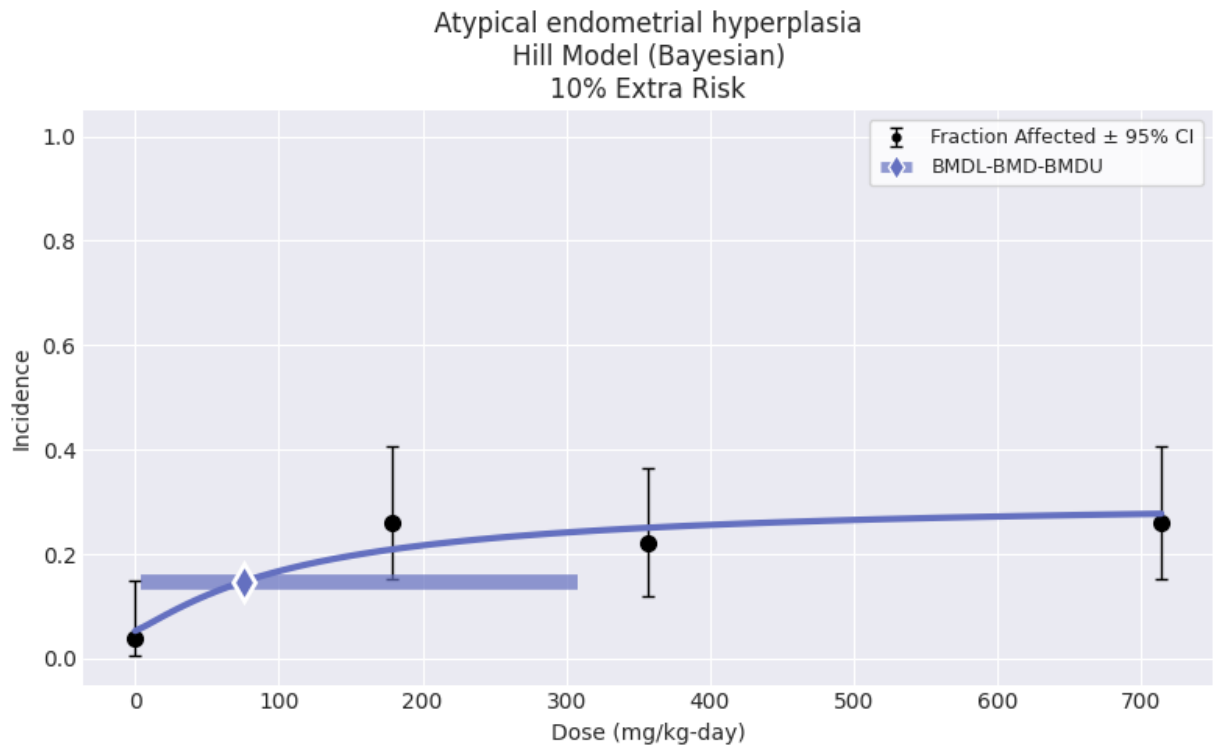
2.2.3 Bayesian Summary

Model	Prior Weights	Posterior Weights	BMDL	BMD	BMDU	Unnormalized Log Posterior Probability	Scaled Residual Near BMD	Scaled Residual at Control
Hill	0.111	0.244	4.264	75.529	308.029	-102.479	-0.401	-0.401
Gamma	0.111	0.033	112.067	299.231	1025.964	-91.395	-1.496	0.139
Logistic	0.111	0.144	316.104	545.391	-	-92.674	-2.158	-0.096
LogLogistic	0.111	0.057	38.335	144.121	404.847	-99.152	-0.742	1.588
LogProbit	0.111	0.005	73.04	215.378	868.602	-100.173	-1.096	1.971
Probit	0.111	0.148	288.489	434.77	1106.662	-90.035	-1.903	0.353
Quantal Linear	0.111	0.286	162.248	265.016	593.95	-89.902	-1.355	1.964
Weibull	0.111	0.08	34.238	159.347	688.062	-96.108	-0.959	1.579
Multistage 2	0.111	0.002	180.31	296.365	506.641	-96.732	-1.428	0.14
Model Average	-	-	18.473	263.973	1036.843	-	-	-



2.2.4 Individual Model Results

2.2.4.1 Hill Model



June 2026

Hill Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	-1	2	-40	40
v	Normal	0	3	-40	40
a	Normal	-3	3.3	-40	40
b	Lognormal	0.693147	0.5	0	40

Modeling Summary:

BMD	75.5288
BMDL	4.26427
BMDU	308.029
AIC	210.16
Log-Likelihood	-101.08
P-Value	0.328413
Overall d.f.	1.24398
Chi ²	1.27189

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0526606	no	0.0391053
v	0.266583	no	0.0286626
a	-5.50477	no	2.73469
b	1.15491	no	0.522204

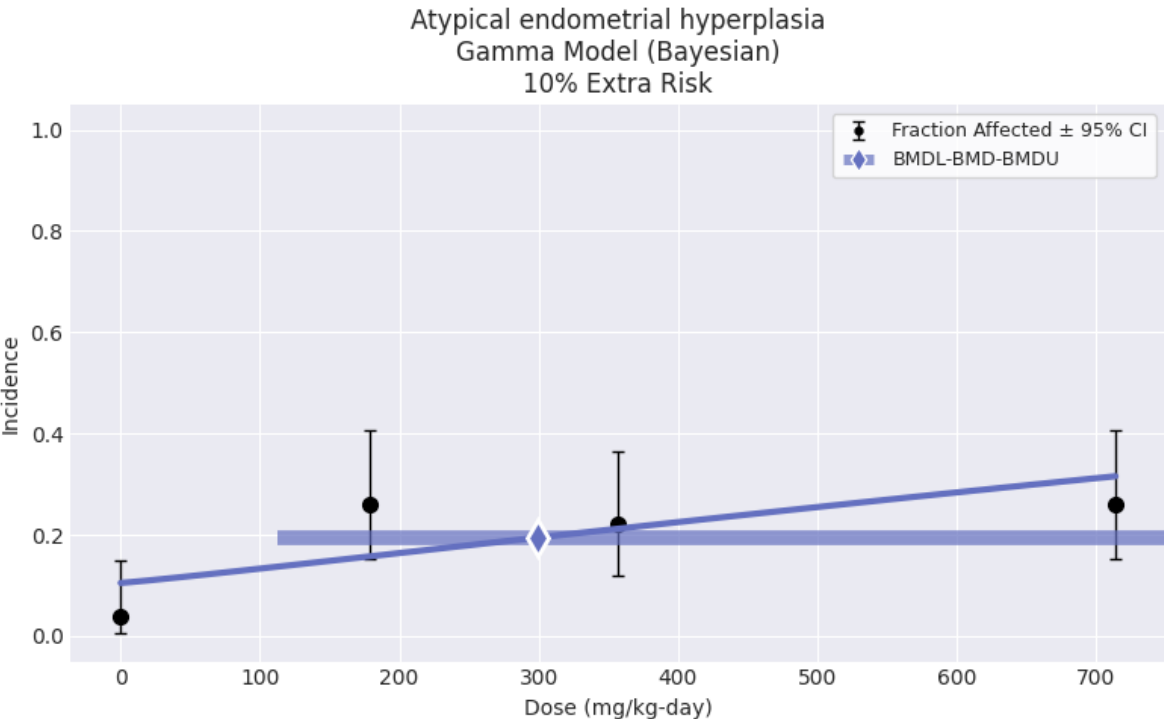
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	2.63303	0.0526606	-0.400814
178.6	50	13	10.4443	0.208886	0.889095
357	50	11	12.5208	0.250415	-0.496403
714	50	13	13.863	0.277259	-0.272632

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-101.08	4	18.0629	0	0
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.2.4.2 Gamma Model



Gamma Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-18	18
a	Lognormal	0.693147	0.424264	0.2	20
b	Lognormal	0	1	0	10000

PUBLIC RELEASE DRAFT
June 2026

Modeling Summary:

BMD	299.231
BMDL	112.067
BMDU	1025.96
AIC	204.732
Log-Likelihood	-99.3661
P-Value	0.0183148
Overall d.f.	1.54276
Chi ²	6.96432

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.104807	no	0.0359167
a	1.09302	no	0.420855
b	0.000450274	no	0.000288524

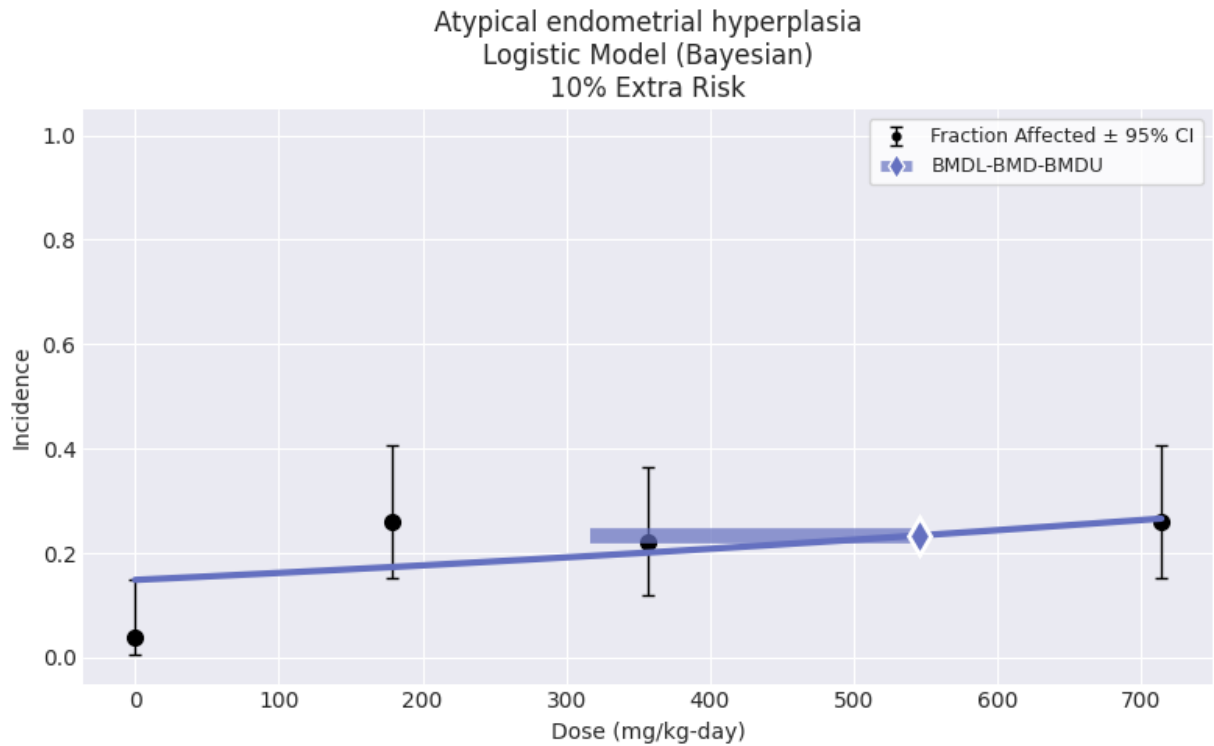
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	5.24035	0.104807	-1.49607
178.6	50	13	7.8587	0.157174	1.99769
357	50	11	10.5973	0.211945	0.139361
714	50	13	15.7806	0.315611	-0.846099

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-99.3661	3	14.6355	1	0.000130431
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.2.4.3 Logistic Model



Logistic Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
a	Normal	0	2	-20	20
b	Lognormal	0	2	0	40

Modeling Summary:

BMD	545.391
BMDL	316.104
BMDU	-9999
AIC	203.451
Log-Likelihood	-99.7255
P-Value	0.0251456
Overall d.f.	2.02146
Chi²	7.41118

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-1.74596	no	0.325746
b	0.00102391	no	0.000773575

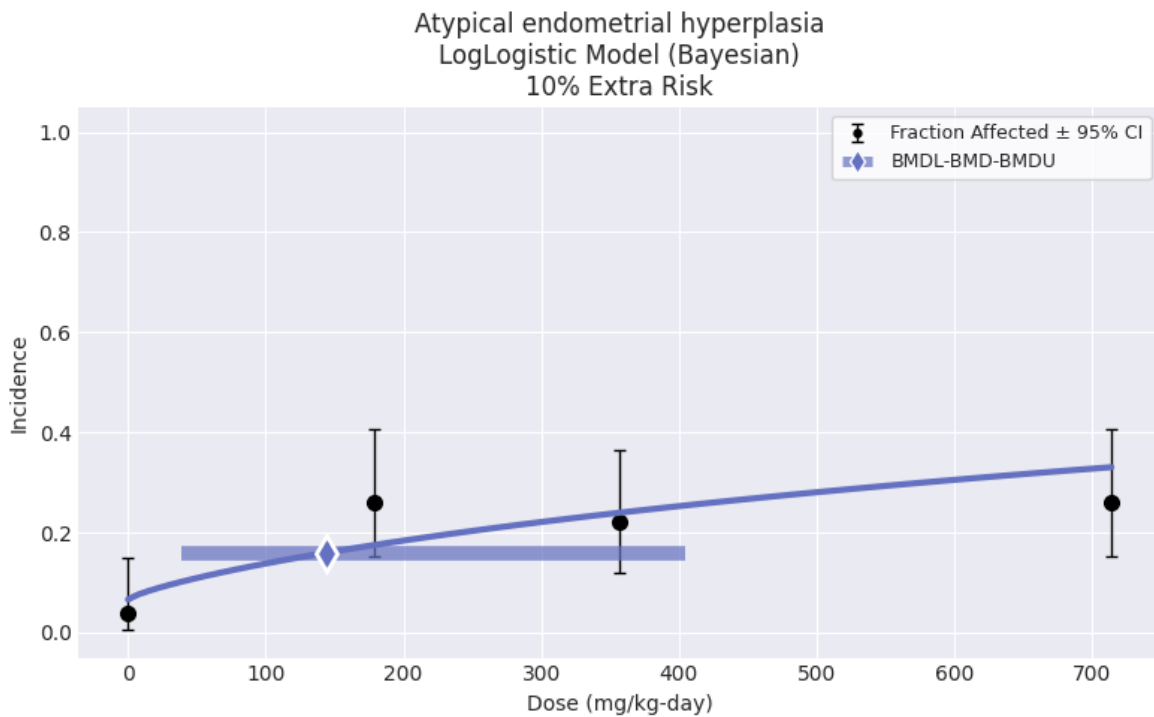
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	7.4279	0.148558	-2.15835
178.6	50	13	8.66022	0.173204	1.62182
357	50	11	10.0471	0.200942	0.336313
714	50	13	13.3013	0.266025	-0.0964212

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-99.7255	2	15.3545	2	0.000463251
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.2.4.4 LogLogistic Model



LogLogistic Model

Version: pybmds 25.1 (bmdscore 25.1)

June 2026

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
a	Normal	0	1	-40	40
b	Lognormal	0.693147	0.5	0	20

Modeling Summary:

BMD	144.121
BMDL	38.3347
BMDU	404.847
AIC	205.364
Log-Likelihood	-99.6818
P-Value	0.0583284
Overall d.f.	1.31168
Chi ²	4.29502

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0660447	no	0.0375508
a	-6.13543	no	1.82614
b	0.792292	no	0.27939

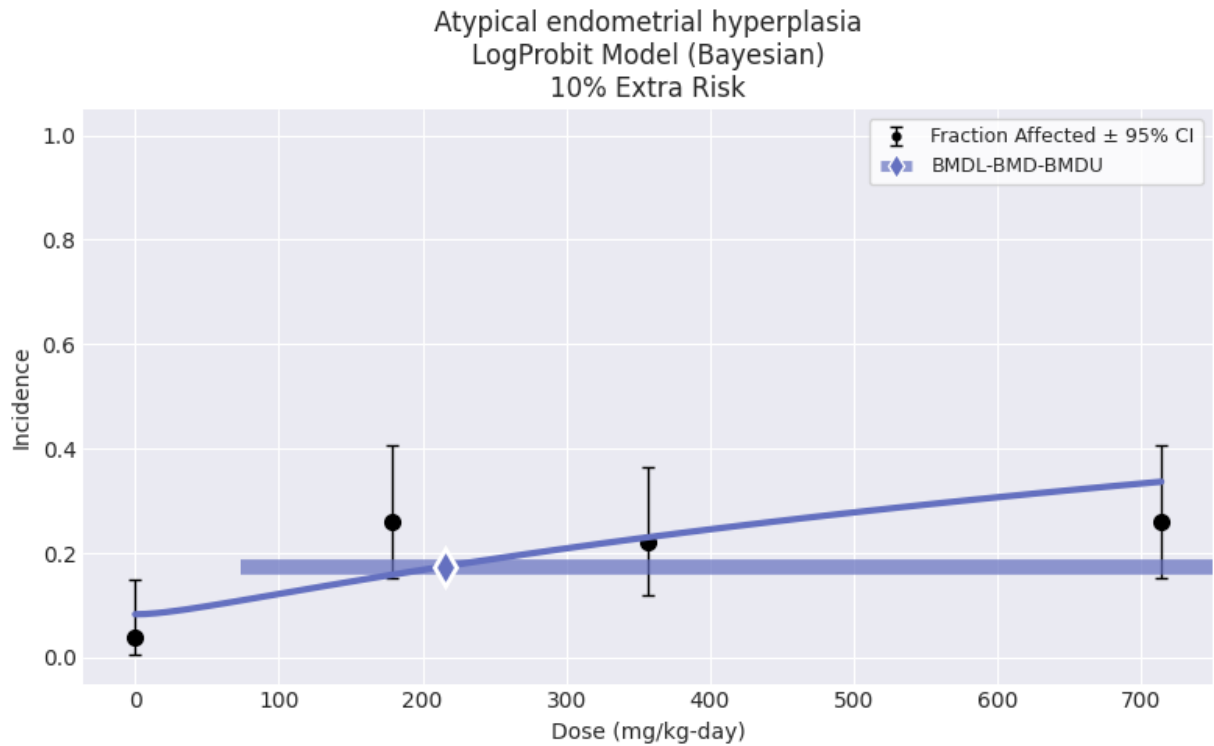
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	3.30224	0.0660447	-0.74152
178.6	50	13	8.73638	0.174728	1.58787
357	50	11	11.9715	0.239431	-0.321966
714	50	13	16.5201	0.330403	-1.05839

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-99.6818	3	15.2669	1	9.33369e-05
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.2.4.5 LogProbit Model



LogProbit Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
a	Normal	0	1	-40	40
b	Lognormal	0.693147	0.5	0	20

Modeling Summary:

BMD	215.378
BMDL	73.0402
BMDU	868.602
AIC	208.756
Log-Likelihood	-101.378
P-Value	0.0146749
Overall d.f.	1.1698
Chi ²	6.43126

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0826881	no	0.0433015
a	-4.37136	no	1.515
b	0.575128	no	0.220223

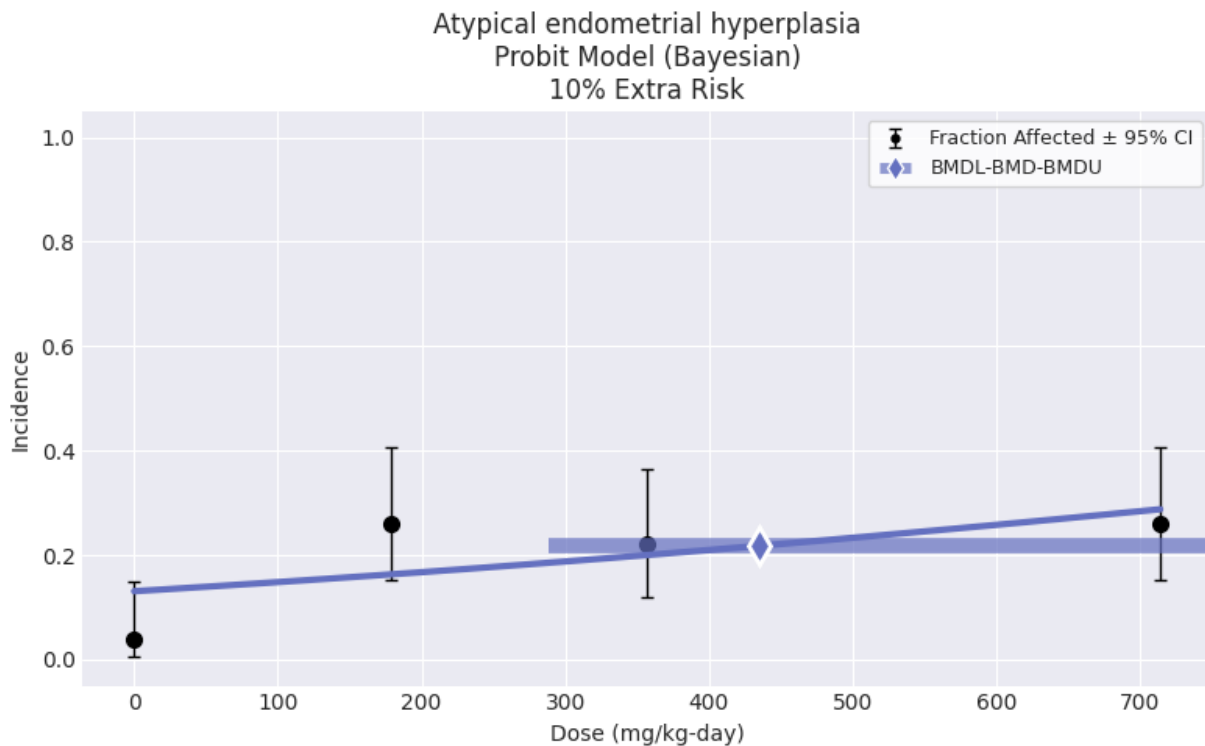
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	4.1344	0.0826881	-1.096
178.6	50	13	7.9128	0.158256	1.97117
357	50	11	11.5125	0.23025	-0.172162
714	50	13	16.8316	0.336633	-1.14669

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-101.378	3	18.6595	1	1.5627e-05
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.2.4.6 Probit Model



June 2026

Probit Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
a	Normal	0	2	-20	20
b	Lognormal	0	1	0	40

Modeling Summary:

BMD	434.77
BMDL	288.489
BMDU	1106.66
AIC	200.786
Log-Likelihood	-98.3929
P-Value	0.025549
Overall d.f.	2.02255
Chi ²	7.38156

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-1.12306	no	0.163354
b	0.000788591	no	0.000363861

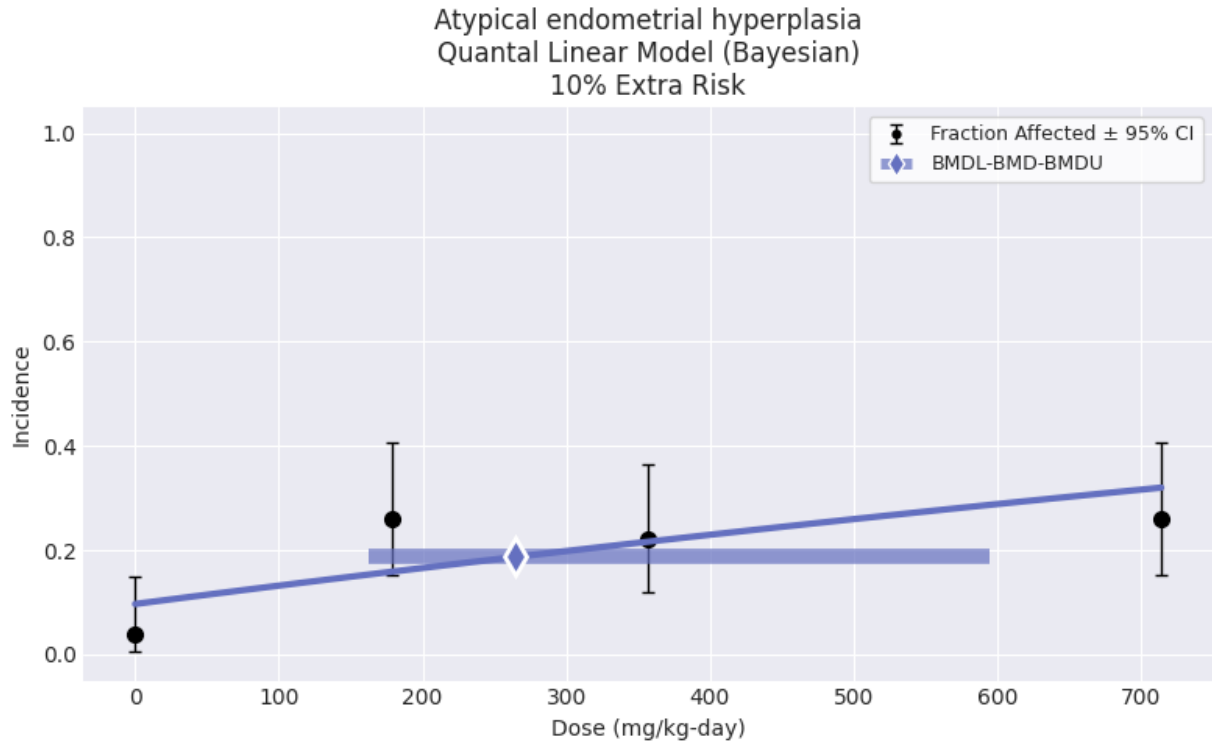
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	6.53531	0.130706	-1.90279
178.6	50	13	8.14982	0.162996	1.85703
357	50	11	10.0012	0.200025	0.353097
714	50	13	14.3869	0.287738	-0.433251

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-98.3929	2	12.6893	2	0.00175613
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.2.4.7 Quantal Linear Model



Quantal Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
b	Lognormal	0	1	0	18

Modeling Summary:

BMD	265.016
BMDL	162.248
BMDU	593.95
AIC	199.996
Log-Likelihood	-97.9981
P-Value	0.0400612
Overall d.f.	2.04422
Chi ²	6.52254

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0966321	no	0.0285306
b	0.000397562	no	0.000146751

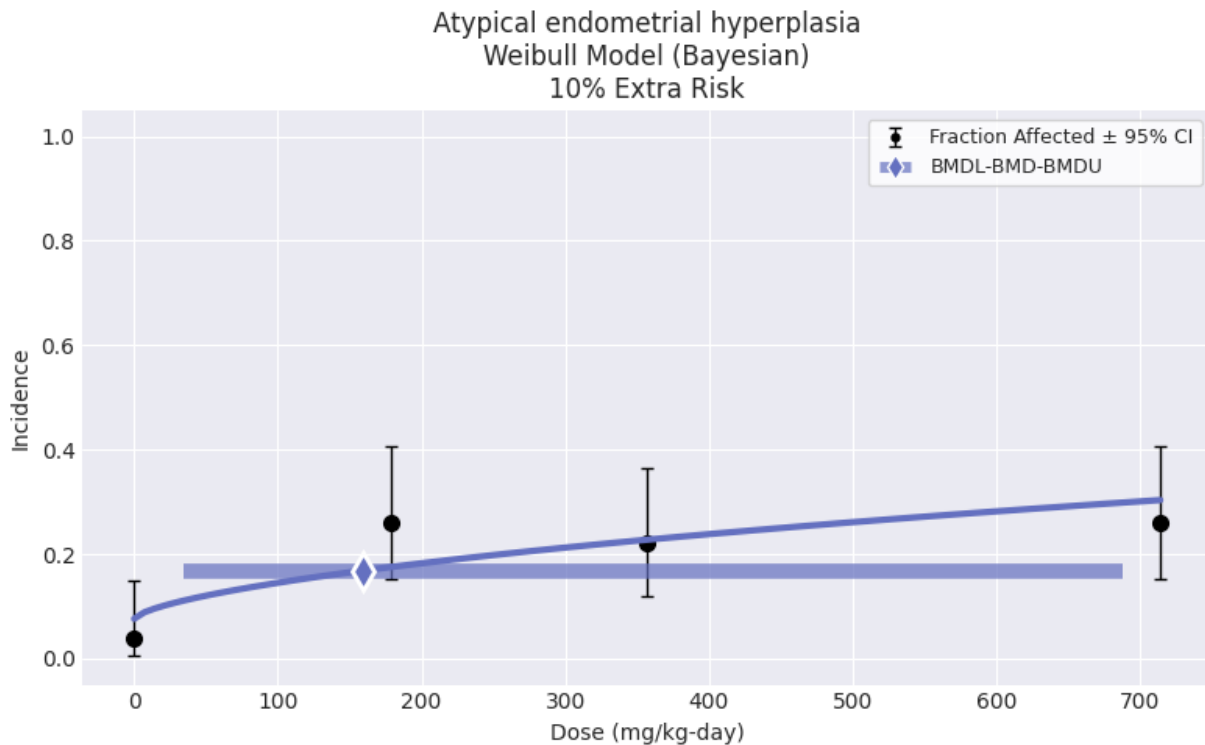
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	4.83161	0.0966321	-1.35536
178.6	50	13	7.92756	0.158551	1.96396
357	50	11	10.8082	0.216164	0.0659001
714	50	13	15.994	0.319879	-0.907769

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-97.9981	2	11.8995	2	0.00260648
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.2.4.8 Weibull Model



June 2026

Weibull Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
a	Lognormal	0.424264	0.5	0	40
b	Lognormal	0	1.5	0	10000

Modeling Summary:

BMD	159.347
BMDL	34.2383
BMDU	688.062
AIC	201.982
Log-Likelihood	-97.9912
P-Value	0.0708435
Overall d.f.	1.27565
Chi ²	3.87319

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0759407	no	0.0385259
a	0.657655	no	0.254194
b	0.00375228	no	0.0982027

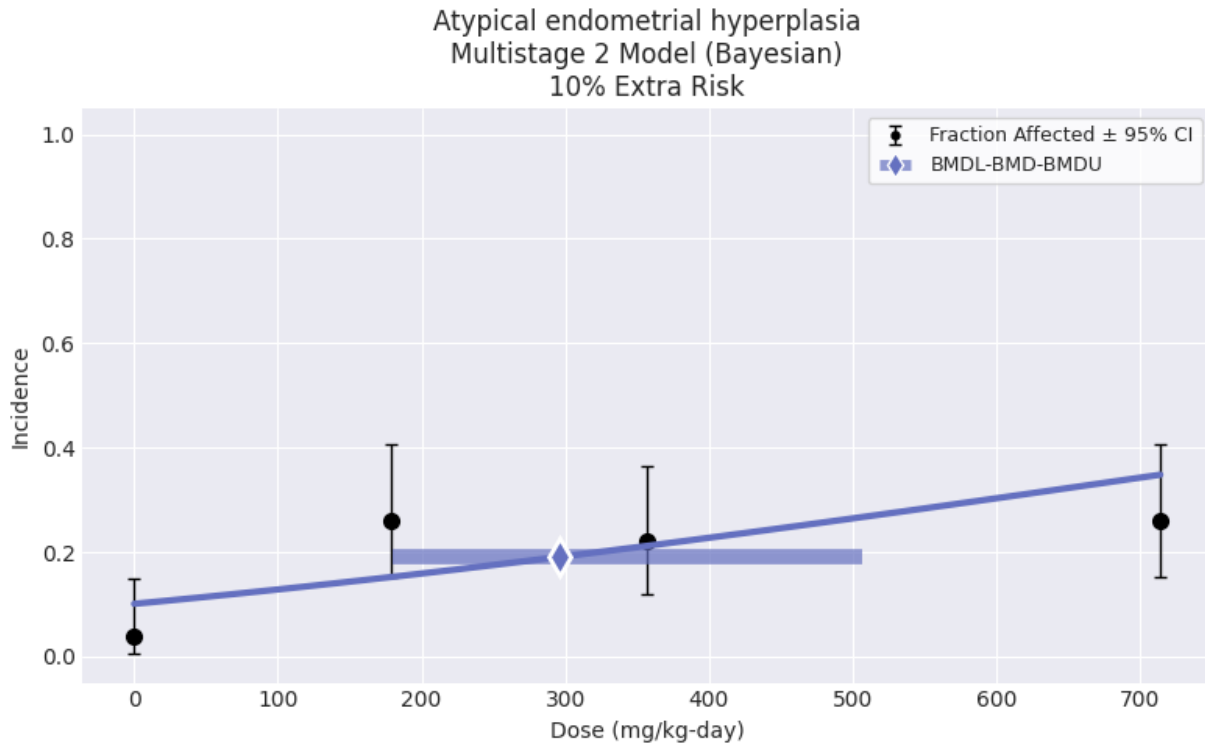
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	50	2	3.79704	0.0759407	-0.959366
178.6	50	13	8.75723	0.175145	1.57862
357	50	11	11.3729	0.227458	-0.125802
714	50	13	15.1683	0.303367	-0.667044

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-97.9912	3	11.8858	1	0.000565632
Reduced model	-98.6785	1	13.2603	3	0.00410613

2.2.4.9 Multistage 2 Model



Multistage 2 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
b1	Lognormal	0	1	0	1e+06
b2	Lognormal	0	1	0	1e+06

Modeling Summary:

BMD	296.365
BMDL	180.31
BMDU	506.641
AIC	204.132
Log-Likelihood	-100.066
P-Value	0.00459151
Overall d.f.	1.0801
Chi ²	8.28627

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.100815	no	0.0263215
b1	0.000288109	no	0.106581
b2	2.27425e-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	2	5.04074	0.100815	-1.42826
178.6	50	13	7.60434	0.152087	2.1249
357	50	11	10.5941	0.211881	0.140488
714	50	13	17.4067	0.348134	-1.30821

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-92.0483	4	-	-	-
Fitted model	-100.066	2	16.0357	2	0.000329521
Reduced model	-98.6785	1	13.2603	3	0.00410613

3 UTERINE ADENOMA, ADENOCARCINOMA, MMTT + ATYPICAL ENDOMETRIAL HYPERPLASIA

Uterine adenoma, adenocarcinoma, and MMTT combined in female Wistar Han rats from NTP 2014 cancer bioassay ([NTP, 2014](#)).

Report Generated: 2026-Mar-24 16:03 UTC

BMDS Online Version: U.S. Environmental Protection Agency (2025). BMDS Online 25.1 (pybmds 25.1; bmdscore 25.1). Available from <https://bmdsonline.epa.gov>.

3.1 Session for Uterine Adenoma, Adenocarcinoma, and MMTT + Atypical Endometrial Hyperplasia

3.1.1 Dataset

Dose (mg/kg-day)	N	Incidence
0	100	8
178.6	100	24
357	100	27
714	100	32

3.1.2 Settings

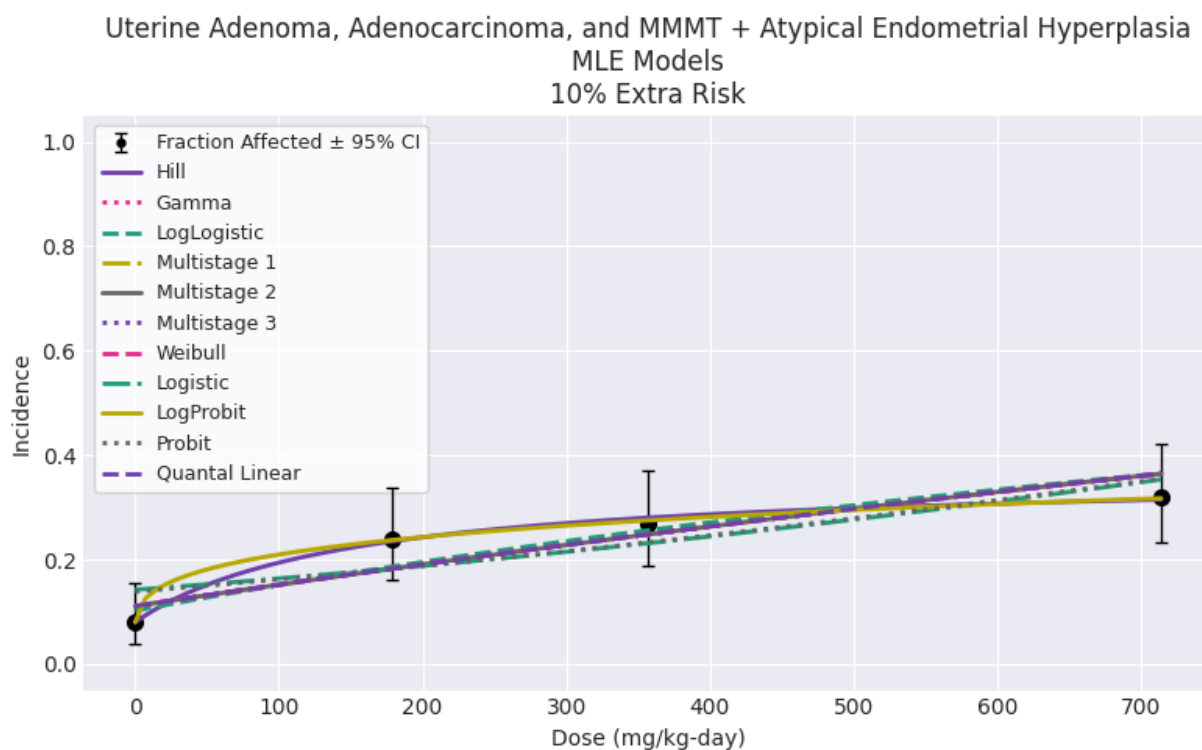
Setting	Value
BMR	10% Extra Risk
Confidence Level (one sided)	0.95
Maximum Multistage Degree	3

3.1.3 Maximum Likelihood Approach

Model	BMDL	BMD	BMDU	P-Value	AIC	Scaled Residual at Control	Scaled Residual Near BMD	Recommendation and Notes
Hill	0	71.33	179.599	0.777	414.076	-0.006	-0.006	Unusable BMDL does not exist
Gamma	158.146	224.065	378.848	0.117	416.233	-0.987	1.486	Viable
LogLogistic ^a	129.906	191.596	336.255	0.182	415.333	-0.733	1.374	Recommended - Lowest AIC
Multistage 1	158.144	224.065	378.88	0.117	416.233	-0.987	1.486	Viable
Multistage 2	158.146	224.065	379.04	0.117	416.233	-0.987	1.486	Viable
Multistage 3	158.144	224.065	381.015	0.117	416.233	-0.987	1.486	Viable
Weibull	158.146	224.065	378.848	0.117	416.233	-0.987	1.486	Viable
Logistic	272.917	345.324	526.513	0.035	419.03	-1.782	0.914	Questionable Goodness of fit p-value < 0.1
LogProbit	0	38.834	200.537	0.889	414.015	-0.001	-0.001	Unusable lowest dose/BMD ratio > 3.0 BMDL does not exist
Probit	258.269	329.739	507.834	0.04	418.7	-1.698	0.873	Questionable Goodness of fit p-value < 0.1
Quantal Linear	158.146	224.065	378.848	0.117	416.233	-0.987	1.486	Viable

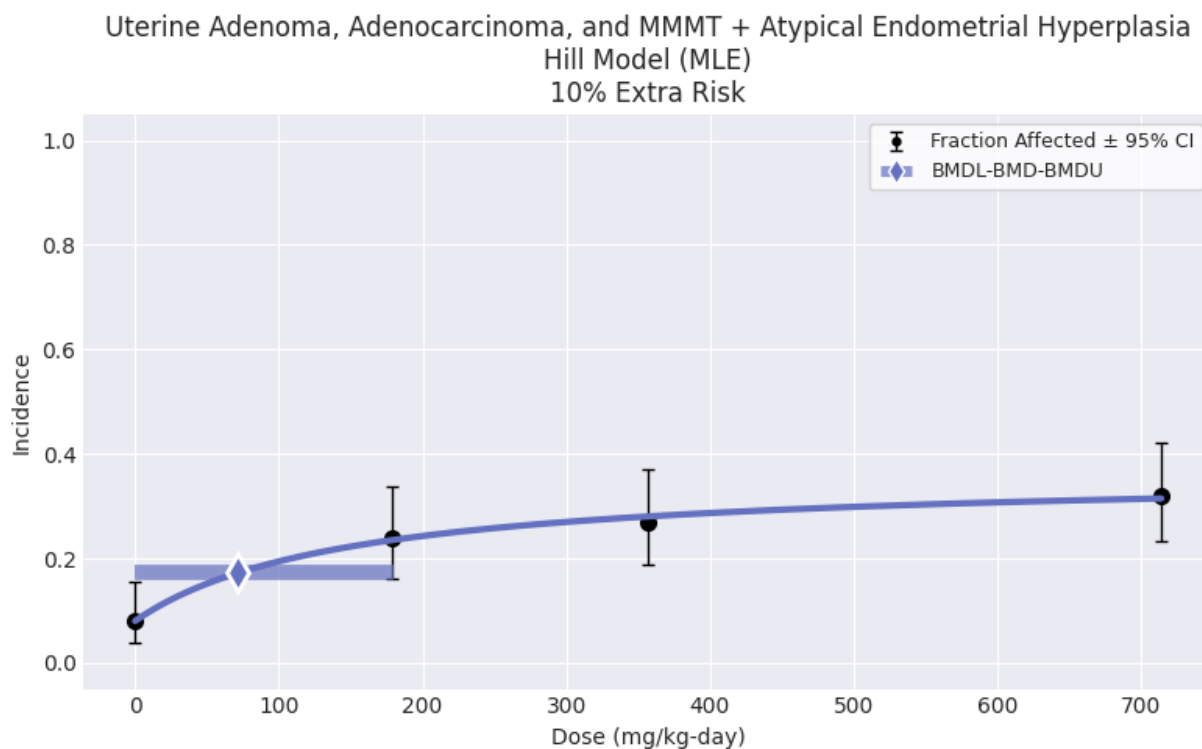
^a BMDS recommended best fitting model

June 2026



3.1.4 Individual Model Results

3.1.4.1 Hill Model



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	71.3304
BMDL	0
BMDU	179.599
AIC	414.076
Log-Likelihood	-204.038
P-Value	0.777481
Overall d.f.	1
Chi ²	0.0798648

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0801614	no	0.0229789
v	0.307908	no	0.0314467
a	-4.99925	no	1.23947
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:

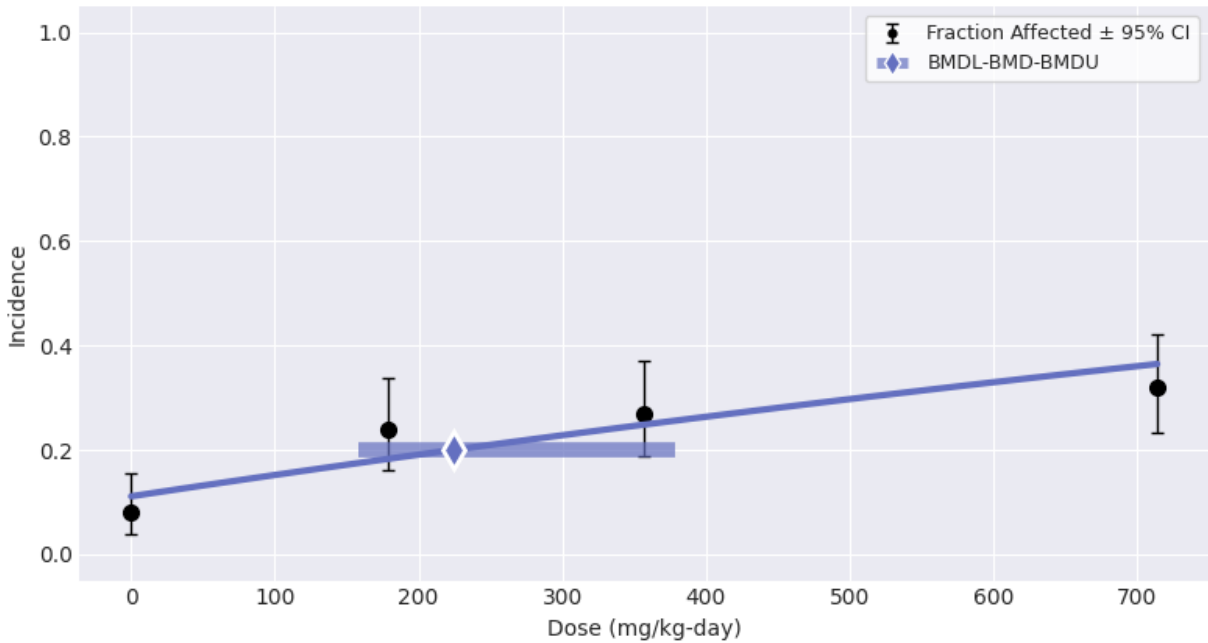
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	8.01614	0.0801614	-0.00594334
178.6	100	24	23.4899	0.234899	0.120317
357	100	27	28.0263	0.280263	-0.228501
714	100	32	31.4677	0.314677	0.114631

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-204.038	3	0.0801517	1	0.777092
Reduced model	-214.495	1	20.9948	3	0.000105539

3.1.4.2 Gamma Model

Uterine Adenoma, Adenocarcinoma, and MMT + Atypical Endometrial Hyperplasia
Gamma Model (MLE)
10% Extra Risk



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

June 2026

Modeling Summary:

BMD	224.065
BMDL	158.146
BMDU	378.848
AIC	416.233
Log-Likelihood	-206.117
P-Value	0.117244
Overall d.f.	2
Chi ²	4.287

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.110992	no	0.0191493
a	1	yes	Not Reported
b	0.000470224	no	0.000117931

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.

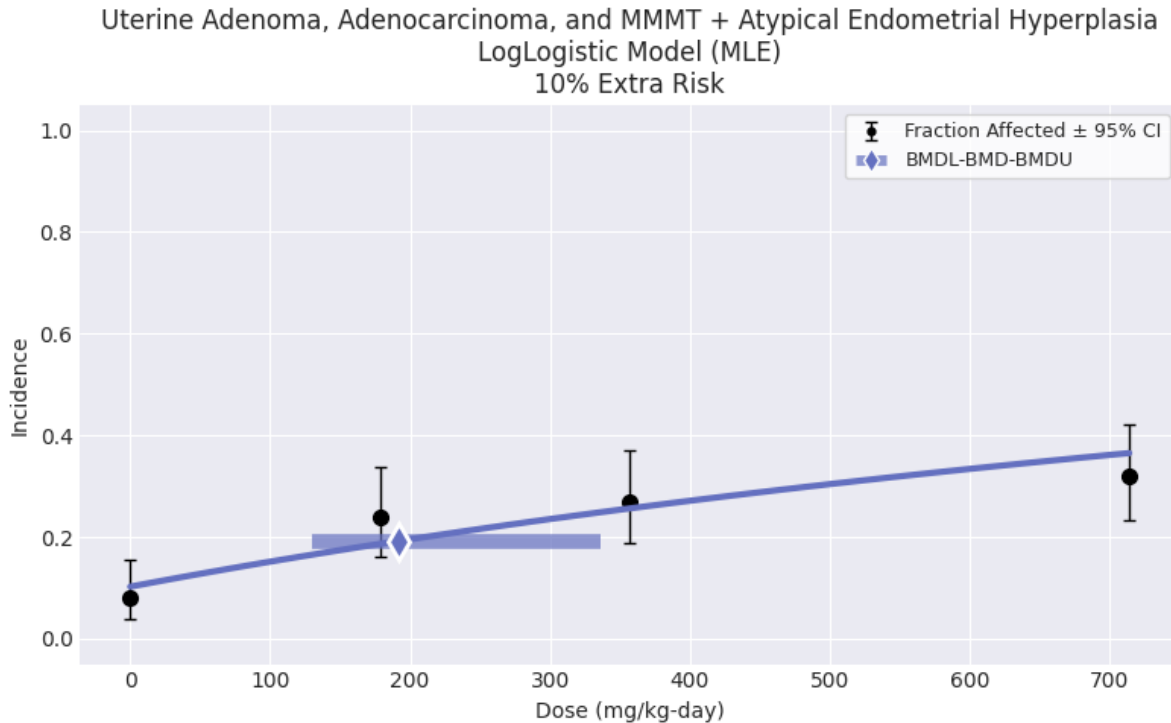
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	11.0992	0.110992	-0.986626
178.6	100	24	18.2604	0.182604	1.48564
357	100	27	24.8376	0.248376	0.500473
714	100	32	36.4529	0.364529	-0.925189

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-206.117	2	4.23764	2	0.120173
Reduced model	-214.495	1	20.9948	3	0.000105539

3.1.4.3 LogLogistic Model



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	191.596
BMDL	129.906
BMDU	336.255
AIC	415.333
Log-Likelihood	-205.667
P-Value	0.182341
Overall d.f.	2
Chi ²	3.40376

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.102215	no	0.0207843
a	-7.45261	no	0.274926
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:

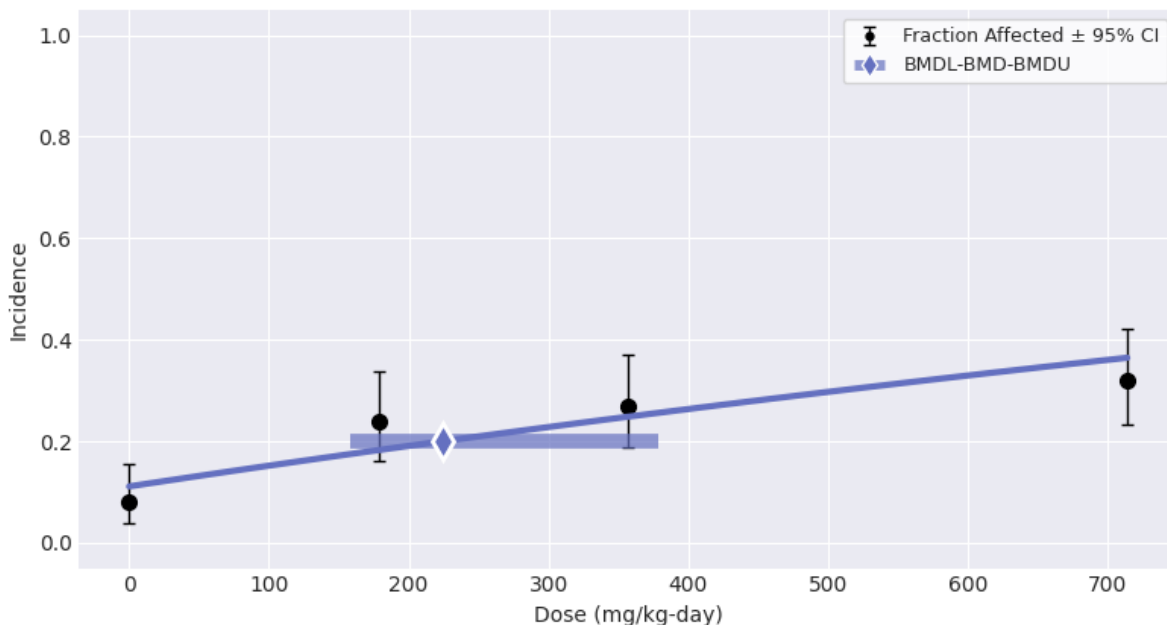
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	10.2215	0.102215	-0.73334
178.6	100	24	18.6476	0.186476	1.37422
357	100	27	25.6205	0.256205	0.316004
714	100	32	36.5104	0.365104	-0.93682

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-205.667	2	3.33771	2	0.188462
Reduced model	-214.495	1	20.9948	3	0.000105539

3.1.4.4 Multistage 1 Model

Uterine Adenoma, Adenocarcinoma, and MMMT + Atypical Endometrial Hyperplasia
Multistage 1 Model (MLE)
10% Extra Risk



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	224.065
BMDL	158.144
BMDU	378.88
AIC	416.233
Log-Likelihood	-206.117
P-Value	0.117244
Overall d.f.	2
Chi ²	4.287

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.110992	no	0.01915
b1	0.000470224	no	0.0839009

Goodness of Fit:

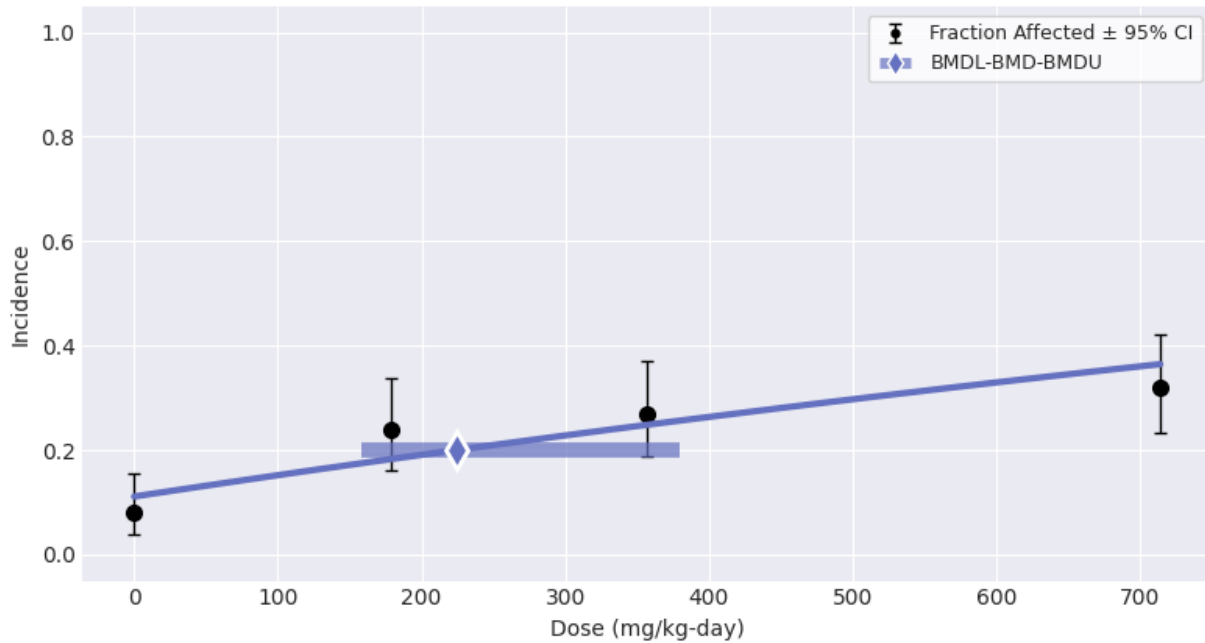
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	11.0992	0.110992	-0.986626
178.6	100	24	18.2604	0.182604	1.48564
357	100	27	24.8376	0.248376	0.500472
714	100	32	36.4529	0.364529	-0.925189

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-206.117	2	4.23764	2	0.120173
Reduced model	-214.495	1	20.9948	3	0.000105539

3.1.4.5 Multistage 2 Model

Uterine Adenoma, Adenocarcinoma, and MMT + Atypical Endometrial Hyperplasia
Multistage 2 Model (MLE)
10% Extra Risk



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

June 2026

Modeling Summary:

BMD	224.065
BMDL	158.146
BMDU	379.04
AIC	416.233
Log-Likelihood	-206.117
P-Value	0.117244
Overall d.f.	2
Chi ²	4.287

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.110992	no	0.0191493
b1	0.000470224	no	0.083897
b2	1.23209e-22	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.

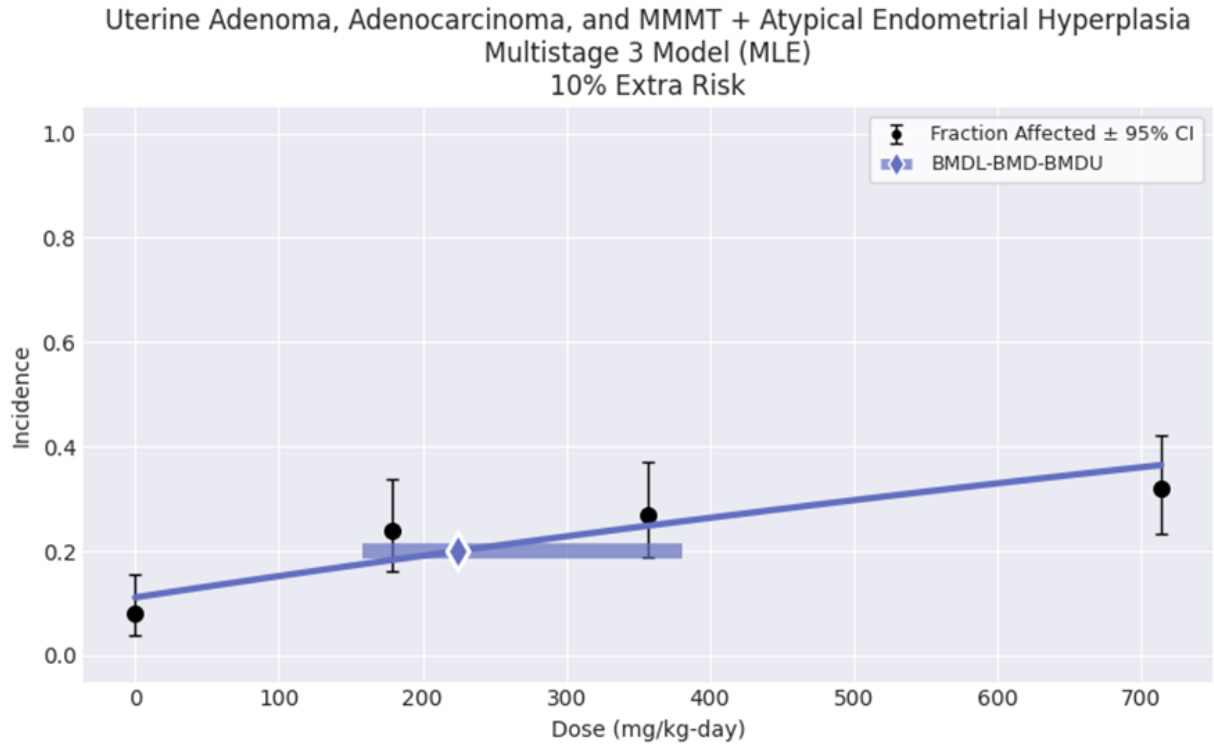
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	11.0992	0.110992	-0.986626
178.6	100	24	18.2604	0.182604	1.48564
357	100	27	24.8376	0.248376	0.500473
714	100	32	36.4529	0.364529	-0.925189

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-206.117	2	4.23764	2	0.120173
Reduced model	-214.495	1	20.9948	3	0.000105539

3.1.4.6 Multistage 3 Model



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

June 2026

Modeling Summary:

BMD	224.065
BMDL	158.144
BMDU	381.015
AIC	416.233
Log-Likelihood	-206.117
P-Value	0.117244
Overall d.f.	2
Chi ²	4.287

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.110992	no	0.0191484
b1	0.000470224	no	0.0838937
b2	1.645e-22	yes	Not Reported
b3	1.99063e-24	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.

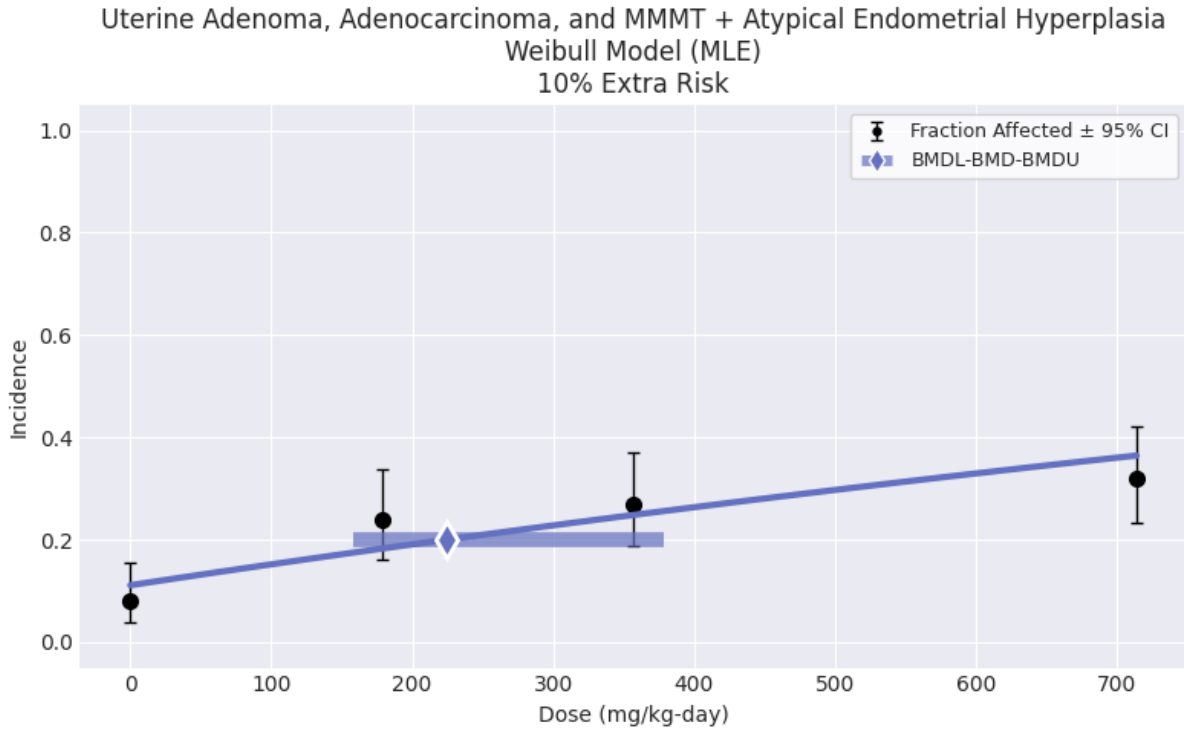
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	11.0992	0.110992	-0.986626
178.6	100	24	18.2604	0.182604	1.48564
357	100	27	24.8376	0.248376	0.500473
714	100	32	36.4529	0.364529	-0.925189

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-206.117	2	4.23764	2	0.120173
Reduced model	-214.495	1	20.9948	3	0.000105539

3.1.4.7 Weibull Model



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	224.065
BMDL	158.146
BMDU	378.848
AIC	416.233
Log-Likelihood	-206.117
P-Value	0.117244
Overall d.f.	2
Chi ²	4.287

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.110992	no	0.0191495
a	1	yes	Not Reported
b	0.000470224	no	0.0842006

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.

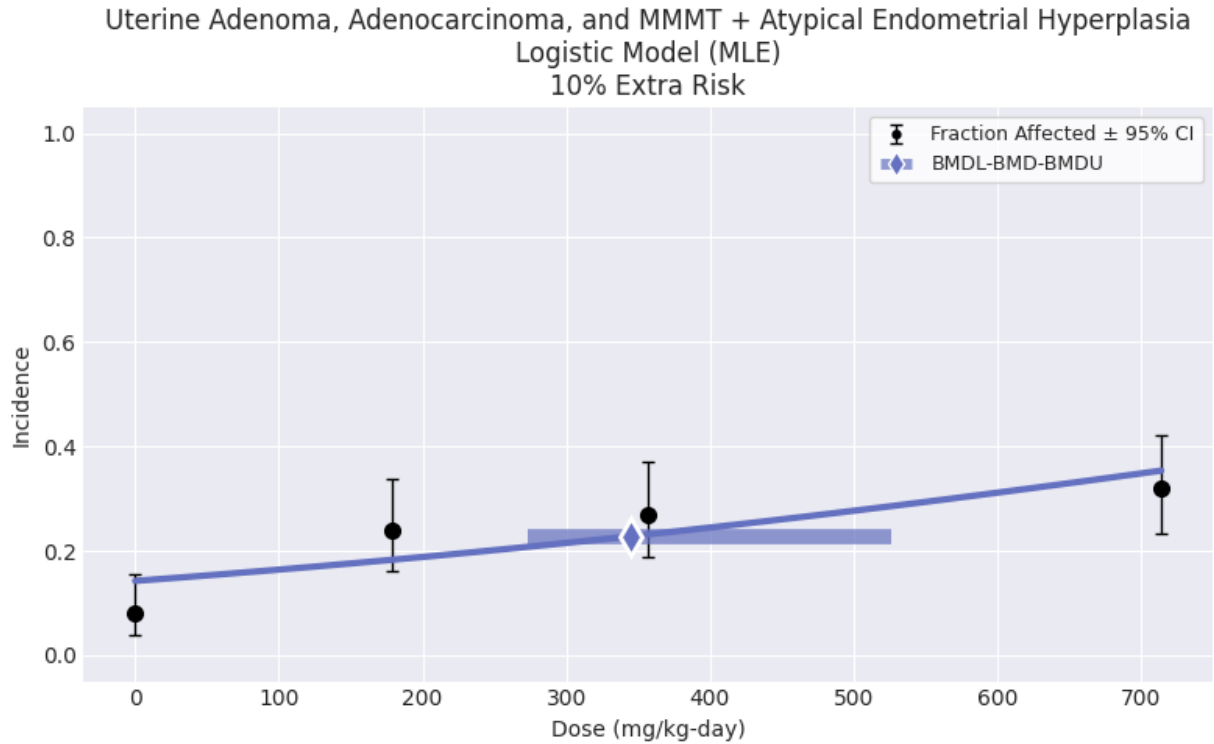
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	11.0992	0.110992	-0.986626
178.6	100	24	18.2604	0.182604	1.48564
357	100	27	24.8376	0.248376	0.500473
714	100	32	36.4529	0.364529	-0.925189

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-206.117	2	4.23764	2	0.120173
Reduced model	-214.495	1	20.9948	3	0.000105539

3.1.4.8 Logistic Model



Logistic 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	100

Modeling Summary:

BMD	345.324
BMDL	272.917
BMDU	526.513
AIC	419.03
Log-Likelihood	-207.515
P-Value	0.0350232
Overall d.f.	2
Chi²	6.70349

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-1.7968	no	0.207658
b	0.00167164	no	0.000450561

Goodness of Fit:

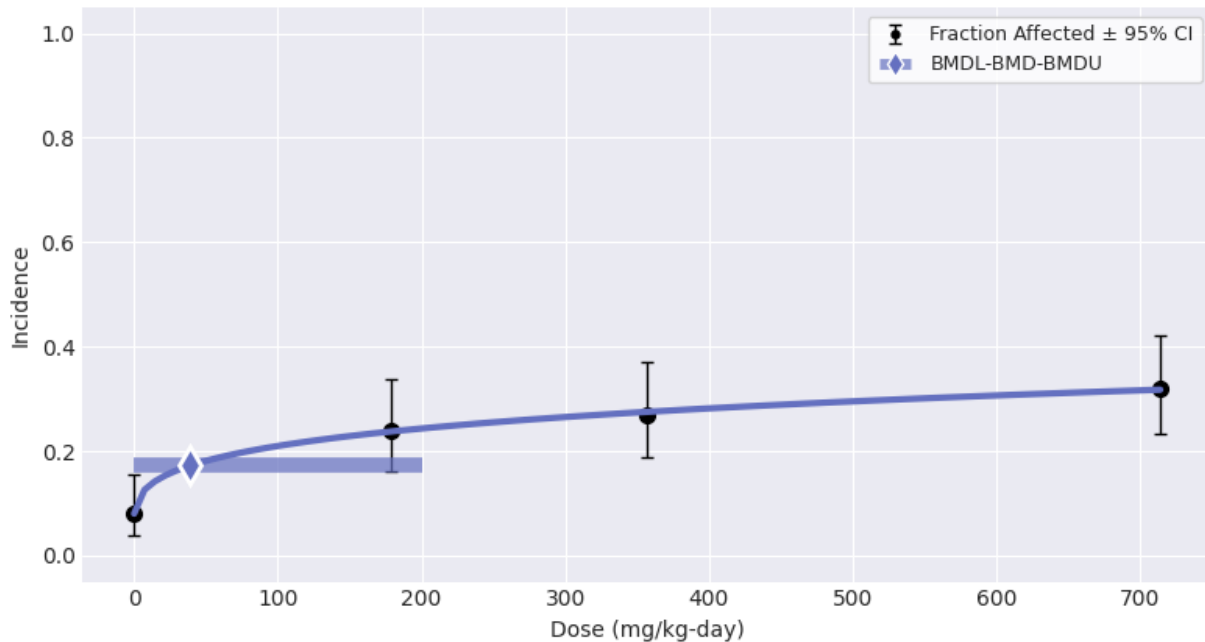
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	14.2241	0.142241	-1.78189
178.6	100	24	18.2687	0.182687	1.48321
357	100	27	23.1471	0.231471	0.913505
714	100	32	35.3601	0.353601	-0.702817

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-207.515	2	7.0344	2	0.0296824
Reduced model	-214.495	1	20.9948	3	0.000105539

3.1.4.9 LogProbit Model

Uterine Adenoma, Adenocarcinoma, and MMT + Atypical Endometrial Hyperplasia
LogProbit Model (MLE)
10% Extra Risk



June 2026

LogProbit 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
g	0	-18	18
a	0	-18	18
b	0.0001	0.0001	18

Modeling Summary:

BMD	38.8343
BMDL	0
BMDU	200.537
AIC	414.015
Log-Likelihood	-204.007
P-Value	0.889451
Overall d.f.	1
Chi ²	0.0193207

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0800324	no	0.0229642
a	-2.07656	no	1.04951
b	0.217258	no	0.173601

Goodness of Fit:

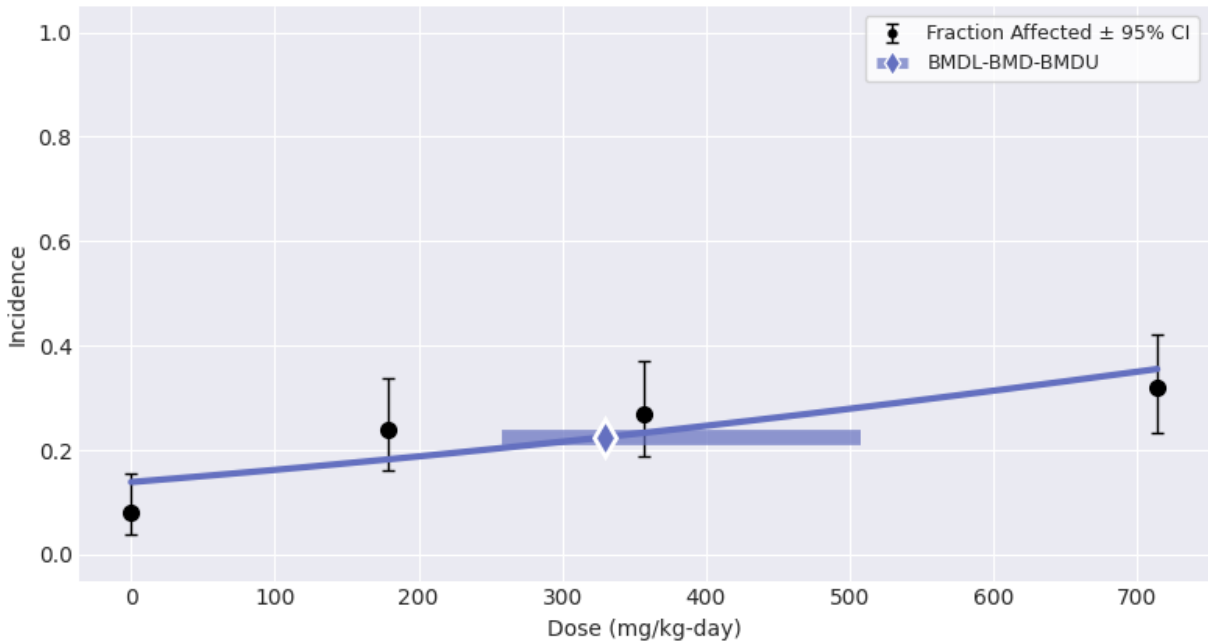
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	8.00324	0.0800324	-0.00119525
178.6	100	24	23.7387	0.237387	0.0614172
357	100	27	27.5044	0.275044	-0.112967
714	100	32	31.7543	0.317543	0.0527787

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-204.007	3	0.0193564	1	0.88935
Reduced model	-214.495	1	20.9948	3	0.000105539

3.1.4.10 Probit Model

Uterine Adenoma, Adenocarcinoma, and MMT + Atypical Endometrial Hyperplasia
Probit Model (MLE)
10% Extra Risk



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

June 2026

Modeling Summary:

BMD	329.739
BMDL	258.269
BMDU	507.834
AIC	418.7
Log-Likelihood	-207.35
P-Value	0.0399837
Overall d.f.	2
Chi ²	6.43857

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-1.08626	no	0.117391
b	0.00100147	no	0.000266543

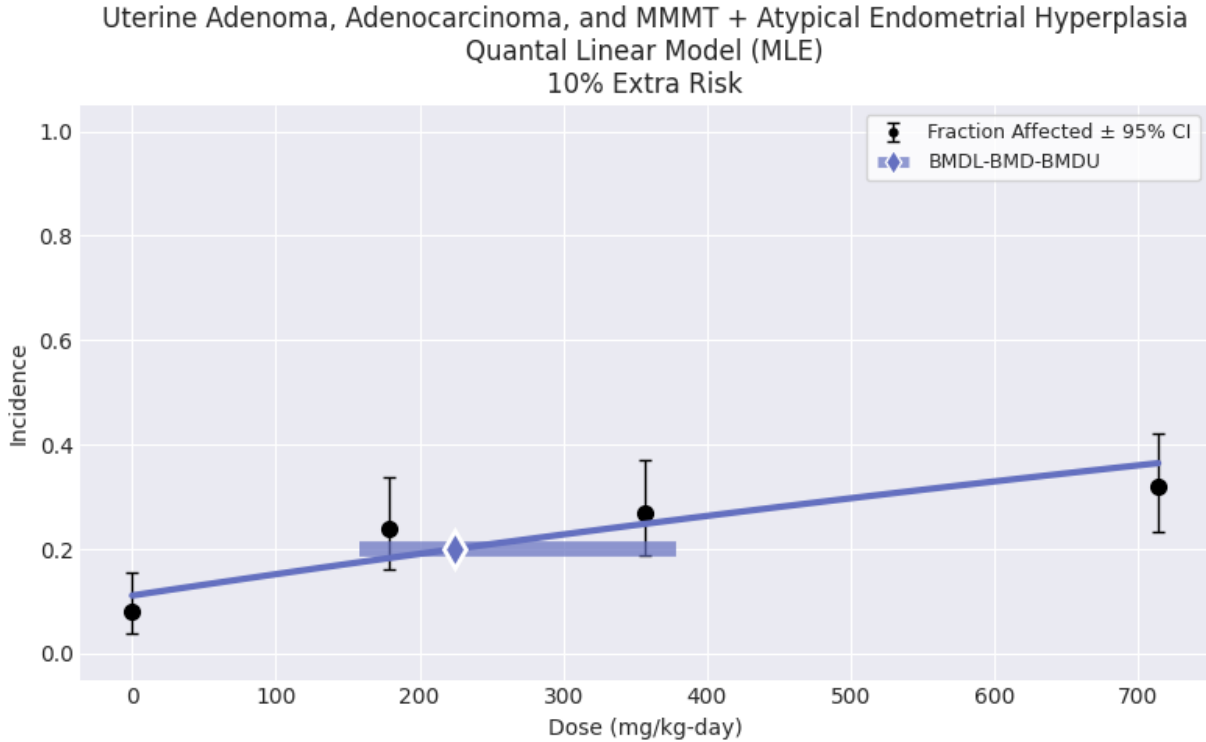
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	13.8681	0.138681	-1.69789
178.6	100	24	18.2098	0.182098	1.50035
357	100	27	23.3081	0.233081	0.87321
714	100	32	35.524	0.35524	-0.73634

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-207.35	2	6.70464	2	0.035003
Reduced model	-214.495	1	20.9948	3	0.000105539

3.1.4.11 Quantal Linear Model



Quantal Linear 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
g	0	-18	18
b	0	0	100

Modeling Summary:

BMD	224.065
BMDL	158.146
BMDU	378.848
AIC	416.233
Log-Likelihood	-206.117
P-Value	0.117244
Overall d.f.	2
Chi ²	4.287

June 2026

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.110992	no	0.01915
b	0.000470224	no	0.000117927

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	11.0992	0.110992	-0.986626
178.6	100	24	18.2604	0.182604	1.48564
357	100	27	24.8376	0.248376	0.500472
714	100	32	36.4529	0.364529	-0.925189

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-206.117	2	4.23764	2	0.120173
Reduced model	-214.495	1	20.9948	3	0.000105539

3.2 Session for Uterine Adenoma, Adenocarcinoma, and MMTT + Atypical Endometrial Hyperplasia

3.2.1 Dataset

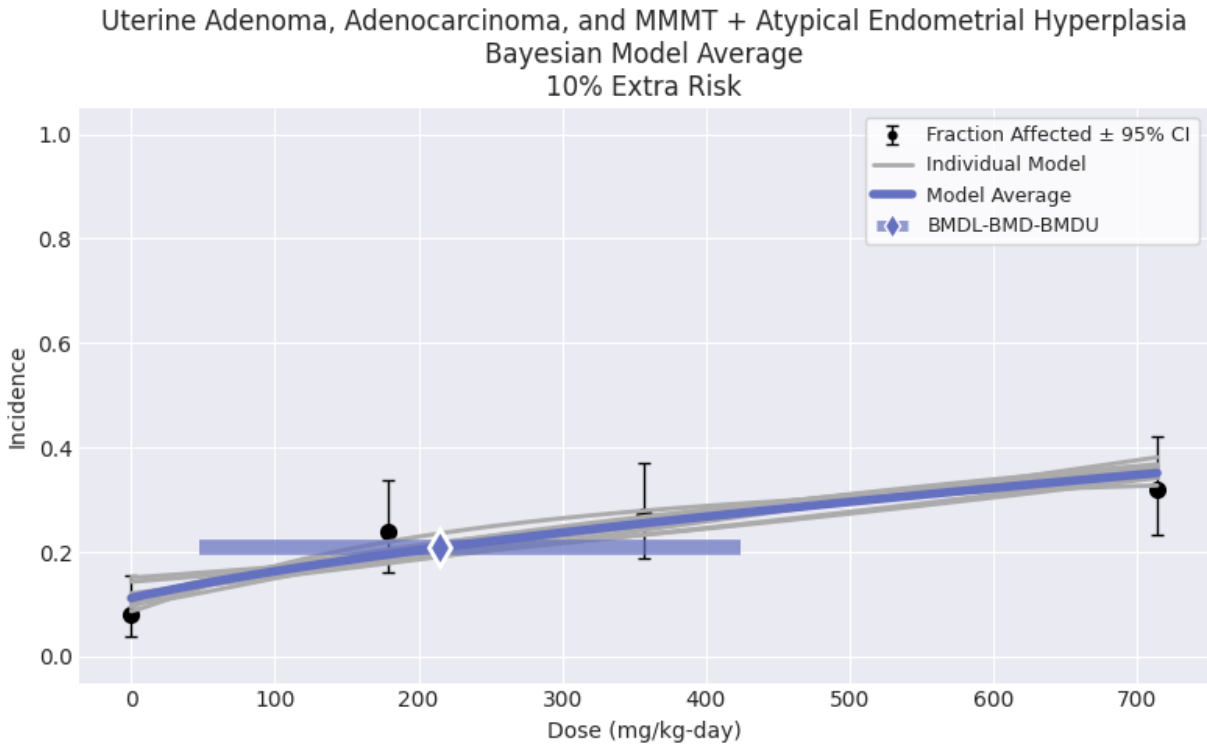
Dose (mg/kg-day)	N	Incidence
0	100	8
178.6	100	24
357	100	27
714	100	32

3.2.2 Settings

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

3.2.3 Bayesian Summary

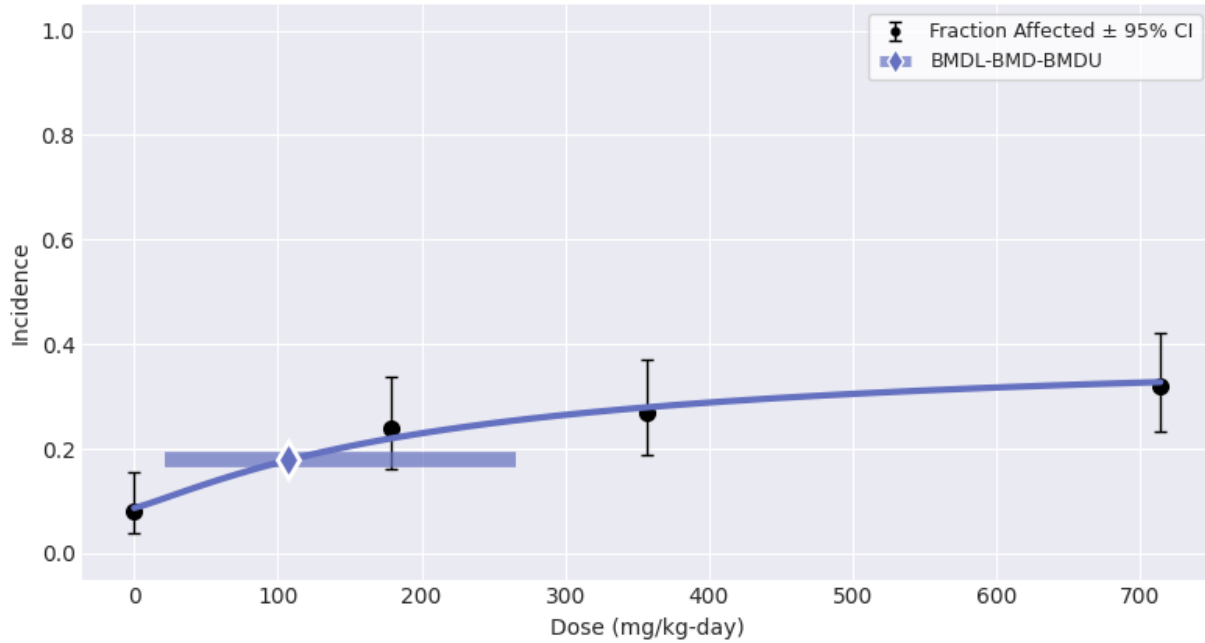
Model	Prior Weights	Posterior Weights	BMDL	BMD	BMDU	Unnormalized Log Posterior Probability	Scaled Residual Near BMD	Scaled Residual at Control
Hill	0.111	0.19	21.175	106.966	265.12	-212.377	-0.235	0.493
Gamma	0.111	0.027	102.953	217.253	438.309	-200.883	-1.026	1.371
Logistic	0.111	0.072	280.797	367.271	637.06	-203.299	-1.98	0.875
LogLogistic	0.111	0.083	46.499	139.507	305.95	-208.638	-0.468	0.948
LogProbit	0.111	0.006	77.284	183.086	401.718	-209.409	-0.721	1.289
Multistage 2	0.111	0.003	180.924	266.245	415.068	-206.834	-1.262	1.609
Probit	0.111	0.109	263.545	341.016	536.256	-200.666	-1.802	0.865
Quantal Linear	0.111	0.41	161.772	228.597	376.696	-199.897	-1.1	1.415
Weibull	0.111	0.1	39.045	137.258	337.308	-205.793	-0.617	0.869
Model Average	-	-	47.018	214.466	424.36	-	-	-



3.2.4 Individual Model Results

3.2.4.1 Hill Model

Uterine Adenoma, Adenocarcinoma, and MMMT + Atypical Endometrial Hyperplasia
Hill Model (Bayesian)
10% Extra Risk



Hill Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	-1	2	-40	40
v	Normal	0	3	-40	40
a	Normal	-3	3.3	-40	40
b	Lognormal	0.693147	0.5	0	40

June 2026

Modeling Summary:

BMD	106.966
BMDL	21.1749
BMDU	265.12
AIC	432.042
Log-Likelihood	-212.021
P-Value	0.553482
Overall d.f.	1.01994
Chi ²	0.365794

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0866019	no	0.0224482
v	0.330731	no	0.0362797
a	-6.26698	no	2.5382
b	1.16231	no	0.527265

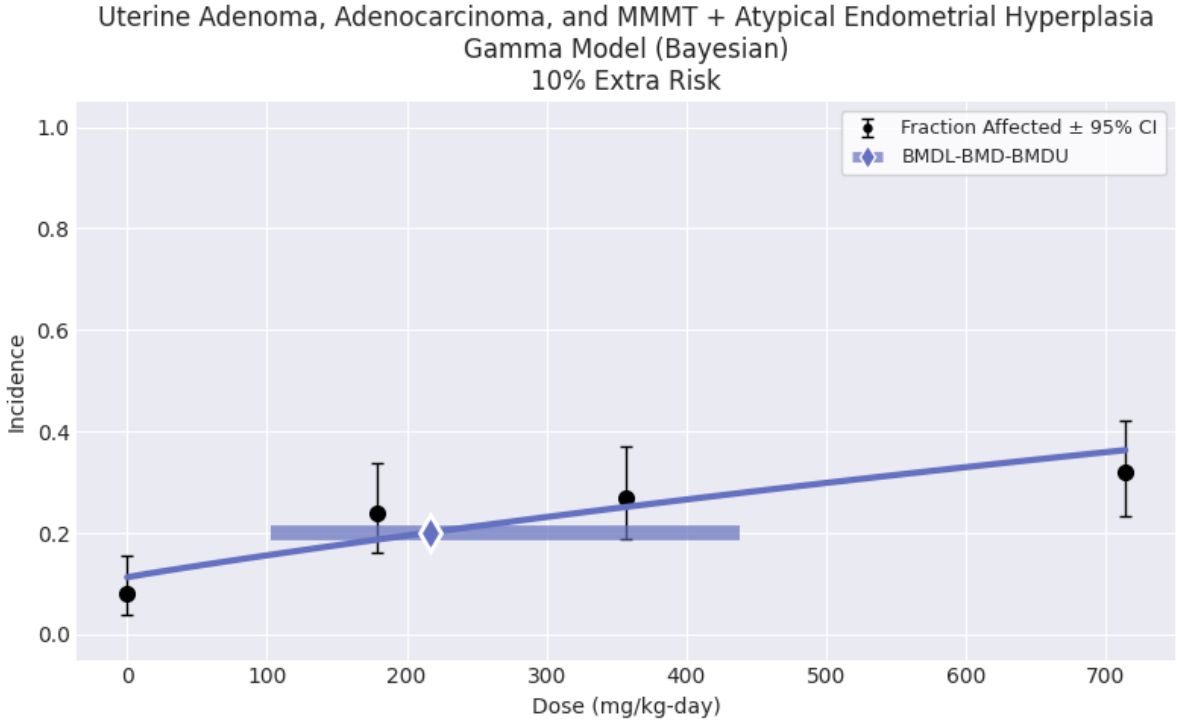
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	8.66019	0.0866019	-0.234734
178.6	100	24	21.959	0.21959	0.493042
357	100	27	27.92	0.2792	-0.20507
714	100	32	32.7502	0.327502	-0.159845

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-212.021	4	16.0467	0	0
Reduced model	-214.495	1	20.9948	3	0.000105539

3.2.4.2 Gamma Model



Gamma Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-18	18
a	Lognormal	0.693147	0.424264	0.2	20
b	Lognormal	0	1	0	10000

Modeling Summary:

BMD	217.253
BMDL	102.953
BMDU	438.309
AIC	426.136
Log-Likelihood	-210.068
P-Value	0.0671918
Overall d.f.	1.25748
Chi ²	3.92734

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.112413	no	0.0214481
a	0.957122	no	0.280737
b	0.000427283	no	0.00024401

Goodness of Fit:

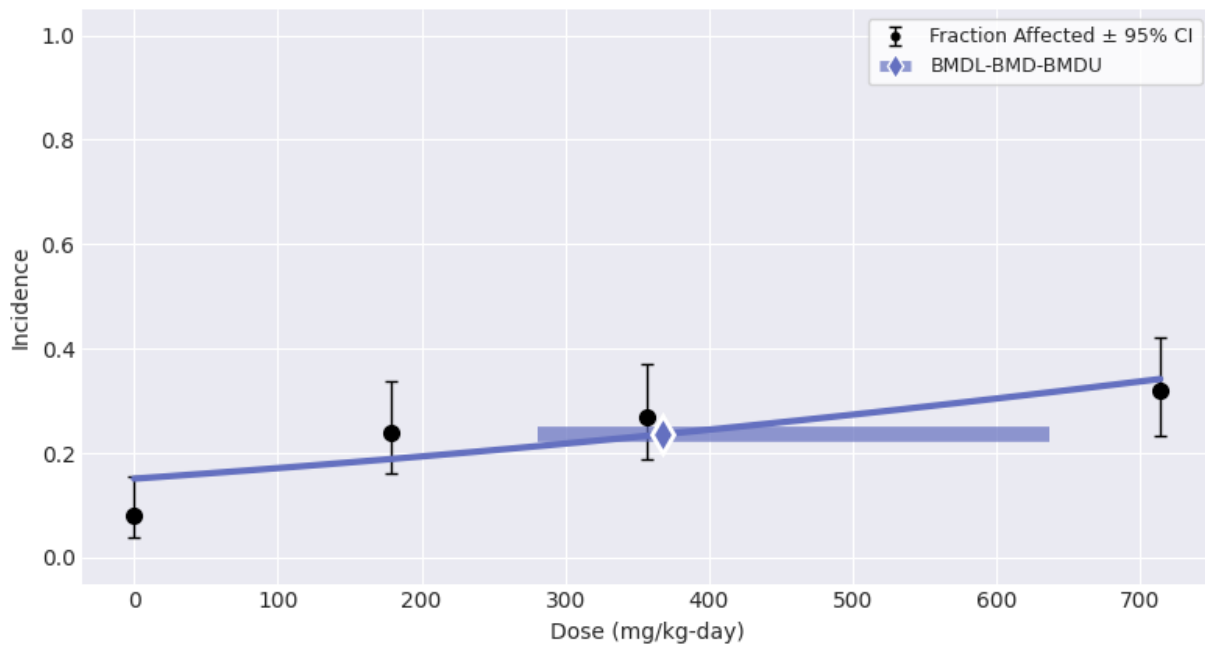
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	11.2413	0.112413	-1.02614
178.6	100	24	18.6584	0.186584	1.37113
357	100	27	25.1169	0.251169	0.434206
714	100	32	36.3171	0.363171	-0.89768

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-210.068	3	12.1409	1	0.000493275
Reduced model	-214.495	1	20.9948	3	0.000105539

3.2.4.3 Logistic Model

Uterine Adenoma, Adenocarcinoma, and MMMT + Atypical Endometrial Hyperplasia
Logistic Model (Bayesian)
10% Extra Risk



June 2026

Logistic Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
a	Normal	0	2	-20	20
b	Lognormal	0	2	0	40

Modeling Summary:

BMD	367.271
BMDL	280.797
BMDU	637.06
AIC	426.51
Log-Likelihood	-211.255
P-Value	0.0367427
Overall d.f.	2.01036
Chi ²	6.62849

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-1.72778	no	0.207976
b	0.00150256	no	0.000462528

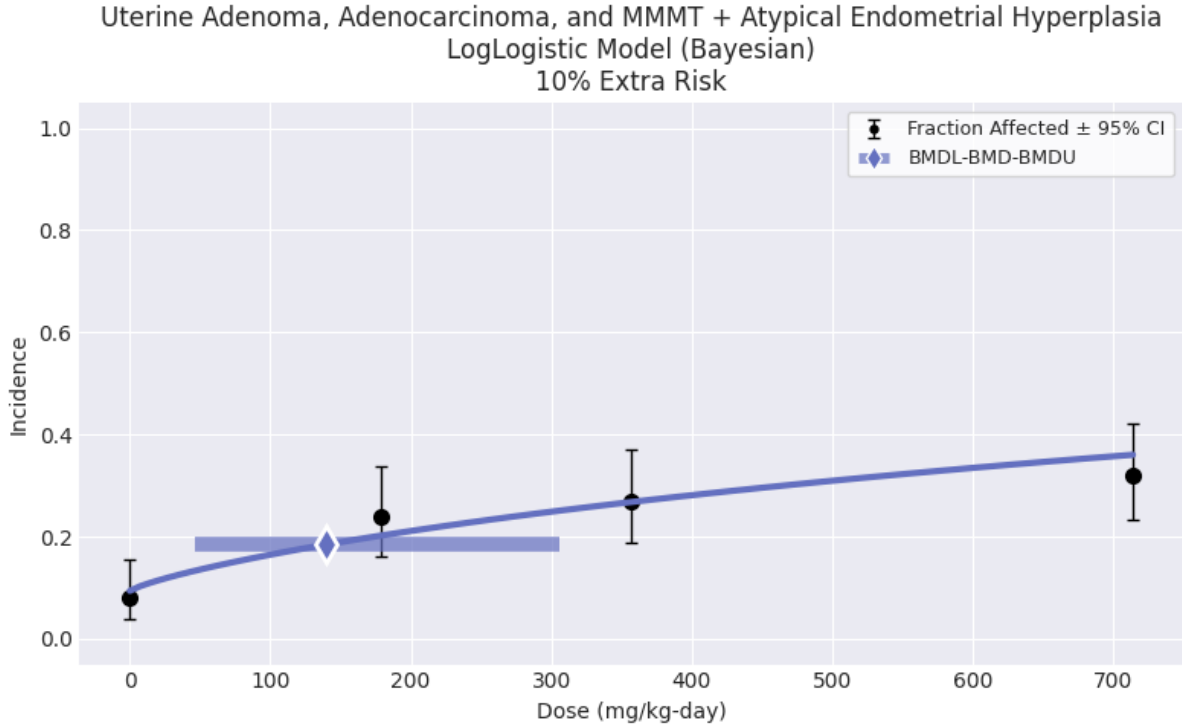
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	15.0872	0.150872	-1.98009
178.6	100	24	18.8556	0.188556	1.31517
357	100	27	23.3015	0.233015	0.874852
714	100	32	34.1875	0.341875	-0.461178

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-211.255	2	14.5148	2	0.000704945
Reduced model	-214.495	1	20.9948	3	0.000105539

3.2.4.4 LogLogistic Model



LogLogistic Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
a	Normal	0	1	-40	40
b	Lognormal	0.693147	0.5	0	20

Modeling Summary:

BMD	139.507
BMDL	46.4994
BMDU	305.95
AIC	426.22
Log-Likelihood	-210.11
P-Value	0.213999
Overall d.f.	1.17093
Chi ²	1.82387

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0936393	no	0.0218179
a	-6.19558	no	1.60755
b	0.809692	no	0.249721

Goodness of Fit:

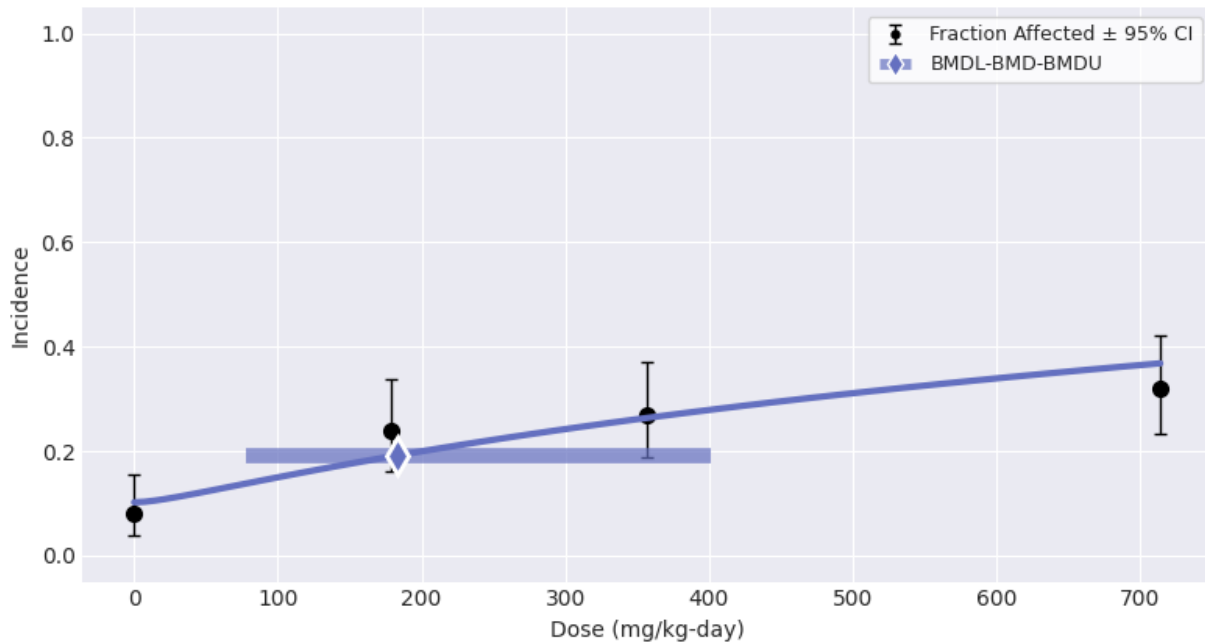
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	9.36393	0.0936393	-0.468179
178.6	100	24	20.1947	0.201947	0.947889
357	100	27	26.7752	0.267752	0.050778
714	100	32	36.027	0.36027	-0.838814

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-210.11	3	12.2248	1	0.00047159
Reduced model	-214.495	1	20.9948	3	0.000105539

3.2.4.5 LogProbit Model

Uterine Adenoma, Adenocarcinoma, and MMMT + Atypical Endometrial Hyperplasia
Logprobit Model (Bayesian)
10% Extra Risk



June 2026

LogProbit Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
a	Normal	0	1	-40	40
b	Lognormal	0.693147	0.5	0	20

Modeling Summary:

BMD	183.086
BMDL	77.2838
BMDU	401.718
AIC	429.623
Log-Likelihood	-211.811
P-Value	0.0826359
Overall d.f.	1.08247
Chi ²	3.19459

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.101792	no	0.0228104
a	-4.14057	no	1.04433
b	0.54876	no	0.159881

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	10.1792	0.101792	-0.7207
178.6	100	24	18.9486	0.189486	1.28898
357	100	27	26.3532	0.263532	0.146819
714	100	32	36.8038	0.368038	-0.996072

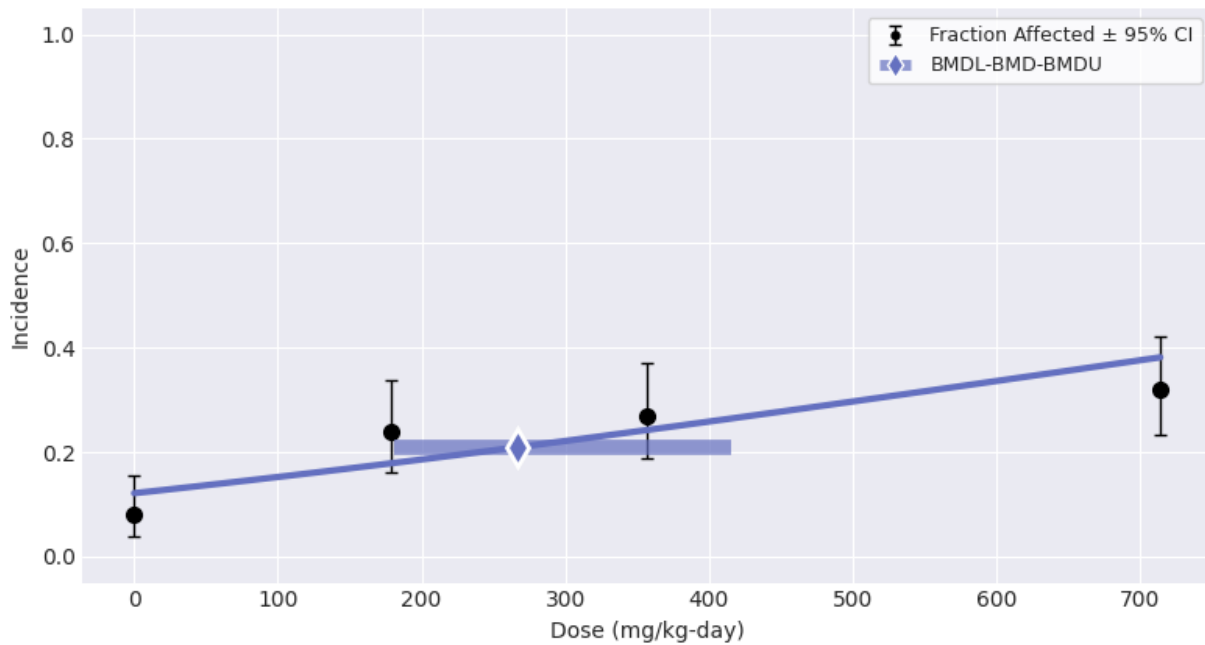
June 2026

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-211.811	3	15.6272	1	7.71363e-05
Reduced model	-214.495	1	20.9948	3	0.000105539

3.2.4.6 Multistage 2 Model

Uterine Adenoma, Adenocarcinoma, and MMT + Atypical Endometrial Hyperplasia
Multistage 2 Model (Bayesian)
10% Extra Risk



Multistage 2 Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
b1	Lognormal	0	1	0	1e+06
b2	Lognormal	0	1	0	1e+06

June 2026

Modeling Summary:

BMD	266.245
BMDL	180.924
BMDU	415.068
AIC	425.744
Log-Likelihood	-210.872
P-Value	0.0136434
Overall d.f.	1.04045
Chi ²	6.20104

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.121174	no	0.0174211
b1	0.000338576	no	0.0950488
b2	2.14657e-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.

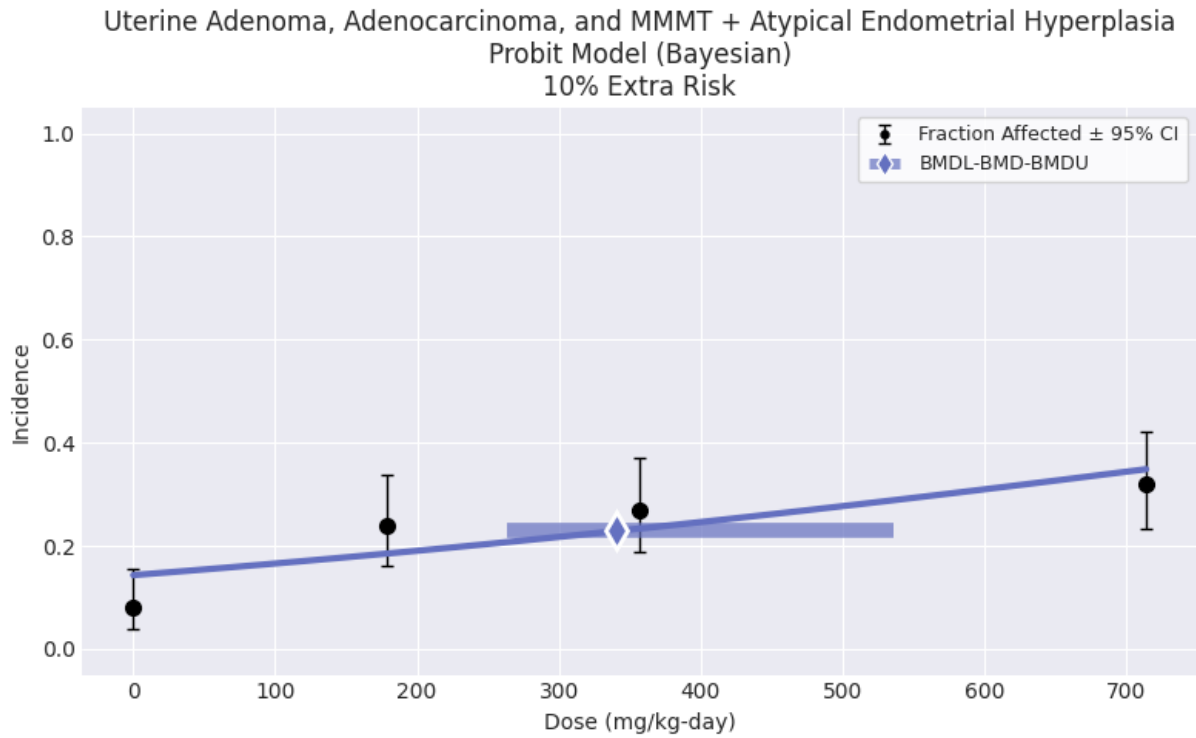
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	12.1174	0.121174	-1.26172
178.6	100	24	17.8386	0.178386	1.6094
357	100	27	24.2247	0.242247	0.647768
714	100	32	38.1429	0.381429	-1.26465

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-210.872	2	13.7489	2	0.00103388
Reduced model	-214.495	1	20.9948	3	0.000105539

3.2.4.7 Probit Model



Probit Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
a	Normal	0	2	-20	20
b	Lognormal	0	1	0	40

Modeling Summary:

BMD	341.016
BMDL	263.545
BMDU	536.256
AIC	423.459
Log-Likelihood	-209.729
P-Value	0.0417026
Overall d.f.	2.01078
Chi ²	6.37575

Model Parameters:

Variable	Estimate	On Bound	Std Error
a	-1.06656	no	0.115607
b	0.000949159	no	0.000261879

Goodness of Fit:

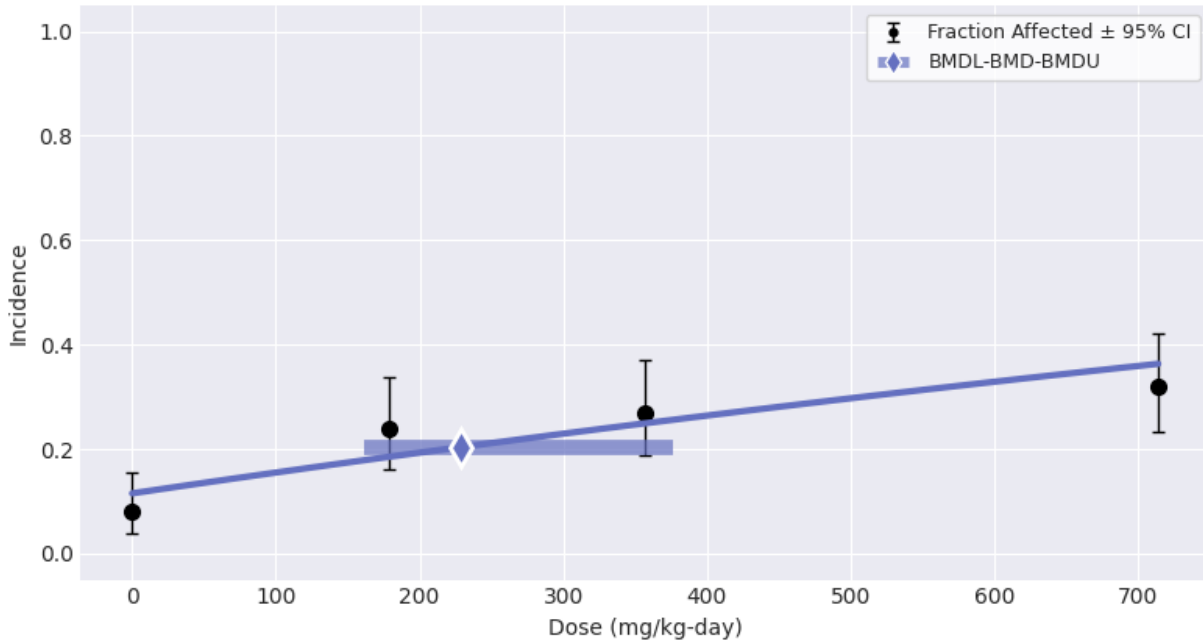
Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	14.3085	0.143085	-1.80161
178.6	100	24	18.4848	0.184848	1.42079
357	100	27	23.3395	0.233395	0.865378
714	100	32	34.8689	0.348689	-0.602016

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-209.729	2	11.4632	2	0.00324183
Reduced model	-214.495	1	20.9948	3	0.000105539

3.2.4.8 Quantal Linear Model

Uterine Adenoma, Adenocarcinoma, and MMMT + Atypical Endometrial Hyperplasia
Quantal Linear Model (Bayesian)
10% Extra Risk



Quantal Linear Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
b	Lognormal	0	1	0	18

Modeling Summary:

BMD	228.597
BMDL	161.772
BMDU	376.696
AIC	421.366
Log-Likelihood	-208.683
P-Value	0.121423
Overall d.f.	2.01976
Chi ²	4.2499

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.115112	no	0.0181054
b	0.000460902	no	0.000113351

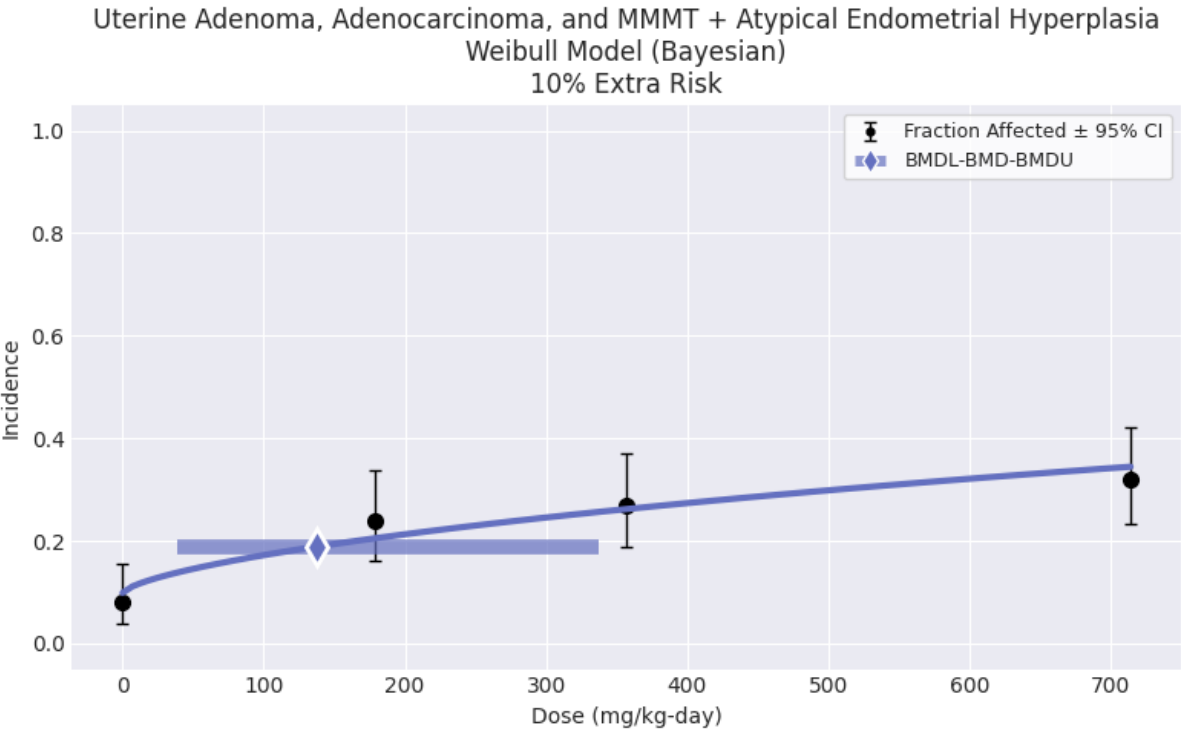
Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	11.5112	0.115112	-1.10015
178.6	100	24	18.5036	0.185036	1.41541
357	100	27	24.9365	0.249365	0.476942
714	100	32	36.325	0.36325	-0.899286

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-208.683	2	9.37055	2	0.00923018
Reduced model	-214.495	1	20.9948	3	0.000105539

3.2.4.9 Weibull Model



Weibull Model

Version: pybmds 25.1 (bmdscore 25.1)

Input Summary:

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

Parameter Settings:

Parameter	Distribution	Initial	Stdev	Min	Max
g	Normal	0	2	-20	20
a	Lognormal	0.424264	0.5	0	40
b	Lognormal	0	1.5	0	10000

Modeling Summary:

BMD	137.258
BMDL	39.0447
BMDU	337.308
AIC	423.185
Log-Likelihood	-208.592
P-Value	0.268141
Overall d.f.	1.14338
Chi²	1.43726

June 2026

Model Parameters:

Variable	Estimate	On Bound	Std Error
g	0.0983819	no	0.0219572
a	0.671615	no	0.221893
b	0.00386435	no	0.0719558

Goodness of Fit:

Dose	Size	Observed	Expected	Est Prob	Scaled Residual
0	100	8	9.83819	0.0983819	-0.617194
178.6	100	24	20.4914	0.204914	0.869255
357	100	27	26.1973	0.261973	0.182554
714	100	32	34.4575	0.344575	-0.517109

Analysis of Deviance:

Model	Log-Likelihood	# Params	Deviance	Test d.f.	P-Value
Full model	-203.998	4	-	-	-
Fitted model	-208.592	3	9.1894	1	0.00243421
Reduced model	-214.495	1	20.9948	3	0.000105539

REFERENCES

- Fukuda, N; Ito, Y; Yamaguchi, M; Mitumori, K; Koizumi, M; Hasegawa, R; Kamata, E; Ema, M.
(2004). Unexpected nephrotoxicity induced by tetrabromobisphenol A in newborn rats. Toxicol
Lett 150: 145-155. <http://dx.doi.org/10.1016/j.toxlet.2004.01.001>
- NTP. (2014). Toxicology studies of tetrabromobisphenol A in F344/NTac rats and B6C3F1/N mice and
toxicology and carcinogenesis studies of tetrabromobisphenol A in Wistar Han [CrI:WI(Han)]
rats and B6C3F1/N mice (gavage studies). (TR-587). Research Triangle Park, NC: U.S.
Department of Health and Human Services. <http://dx.doi.org/10.22427/NTP-TR-587>