

Table A-1. Benzo(a)pyrene Dose-response Models and Benchmark Dose Estimates at 10% Effect Levels Applied to Study Results

Source	Effect Endpoint		Dose-Response Model (1, 2)	Parameters (2)			Goodness-of-Fit			POD (% Effect)	Dose (mg/kg-day)		Human CSF (mg/kg-day) ⁻¹	Notes
	Animal	Tissue		β_0	β_1	β_2	p-value (3)	AIC (4)	Maximum Residual (5)		BMD	BMDL		
Culp, 1998 Table IV	female B6C3F1 mouse	Liver (hepatocellular adenomas)	multistage cancer	0.074	0	0	0.035	102	-1.9	10%	--	--	--	BMD computation failed. BMD is larger than three times maximum input doses.
Culp, 1998 Table IV	female B6C3F1 mouse	Lung (alveolar/bronchiolar adenomas and/or carcinomas)	multistage cancer	0.048	0	0	0.020	74	1.8	10%	--	--	--	BMD computation failed. BMD is larger than three times maximum input doses.
Culp, 1998 Table IV without 100ppm Dose	female B6C3F1 mouse	Lung (alveolar/bronchiolar adenomas and/or carcinomas)	multistage cancer	0.053	0	0.14	0.022	70	-1.7	10%	0.9	0.4	0.23	
Culp, 1998 Table IV	female B6C3F1 mouse	Forestomach (papillomas and/or carcinomas)	multistage cancer	0.014	2.2	0	0.011	105	-2.4	10%	0.049	0.038	2.61	
Culp, 1998 Table IV without 100ppm Dose	female B6C3F1 mouse	Forestomach (papillomas and/or carcinomas)	multistage cancer	0.019	0	6.0	0.77	84	-0.26	10%	0.133	0.081	1.23	
Culp, 1998 Table IV	female B6C3F1 mouse	Esophagus (papillomas and/or carcinomas)	multistage cancer	0	0	0.21	0.99	81	-0.31	10%	0.72	0.52	0.19	
Culp, 1998 Table IV	female B6C3F1 mouse	Tongue (papillomas and/or carcinomas)	multistage cancer	0	0	0.15	0.99	85	-0.27	10%	0.83	0.55	0.18	
Culp, 1998 Table IV	female B6C3F1 mouse	Larynx (papillomas and/or carcinomas)	multistage cancer	0	0.09	0	0.50	54	1.3	10%	1.2	0.72	0.14	
Culp, 1998 Table IV	female B6C3F1 mouse	Hemangiosarcomas	multistage cancer	0.031	0	0	0.32	55	1.3	10%	--	--	--	BMD computation failed. BMD is larger than three times maximum input doses.
Culp, 1998 Table IV	female B6C3F1 mouse	Histiocytic sarcomas	multistage cancer	0.026	0	0	0.52	48	-1.14	10%	--	--	--	BMD computation failed. BMD is larger than three times maximum input doses.
Culp, 1998 Table IV	female B6C3F1 mouse	Sarcomas	multistage cancer	0.053	0	0	0.0059	80	3.0	10%	--	--	--	BMD computation failed. BMD is larger than three times maximum input doses.

Abbreviations

AIC = Akaike's Information Criterion CSF = cancer slope factor
 BMD = benchmark dose POD = point of departure
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.1.1 was used to determine dose-response dichotomous data.
- Dose response functions for multistage cancer: $P[\text{response}] = \beta_0 + (1 - \beta_0) \cdot [1 - \text{EXP}(-\beta_1 \cdot \text{dose} - \beta_2 \cdot \text{dose}^2)]$;
 Dose response function for Hill Model: $y + (v \cdot d^n) / (k^n + d^n)$, where v=sign, n=power, and k=slope.
- For dichotomous data, Chi-square test is a hypothesis test in which the null hypothesis is that data fit the dose-response function. Higher p-values indicate better fits.
 For continuous data, there are four Maximum Likelihood tests performed by BMDS that test the null hypothesis that the model fits the data as well as the "true" model.
 Test 1. Tests the hypothesis that response and variance don't differ among dose levels. If this test accepts, there may not be a dose-response. P-values less than 0.1 indicate a model fit.
 Test 2. Tests the hypothesis that variances are homogeneous. If this test accepts, the simpler constant variance model may be appropriate. P-values less than 0.1 indicate a model fit.
 Test 3. (non-constant variance model) Test the hypothesis that the variances are adequately modeled. If this test accepts, it may be appropriate to conclude that the variances have been modeled
 Test 4. (non-constant variance model). Tests the hypothesis that the model for the mean fits the data. If this tests accepts, the user has support for the selected model. P-values greater than 0.1 indicate a model fit.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Culp, S.J. et al. 1998. Carcinogenesis 19(1):117-124; Table III and Table IV.

Table A-2. Benchmark Dose Modeling results from Thyssen (1981), total URT tumors

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (mg/m ³)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Gamma	10%	0.00	110	-1.41	0.373	0.283	No fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Logistic	10%	0.00	125	5.15	1.11	0.851	No fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	LogLogistic	10%	0.00	103	-1.84	0.222	0.147	No fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	LogProbit	10%	0.00	112	-0.77	0.527	0.407	No fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Multistage-Cancer 1	10%	0.00	110	-1.41	0.373	0.283	No fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Multistage-Cancer 2	10%	0.00	110	-1.41	0.373	0.283	No fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Multistage-Cancer 3	10%	0.00	110	-1.41	0.373	0.283	No fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Multistage-Cancer 4	10%	0.00	110	-1.41	0.373	0.283	No fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Probit	10%	0.00	125	5.21	1.04	0.814	No fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Weibull	10%	0.00	110	-1.41	0.373	0.283	No fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Quantal-Linear	10%	0.00	110	-1.41	0.373	0.283	No fit

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Thyssen, 1981

BMDL Ratio = 0.00

No models fit this data.

Table A-3. Benchmark Dose Modeling results from Thyssen (1981), total URT tumors

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (mg/m ³)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Gamma	10%	1.00	35.5	0	0.672	0.337	Best fit: lowest AIC, highest p-value
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Logistic	10%	1.000	37.5	0	0.907	0.470	Good fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	LogLogistic	10%	1.000	37.5	0	0.829	0.337	Good fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	LogProbit	10%	1.000	37.5	0	0.692	0.322	Good fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Multistage-Cancer 1	10%	0.0273	47.2	-2.32	0.146	0.0991	No fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Multistage-Cancer 2	10%	0.412	38.8	-1.27	0.337	0.241	Good fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Multistage-Cancer 3	10%	0.807	36.4	-0.65	0.475	0.317	Good fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Multistage-Cancer 4	10%	0.949	35.8	-0.32	0.571	0.345	Good fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Probit	10%	1.000	37.5	0	0.804	0.421	Good fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Weibull	10%	1.000	37.5	0	0.857	0.351	Good fit
Thyssen, 1981	B(a)P	Syrian Golden	Total URT tumors	Quantal-Linear	10%	0.0273	47.2	-2.32	0.146	0.0991	No fit
									BMDL Ratio = 1.95		BMDL Ratio less than 3; Mean BMDL = 0.35

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

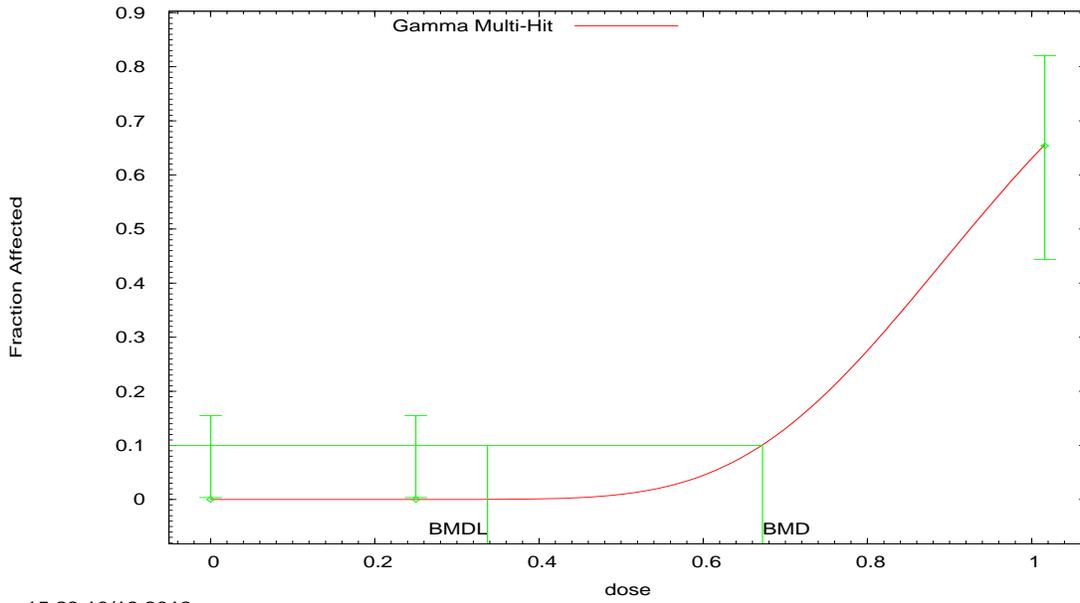
- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Thyssen, 1981

Gamma_Thyssen1981TotalTumors-woutHigh_Gam-BMR10-Restrict

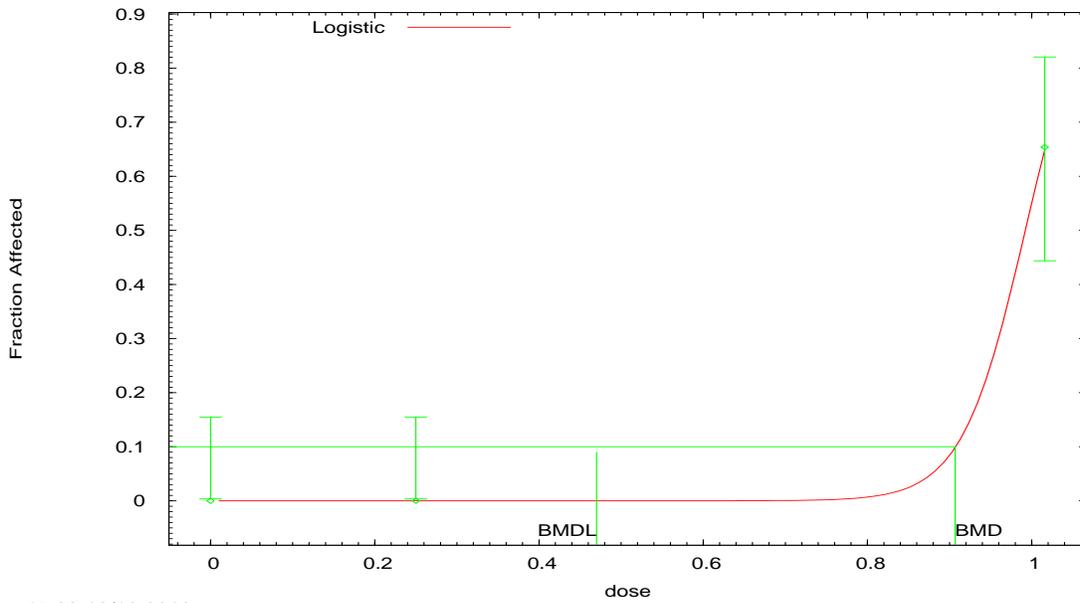
Gamma Multi-Hit Model, with BMR of 10% Extra Risk for the BMD and 0.95 Lower Confidence Limit for the BMI



15:28 10/18 2013

Logistic_Thyssen1981TotalTumors-woutHigh_Log-BMR10

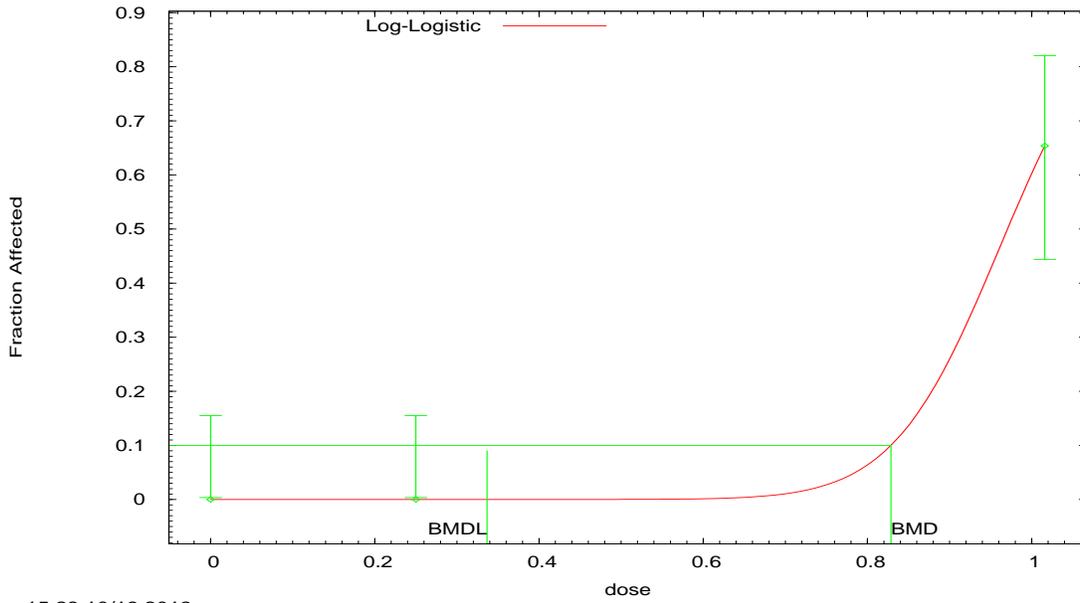
Logistic Model, with BMR of 10% Extra Risk for the BMD and 0.95 Lower Confidence Limit for the BMDL



15:28 10/18 2013

LogLogistic_Thyssen1981TotalTumors-woutHigh_Lnl-BMR10-Restrict

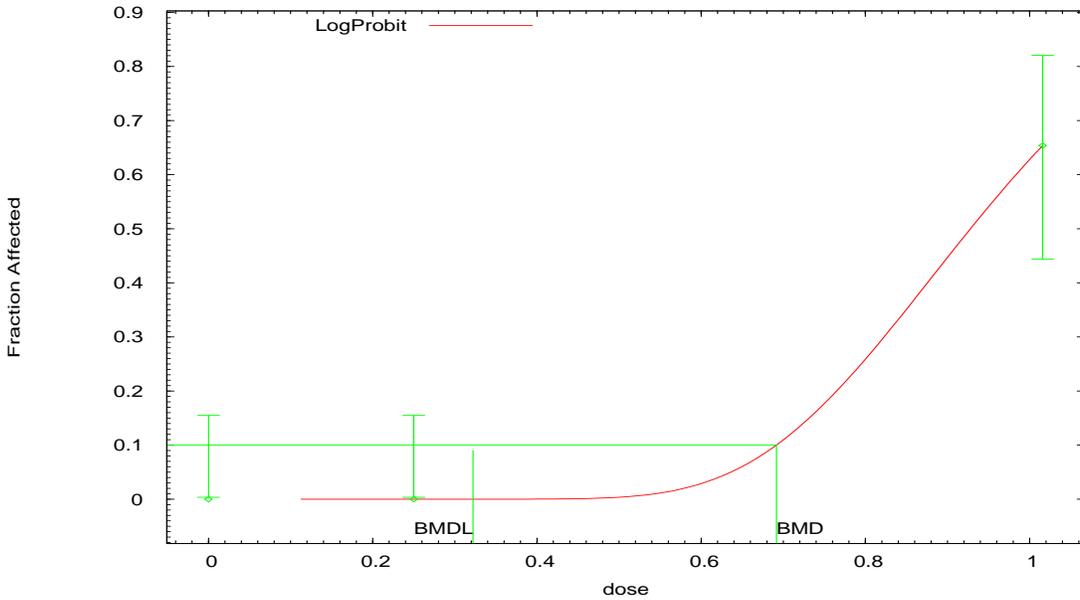
Log-Logistic Model, with BMR of 10% Extra Risk for the BMD and 0.95 Lower Confidence Limit for the BMDL



15:28 10/18 2013

LogProbit_Thyssen1981TotalTumors-woutHigh_Lnp-BMR10-Restrict

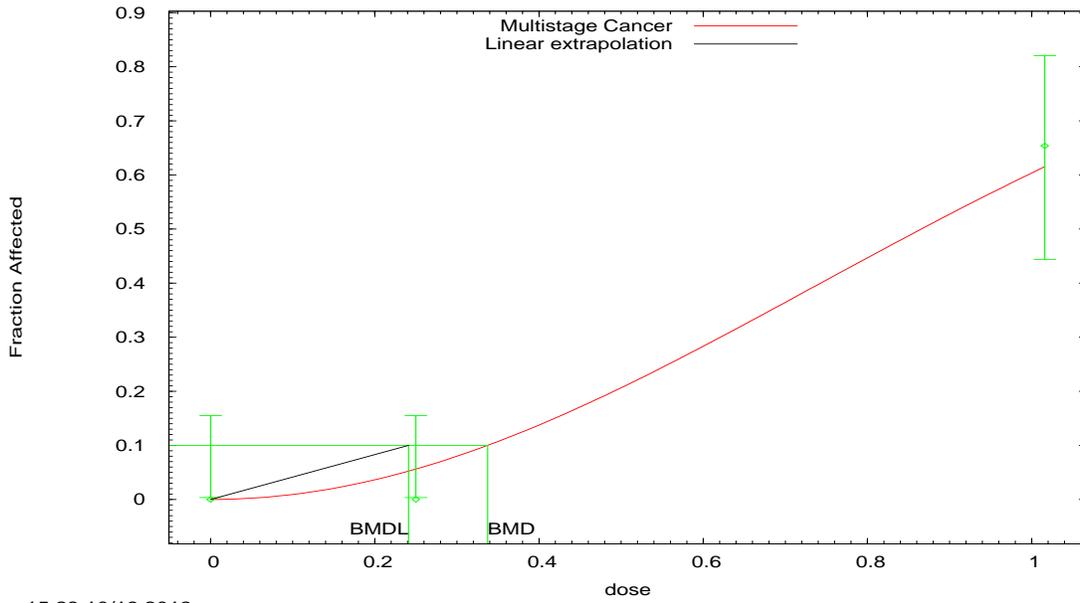
LogProbit Model, with BMR of 10% Extra Risk for the BMD and 0.95 Lower Confidence Limit for the BMDL



15:28 10/18 2013

Multistage-Cancer_Thyssen1981TotalTumors-woutHigh_Msc2-BMR10

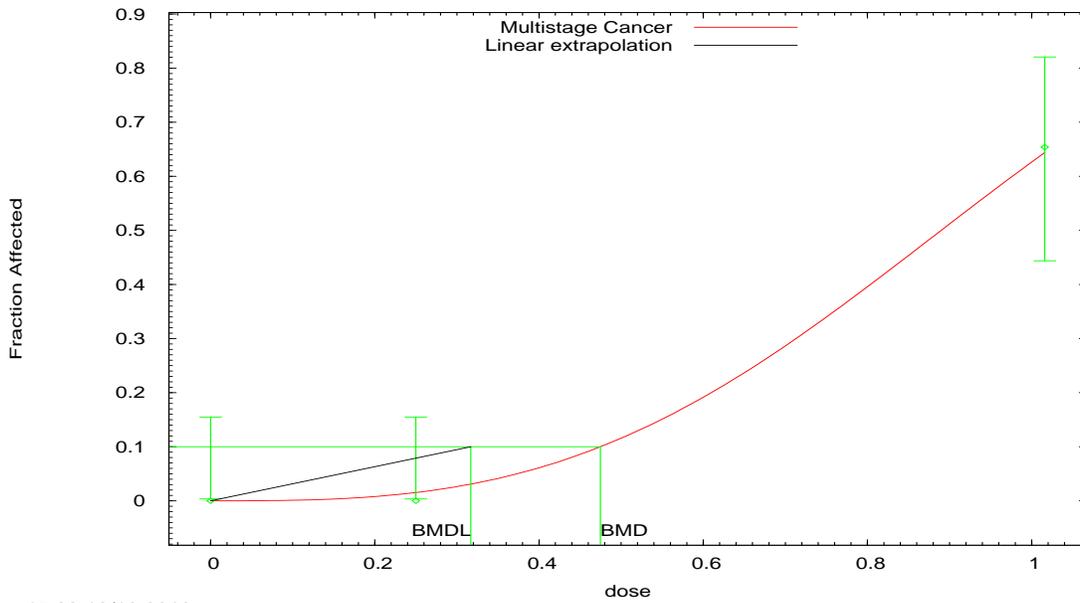
Multistage Cancer Model, with BMR of 10% Extra Risk for the BMD and 0.95 Lower Confidence Limit for the BM



15:28 10/18 2013

Multistage-Cancer_Thyssen1981TotalTumors-woutHigh_Msc3-BMR10

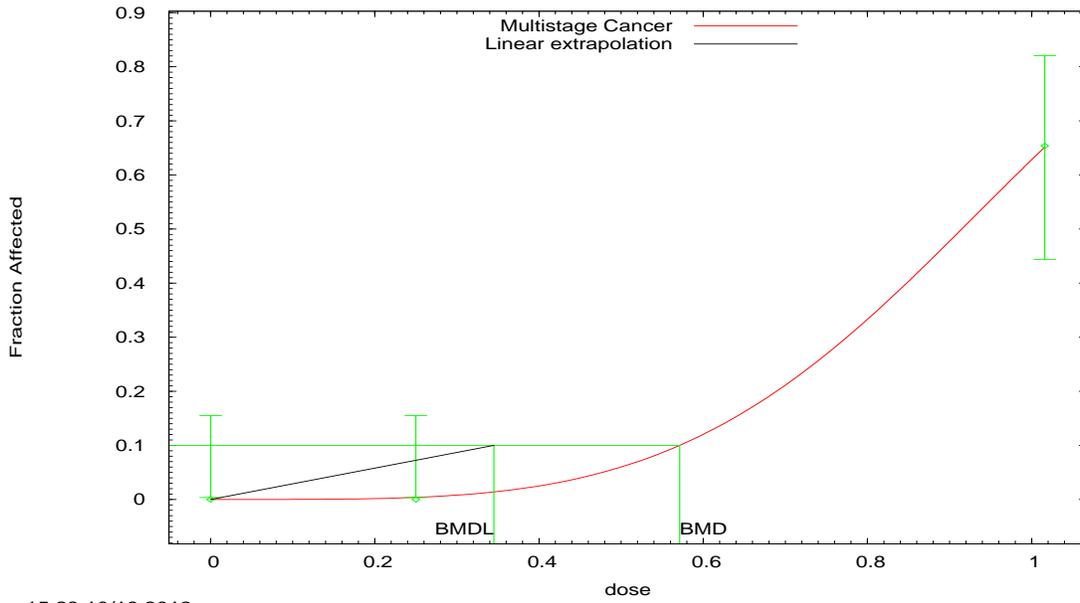
Multistage Cancer Model, with BMR of 10% Extra Risk for the BMD and 0.95 Lower Confidence Limit for the BM



15:28 10/18 2013

Multistage-Cancer_Thyssen1981TotalTumors-woutHigh_Msc4-BMR10_gh

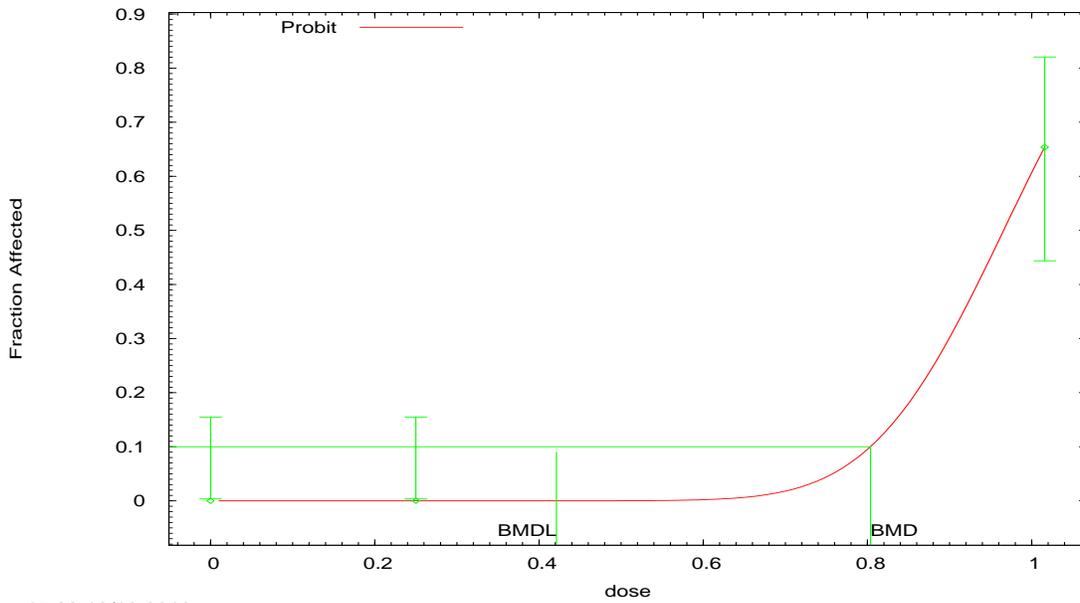
Multistage Cancer Model, with BMR of 10% Extra Risk for the BMD and 0.95 Lower Confidence Limit for the BM



15:28 10/18 2013

Probit_Thyssen1981TotalTumors-woutHigh_Pro-BMR10

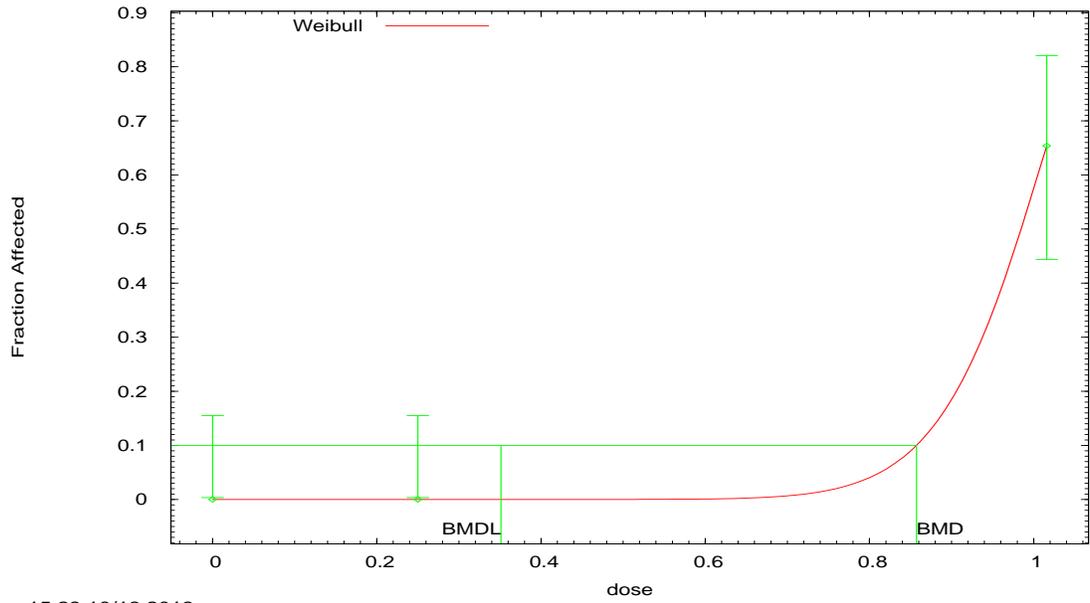
Probit Model, with BMR of 10% Extra Risk for the BMD and 0.95 Lower Confidence Limit for the BMDL



15:28 10/18 2013

Weibull_Thyssen1981TotalTumors-woutHigh_Wei-BMR10-Restrict

Weibull Model, with BMR of 10% Extra Risk for the BMD and 0.95 Lower Confidence Limit for the BMDL



15:28 10/18 2013

Table A-4. Benchmark Dose Modeling results from Sivak (1997), total skin tumors

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	Goodness-of-Fit			POD (% Effect)	Dose of B(a)P (µg)		Notes
		Animal	Tissue		p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)		BMD	BMDL	
Sivak, 1997	B(a)P	C3H/HeJ male mice	Total skin tumors	Gamma	0.83	51	0.32	10%	0.10	0.054	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Total skin tumors	Logistic	0.03	59	2.05	10%	0.34	0.24	
Sivak, 1997	B(a)P	C3H/HeJ male mice	Total skin tumors	LogLogistic	0.94	51	0.11	10%	0.10	0.057	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Total skin tumors	LogProbit	1.00	49	0.09	10%	0.11	0.076	Best fit. Lowest AIC of fitting models.
Sivak, 1997	B(a)P	C3H/HeJ male mice	Total skin tumors	Multistage 2	0.77	52	0.25	10%	0.09	0.053	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Total skin tumors	Multistage 3	0.77	52	0.25	10%	0.09	0.053	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Total skin tumors	Multistage-Cancer 2	0.77	52	0.25	10%	0.09	0.053	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Total skin tumors	Multistage-Cancer 3	0.765	52	0.25	10%	0.09	0.053	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Total skin tumors	Probit	0.04	58	2.02	10%	0.31	0.23	
Sivak, 1997	B(a)P	C3H/HeJ male mice	Total skin tumors	Weibull	0.81	51	0.31	10%	0.10	0.054	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Total skin tumors	Quantal-Linear	0.83	50	-0.80	10%	0.07	0.051	Good fit
									BMDL Ratio = 0.00		

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Sivak, 1997

Table A-5. Benchmark Dose Modeling results from Sivak (1997), carcinomas

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	Goodness-of-Fit			POD (% Effect)	Dose of B(a)P (µg)		Notes
		Animal	Tissue		p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)		BMD	BMDL	
Sivak, 1997	B(a)P	C3H/HeJ male mice	Carcinomas	Gamma	0.95	43	0.12	10%	0.15	0.075	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Carcinomas	Logistic	0.15	48	1.50	10%	0.41	0.29	Exclude model despite fit; model has higher AIC, higher residual and lower p-value.
Sivak, 1997	B(a)P	C3H/HeJ male mice	Carcinomas	LogLogistic	0.98	43	0.05	10%	0.15	0.083	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Carcinomas	LogProbit	1.00	43	0.01	10%	0.14	0.091	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Carcinomas	Multistage 2	0.87	44	0.19	10%	0.16	0.071	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Carcinomas	Multistage 3	0.87	44	0.19	10%	0.16	0.070	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Carcinomas	Multistage-Cancer 2	0.87	44	0.19	10%	0.16	0.071	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Carcinomas	Multistage-Cancer 3	0.87	44	0.19	10%	0.16	0.070	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Carcinomas	Probit	0.18	47	1.44	10%	0.36	0.26	Exclude model despite fit; model has higher AIC, higher residual and lower p-value.
Sivak, 1997	B(a)P	C3H/HeJ male mice	Carcinomas	Weibull	0.93	43	0.15	10%	0.15	0.074	Good fit
Sivak, 1997	B(a)P	C3H/HeJ male mice	Carcinomas	Quantal-Linear	0.52	44	-0.76	10%	0.08	0.056	Good fit

Abbreviations

AIC = Akaike's Information Criterion
 BMD = benchmark dose
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

POD = point of departure
 SD = standard deviation

B(a)P = Benzo (a) pyrene

BMDL Ratio = 1.63

Average of BMDLs from best fitting models is 0.073.

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Sivak, 1997

Table A-6. Benchmark Dose Modeling results from Poel (1959), total skin tumors

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	Goodness-of-Fit			POD (% Effect)	Dose of B(a)P (µg)		Notes
		Animal	Tissue		p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)		BMD	BMDL	
Poel, 1959	B(a)P	C57L male mice	Total skin tumors	Gamma	0.07	188	1.00	10%	0.11	0.088	
Poel, 1959	B(a)P	C57L male mice	Total skin tumors	Logistic	0.12	188	-0.74	10%	0.35	0.29	Good fit
Poel, 1959	B(a)P	C57L male mice	Total skin tumors	LogLogistic	0.03	192	-0.55	10%	0.40	0.15	
Poel, 1959	B(a)P	C57L male mice	Total skin tumors	LogProbit	0.03	192	-0.14	10%	0.47	0.18	
Poel, 1959	B(a)P	C57L male mice	Total skin tumors	Multistage 2	0.06	189	1.70	10%	0.16	0.092	
Poel, 1959	B(a)P	C57L male mice	Total skin tumors	Multistage 3	0.07	188	1.76	10%	0.17	0.095	
Poel, 1959	B(a)P	C57L male mice	Total skin tumors	Multistage-Cancer 2	0.06	189	1.70	10%	0.16	0.092	
Poel, 1959	B(a)P	C57L male mice	Total skin tumors	Multistage-Cancer 3	0.07	188	1.76	10%	0.17	0.095	
Poel, 1959	B(a)P	C57L male mice	Total skin tumors	Probit	0.12	188	-0.84	10%	0.32	0.27	Good fit
Poel, 1959	B(a)P	C57L male mice	Total skin tumors	Weibull	0.07	188	1.28	10%	0.12	0.088	
Poel, 1959	B(a)P	C57L male mice	Total skin tumors	Quantal-Linear	0.13	186	0.95	10%	0.11	0.088	Good fit
									BMDL Ratio = 3.25		Average of three fitting models = 0.216.

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation

BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Poel, 1959

Table A-7. Benchmark Dose Modeling results from Poel (1959), epidermoid carcinoma

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	Goodness-of-Fit			POD (% Effect)	Dose of B(a)P (µg)		Notes
		Animal	Tissue		p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)		BMD	BMDL	
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Gamma	0.096	128	-0.53	10%	0.34	0.24	
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Logistic	0	151	0.06	10%	0.66	0.54	
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	LogLogistic	0.96	123	-0.26	10%	0.36	0.27	Best fit. Lowest AIC of fitting models
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	LogProbit	0.91	124	-0.59	10%	0.33	0.26	Good fit
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Multistage 2				10%			
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Multistage 3				10%			
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Multistage-Cancer 2	0.09	133	-0.97	10%	0.24	0.18	
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Multistage-Cancer 3	0.09	133	-0.97	10%	0.24	0.18	
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Probit	0	168	-0.61	10%	0.74	0.60	
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Weibull	0.08	130	-0.80	10%	0.31	0.21	
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Quantal-Linear	0.17	131	-1.05	10%	0.23	0.18	Good fit
									BMDL Ratio = 1.49		

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation

BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Poel, 1959

Table A-8. Benchmark Dose Modeling results from Poel (1959), epidermoid carcinoma

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	Goodness-of-Fit			POD (% Effect)	Dose of B(a)P (µg)		Notes
		Animal	Tissue		p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)		BMD	BMDL	
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Gamma	0.16	128	-0.53	10%	0.34	0.24	Good fit
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Logistic	0	151	0.06	10%	0.66	0.54	
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	LogLogistic	0.98	123	-0.25	10%	0.36	0.27	Best fit. Lowest AIC of fitting models.
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	LogProbit	0.96	124	-0.59	10%	0.33	0.26	Good fit
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Multistage 2	0.16	133	-0.97	10%	0.24	0.18	Good fit
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Multistage 3	0.16	133	-0.97	10%	0.24	0.18	Good fit
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Multistage-Cancer 2	0.16	133	-0.97	10%	0.24	0.18	Good fit
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Multistage-Cancer 3	0.16	133	-0.97	10%	0.24	0.18	Good fit
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Probit	0	168	-0.61	10%	0.74	0.60	
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Weibull	0.14	130	-0.80	10%	0.31	0.21	Good fit
Poel, 1959	B(a)P	C57L male mice	Epidermoid carcinoma	Quantal-Linear	0.25	131	-1.05	10%	0.23	0.18	Good fit
									BMDL Ratio = 1.5		

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Poel, 1959

Table A-9. Benchmark Dose Modeling results from Poel (1960), total skin tumors

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (µg)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Poel, 1960	B(a)P	Male SWR mice	Total skin tumors	Gamma	10%	1.00	34	0.01	0.17	0.13	
Poel, 1960	B(a)P	Male SWR mice	Total skin tumors	Logistic	10%	0.89	34	0.24	0.17	0.13	
Poel, 1960	B(a)P	Male SWR mice	Total skin tumors	LogLogistic	10%	0.99	34	0.02	0.17	0.13	
Poel, 1960	B(a)P	Male SWR mice	Total skin tumors	LogProbit	10%	1.00	34	0	0.17	0.13	Best fit model (highest p-value, lowest AIC, lowest residual)
Poel, 1960	B(a)P	Male SWR mice	Total skin tumors	Multistage-Cancer 1	10%	0.001	53	-1.89	0.05	0.03	
Poel, 1960	B(a)P	Male SWR mice	Total skin tumors	Multistage-Cancer 2	10%	0.10	40	-1.05	0.10	0.08	
Poel, 1960	B(a)P	Male SWR mice	Total skin tumors	Multistage-Cancer 3	10%	0.62	34	-1.02	0.13	0.11	
Poel, 1960	B(a)P	Male SWR mice	Total skin tumors	Multistage-Cancer 4	10%	0.98	32	-0.26	0.16	0.12	
Poel, 1960	B(a)P	Male SWR mice	Total skin tumors	Probit	10%	0.97	34	0.11	0.17	0.13	
Poel, 1960	B(a)P	Male SWR mice	Total skin tumors	Weibull	10%	0.98	34	0.06	0.17	0.13	
Poel, 1960	B(a)P	Male SWR mice	Total skin tumors	Quantal-Linear	10%	0.001	53	-1.89	0.05	0.03	
										BMDL Ratio = 1.69	

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0 .

References

Poel, 1960

Table A-10. Benchmark Dose Modeling results from Poel (1960), total skin tumors

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (µg)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Poel, 1960	B(a)P	Male C3HeB	Total skin tumors	Gamma	10%	0.69	63	1.02	0.16	0.11	Good fit
Poel, 1960	B(a)P	Male C3HeB	Total skin tumors	Logistic	10%	0.10	71	1.36	0.49	0.35	
Poel, 1960	B(a)P	Male C3HeB	Total skin tumors	LogLogistic	10%	0.67	65	0.76	0.14	0.07	
Poel, 1960	B(a)P	Male C3HeB	Total skin tumors	LogProbit	10%	0.13	66	1.99	0.21	0.15	
Poel, 1960	B(a)P	Male C3HeB	Total skin tumors	Multistage-Cancer 1	10%	0.69	63	1.02	0.16	0.11	Good fit
Poel, 1960	B(a)P	Male C3HeB	Total skin tumors	Multistage-Cancer 2	10%	0.69	63	1.02	0.16	0.11	
Poel, 1960	B(a)P	Male C3HeB	Total skin tumors	Multistage-Cancer 3	10%	0.69	63	1.02	0.16	0.11	
Poel, 1960	B(a)P	Male C3HeB	Total skin tumors	Multistage-Cancer 4	10%	0.69	63	1.02	0.16	0.11	
Poel, 1960	B(a)P	Male C3HeB	Total skin tumors	Probit	10%	0.11	70	1.32	0.44	0.33	
Poel, 1960	B(a)P	Male C3HeB	Total skin tumors	Weibull	10%	0.69	63	1.02	0.16	0.11	Good fit
Poel, 1960	B(a)P	Male C3HeB	Total skin tumors	Quantal-Linear	10%	0.69	63	1.02	0.16	0.11	Good fit
									BMDL Ratio = 4.79		

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Poel, 1960

Table A-11. Benchmark Dose Modeling results from Poel (1960), total skin tumors

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (µg)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Poel, 1960	B(a)P	Male A/He Mice	Total skin tumors	Gamma	10%	1.00	16	-0.01	4.35	1.82	Good fit
Poel, 1960	B(a)P	Male A/He Mice	Total skin tumors	Logistic	10%	1.00	18	0	6.77	2.93	Good fit
Poel, 1960	B(a)P	Male A/He Mice	Total skin tumors	LogLogistic	10%	1.00	18	0	5.79	1.80	Good fit
Poel, 1960	B(a)P	Male A/He Mice	Total skin tumors	LogProbit	10%	1.00	18	0	4.47	1.77	Good fit
Poel, 1960	B(a)P	Male A/He Mice	Total skin tumors	Multistage-Cancer 1	10%	0.07	32	-0.99	0.60	0.41	
Poel, 1960	B(a)P	Male A/He Mice	Total skin tumors	Multistage-Cancer 2	10%	0.88	19	-1.24	1.80	1.30	Good fit
Poel, 1960	B(a)P	Male A/He Mice	Total skin tumors	Multistage-Cancer 3	10%	1.00	16	-0.57	2.88	1.72	Good fit
Poel, 1960	B(a)P	Male A/He Mice	Total skin tumors	Multistage-Cancer 4	10%	1.00	16	-0.26	3.72	1.87	Good fit
Poel, 1960	B(a)P	Male A/He Mice	Total skin tumors	Probit	10%	1.00	18	0	5.72	2.56	Good fit
Poel, 1960	B(a)P	Male A/He Mice	Total skin tumors	Weibull	10%	1.00	18	0	6.32	1.89	Good fit
Poel, 1960	B(a)P	Male A/He Mice	Total skin tumors	Quantal-Linear	10%	0.07	32	-0.99	0.60	0.41	
BMDL Ratio = 2.25										Average of fitting models is 1.96.	

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

1. USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
2. The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
3. For each dataset, models with relatively low AIC are indicative of better fits.
4. A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Poel, 1960

Table A-12. Benchmark Dose Modeling results from Schmidt (1973), skin carcinomas

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (µg)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Schmidt, 1973	B(a)P	Female Swiss	Skin carcinomas	Gamma	10%	1.00	151	0.05	0.27	0.22	
Schmidt, 1973	B(a)P	Female Swiss	Skin carcinomas	Logistic	10%	0.39	155	1.28	0.34	0.29	
Schmidt, 1973	B(a)P	Female Swiss	Skin carcinomas	LogLogistic	10%	0.99	151	0.08	0.27	0.22	
Schmidt, 1973	B(a)P	Female Swiss	Skin carcinomas	LogProbit	10%	1.00	151	0.01	0.26	0.22	Best fit model
Schmidt, 1973	B(a)P	Female Swiss	Skin carcinomas	Multistage-Cancer 1	10%	0.0001	181	-2.27	0.12	0.10	
Schmidt, 1973	B(a)P	Female Swiss	Skin carcinomas	Multistage-Cancer 2	10%	0.51	153	-1.38	0.22	0.19	
Schmidt, 1973	B(a)P	Female Swiss	Skin carcinomas	Multistage-Cancer 3	10%	0.98	151	0.27	0.28	0.22	
Schmidt, 1973	B(a)P	Female Swiss	Skin carcinomas	Multistage-Cancer 4	10%	0.98	151	0.27	0.28	0.22	
Schmidt, 1973	B(a)P	Female Swiss	Skin carcinomas	Probit	10%	0.69	153	0.85	0.31	0.27	
Schmidt, 1973	B(a)P	Female Swiss	Skin carcinomas	Weibull	10%	0.99	151	0.14	0.28	0.22	
Schmidt, 1973	B(a)P	Female Swiss	Skin carcinomas	Quantal-Linear	10%	0.0001	181	-2.27	0.12	0.10	
									BMDL Ratio = 1.52		Avg BMDL is 0.23

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Schmidt, 1973

Table A-13. Benchmark Dose Modeling results from Schmidt (1973), skin carcinomas

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (µg)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Schmidt, 1973	B(a)P	Female NMRI mice	Skin carcinomas	Gamma	10%	1.00	146	0.02	0.37	0.31	Good fit
Schmidt, 1973	B(a)P	Female NMRI mice	Skin carcinomas	Logistic	10%	0.82	147	-0.06	0.44	0.39	Good fit
Schmidt, 1973	B(a)P	Female NMRI mice	Skin carcinomas	LogLogistic	10%	1.00	146	0.04	0.38	0.32	Good fit
Schmidt, 1973	B(a)P	Female NMRI mice	Skin carcinomas	LogProbit	10%	1.00	146	0.002	0.36	0.30	Good fit
Schmidt, 1973	B(a)P	Female NMRI mice	Skin carcinomas	Multistage-Cancer 1	10%	0.01	163	-2.44	0.26	0.19	
Schmidt, 1973	B(a)P	Female NMRI mice	Skin carcinomas	Multistage-Cancer 2	10%	0.63	147	-1.36	0.33	0.29	Good fit
Schmidt, 1973	B(a)P	Female NMRI mice	Skin carcinomas	Multistage-Cancer 3	10%	1.00	144	-0.16	0.38	0.33	Good fit
Schmidt, 1973	B(a)P	Female NMRI mice	Skin carcinomas	Multistage-Cancer 4	10%	1.00	146	0.03	0.39	0.33	Good fit
Schmidt, 1973	B(a)P	Female NMRI mice	Skin carcinomas	Probit	10%	0.93	146	-0.06	0.41	0.37	Good fit
Schmidt, 1973	B(a)P	Female NMRI mice	Skin carcinomas	Weibull	10%	1.00	146	0.04	0.39	0.32	Good fit
Schmidt, 1973	B(a)P	Female NMRI mice	Skin carcinomas	Quantal-Linear	10%	0.01	163	-2.44	0.26	0.19	
									BMDL Ratio = 1.38		Average BMDL is 0.33.

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Schmidt, 1973

Table A-14 Benchmark Dose Modeling results from Schmahl (1977), total skin tumors

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (µg)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Schmahl, 1977	B(a)P	NMRI Mice	Total skin tumors	Gamma	10%	0.69	337	-0.22	0.28	0.183	Good fit
Schmahl, 1977	B(a)P	NMRI Mice	Total skin tumors	Logistic	10%	0.10	340	0.21	0.37	0.33	Good fit
Schmahl, 1977	B(a)P	NMRI Mice	Total skin tumors	LogLogistic	10%	0.75	337	-0.18	0.28	0.192	Good fit
Schmahl, 1977	B(a)P	NMRI Mice	Total skin tumors	LogProbit	10%	0.87	337	-0.08	0.28	0.241	Best fit (lowest AIC, lowest residuals, highest p-value of fitting models)
Schmahl, 1977	B(a)P	NMRI Mice	Total skin tumors	Multistage 2	10%	0.54	337	-0.35	0.26	0.175	Good fit
Schmahl, 1977	B(a)P	NMRI Mice	Total skin tumors	Multistage 3	10%	0.54	337	-0.35	0.26	0.173	Good fit
Schmahl, 1977	B(a)P	NMRI Mice	Total skin tumors	Multistage-Cancer 2	10%	0.54	337	-0.35	0.26	0.175	Good fit
Schmahl, 1977	B(a)P	NMRI Mice	Total skin tumors	Multistage-Cancer 3	10%	0.54	337	-0.35	0.26	0.173	Good fit
Schmahl, 1977	B(a)P	NMRI Mice	Total skin tumors	Probit	10%	0.19	338	0.24	0.35	0.31	Good fit
Schmahl, 1977	B(a)P	NMRI Mice	Total skin tumors	Weibull	10%	0.63	337	-0.28	0.27	0.181	Good fit
Schmahl, 1977	B(a)P	NMRI Mice	Total skin tumors	Quantal-Linear	10%	0.208	338	-1.44	0.18	0.149	Good fit
									BMDL Ratio = 2.1		

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Schmahl, 1977

Table A-15. Benchmark Dose Modeling results from Habs (1980), total skin tumors

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (µg)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Habs, 1980	B(a)P	Female NMRI mice	Total skin tumors	Gamma	10%	1.0	85	0	0.38	0.229	Best fit
Habs, 1980	B(a)P	Female NMRI mice	Total skin tumors	Logistic	10%	0.50	85	0.33	0.38	0.28	Good fit
Habs, 1980	B(a)P	Female NMRI mice	Total skin tumors	LogLogistic	10%	1.0	85	0	0.38	0.246	Best fit
Habs, 1980	B(a)P	Female NMRI mice	Total skin tumors	LogProbit	10%	1.0	85	0	0.39	0.261	Best fit
Habs, 1980	B(a)P	Female NMRI mice	Total skin tumors	Multistage 2	10%	0.50	84	-1.0	0.26	0.140	
Habs, 1980	B(a)P	Female NMRI mice	Total skin tumors	Multistage 3	10%	NA	87	0	0.36	0.150	
Habs, 1980	B(a)P	Female NMRI mice	Total skin tumors	Multistage-Cancer 2	10%	0.50	84	-1.0	0.26	0.140	
Habs, 1980	B(a)P	Female NMRI mice	Total skin tumors	Multistage-Cancer 3	10%	NA	87	0	0.36	0.150	
Habs, 1980	B(a)P	Female NMRI mice	Total skin tumors	Probit	10%	0.71	85	0.18	0.37	0.26	
Habs, 1980	B(a)P	Female NMRI mice	Total skin tumors	Weibull	10%	1.0	85	0	0.36	0.210	Best fit
Habs, 1980	B(a)P	Female NMRI mice	Total skin tumors	Quantal-Linear	10%	0.053	89	0	0.10	0.078	
										BMDL Ratio = 1.99	Average of best fitting models = 0.24.

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Habs, 1980

Table A-16. Benchmark Dose Modeling results from Habs (1984), carcinomas

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (µg)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Habs, 1984	B(a)P	Mice	Carcinomas	Gamma	10%	1	48	0	0.24	0.060	Best fit
Habs, 1984	B(a)P	Mice	Carcinomas	Logistic	10%	0.19	51	0.75	0.29	0.19	Good fit
Habs, 1984	B(a)P	Mice	Carcinomas	LogLogistic	10%	1	48	0	0.28	0.054	Best fit
Habs, 1984	B(a)P	Mice	Carcinomas	LogProbit	10%	1	48	0	0.29	0.113	Best fit
Habs, 1984	B(a)P	Mice	Carcinomas	Multistage 2	10%	1	48	0	0.17	0.060	Best fit
Habs, 1984	B(a)P	Mice	Carcinomas	Multistage 3	10%	NA	50	0	0.12	0.060	
Habs, 1984	B(a)P	Mice	Carcinomas	Multistage-Cancer 1	10%	0.58	48	0	0.08	0.056	Good fit
Habs, 1984	B(a)P	Mice	Carcinomas	Multistage-Cancer 2	10%	1	48	0	0.17	0.060	Best fit
Habs, 1984	B(a)P	Mice	Carcinomas	Multistage-Cancer 3	10%	NA	50	0	0.12	0.060	
Habs, 1984	B(a)P	Mice	Carcinomas	Probit	10%	0.22	50	-0.78	0.28	0.18	Good fit
Habs, 1984	B(a)P	Mice	Carcinomas	Weibull	10%	1	48	0	0.20	0.060	Best fit
Habs, 1984	B(a)P	Mice	Carcinomas	Quantal-Linear	10%	0.58	48	0	0.08	0.056	Good fit
										BMDL Ratio = 3.58	Average of best fitting models = 0.068.

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Habs, 1984

Table A-17. Benchmark Dose Modeling results from Grimmer (1983), carcinomas

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (µg)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Grimmer, 1983	B(a)P	Female CFLP mice	Carcinomas	Gamma	10%	1.00	227	0	0.34	0.22	Good fit
Grimmer, 1983	B(a)P	Female CFLP mice	Carcinomas	Logistic	10%	0.0003	249	1.74	0.74	0.63	
Grimmer, 1983	B(a)P	Female CFLP mice	Carcinomas	LogLogistic	10%	0.88	227	0	0.48	0.27	Good fit
Grimmer, 1983	B(a)P	Female CFLP mice	Carcinomas	LogProbit	10%	0.92	227	0	0.50	0.39	Good fit
Grimmer, 1983	B(a)P	Female CFLP mice	Carcinomas	Multistage-Cancer 1	10%	0.93	225	0	0.25	0.21	Good fit
Grimmer, 1983	B(a)P	Female CFLP mice	Carcinomas	Multistage-Cancer 2	10%	0.98	227	0	0.29	0.22	Good fit
Grimmer, 1983	B(a)P	Female CFLP mice	Carcinomas	Multistage-Cancer 3	10%	0.98	227	0	0.29	0.22	
Grimmer, 1983	B(a)P	Female CFLP mice	Carcinomas	Multistage-Cancer 4	10%	0.98	227	0	0.29	0.22	
Grimmer, 1983	B(a)P	Female CFLP mice	Carcinomas	Probit	10%	0.0004	249	1.80	0.71	0.61	
Grimmer, 1983	B(a)P	Female CFLP mice	Carcinomas	Weibull	10%	1.00	227	0	0.33	0.22	Good fit
Grimmer, 1983	B(a)P	Female CFLP mice	Carcinomas	Quantal-Linear	10%	0.93	225	0	0.25	0.21	Good fit

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Grimmer, 1983

BMDL Ratio = 1.82
 Scaled residuals = 0 for 9 models. MSC2,3, and 4 all provide same fit (exclude MSC3 and MSC4). All models have good fits: take average: 0.25

Table A-18. Benchmark Dose Modeling results from Cavalieri (1983), tumors

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (µg)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Cavalieri, 1983	B(a)P	Mice	Tumors	Gamma	10%	0.14	79	-0.15	0.62	0.187	
Cavalieri, 1983	B(a)P	Mice	Tumors	Logistic	10%	0.44	76	-0.18	0.63	0.49	
Cavalieri, 1983	B(a)P	Mice	Tumors	LogLogistic	10%	0.14	79	-0.19	0.61	0.201	
Cavalieri, 1983	B(a)P	Mice	Tumors	LogProbit	10%	0.15	79	-0.02	0.62	0.297	
Cavalieri, 1983	B(a)P	Mice	Tumors	Multistage 2	10%	0.38	76	-0.96	0.38	0.207	
Cavalieri, 1983	B(a)P	Mice	Tumors	Multistage 3	10%	0.48	75	-0.71	0.43	0.218	
Cavalieri, 1983	B(a)P	Mice	Tumors	Multistage-Cancer 2	10%	0.38	76	-0.96	0.38	0.207	
Cavalieri, 1983	B(a)P	Mice	Tumors	Multistage-Cancer 3	10%	0.48	75	-0.71	0.43	0.218	Best Fit
Cavalieri, 1983	B(a)P	Mice	Tumors	Probit	10%	0.42	76	-0.34	0.57	0.44	
Cavalieri, 1983	B(a)P	Mice	Tumors	Weibull	10%	0.28	77	-1.09	0.37	0.193	
Cavalieri, 1983	B(a)P	Mice	Tumors	Quantal-Linear	10%	0.303	76	-0.04	0.24	0.167	
									BMDL Ratio = 0.00		

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Cavalieri, 1983

Table A-19. Benchmark Dose Modeling results from Levin (1977), total skin tumors

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (µg)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Levin, 1977	B(a)P	C57BL/6J mice	Total skin tumors	Gamma	10%	0.29	81	-0.81	0.43	0.293	
Levin, 1977	B(a)P	C57BL/6J mice	Total skin tumors	Logistic	10%	0.02	86	-1.05	0.43	0.331	
Levin, 1977	B(a)P	C57BL/6J mice	Total skin tumors	LogLogistic	10%	0.58	80	-0.54	0.46	0.337	Best fit; lowest AIC, highest p-value
Levin, 1977	B(a)P	C57BL/6J mice	Total skin tumors	LogProbit	10%	0.54	80	-0.53	0.46	0.344	
Levin, 1977	B(a)P	C57BL/6J mice	Total skin tumors	Multistage 2	10%	0.29	81	-1.28	0.36	0.222	
Levin, 1977	B(a)P	C57BL/6J mice	Total skin tumors	Multistage 3	10%	0.29	81	-1.28	0.36	0.219	
Levin, 1977	B(a)P	C57BL/6J mice	Total skin tumors	Multistage-Cancer 2	10%	0.29	81	-1.28	0.36	0.222	
Levin, 1977	B(a)P	C57BL/6J mice	Total skin tumors	Multistage-Cancer 3	10%	0.29	81	-1.28	0.36	0.219	
Levin, 1977	B(a)P	C57BL/6J mice	Total skin tumors	Probit	10%	0.03	86	-1.05	0.42	0.315	
Levin, 1977	B(a)P	C57BL/6J mice	Total skin tumors	Weibull	10%	0.15	83	-1.22	0.37	0.240	
Levin, 1977	B(a)P	C57BL/6J mice	Total skin tumors	Quantal-Linear	10%	0.009	91	0.00	0.12	0.095	
										BMDL Ratio = 0.00	

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Levin, 1977

Table A-20. Benchmark Dose Modeling results from Nesnow (1983), carcinomas

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (µg)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Nesnow, 1983	B(a)P	Male SENCAR	Carcinomas	Gamma	10%	0.37	106	-0.68	1.59	1.14	
Nesnow, 1983	B(a)P	Male SENCAR	Carcinomas	Logistic	10%	0.02	112	-0.79	1.63	1.28	
Nesnow, 1983	B(a)P	Male SENCAR	Carcinomas	LogLogistic	10%	0.79	105	-0.32	1.71	1.32	Best fit; lowest AIC, highest p-value
Nesnow, 1983	B(a)P	Male SENCAR	Carcinomas	LogProbit	10%	0.70	105	-0.38	1.71	1.34	
Nesnow, 1983	B(a)P	Male SENCAR	Carcinomas	Multistage 2	10%	0.33	106	-1.16	1.36	0.87	
Nesnow, 1983	B(a)P	Male SENCAR	Carcinomas	Multistage 3	10%	0.33	106	-1.16	1.36	0.86	
Nesnow, 1983	B(a)P	Male SENCAR	Carcinomas	Multistage-Cancer 2	10%	0.33	106	-1.16	1.36	0.87	
Nesnow, 1983	B(a)P	Male SENCAR	Carcinomas	Multistage-Cancer 3	10%	0.33	106	-1.16	1.36	0.86	
Nesnow, 1983	B(a)P	Male SENCAR	Carcinomas	Probit	10%	0.02	113	-0.88	1.55	1.21	
Nesnow, 1983	B(a)P	Male SENCAR	Carcinomas	Weibull	10%	0.18	108	-1.14	1.37	0.94	
Nesnow, 1983	B(a)P	Male SENCAR	Carcinomas	Quantal-Linear	10%	0.003	120	0.00	0.45	0.36	
									BMDL Ratio = 1.56		

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Nesnow, 1983

Table A-21. Benchmark Dose Modeling results from Nesnow (1983), carcinomas

Source	Substance	Effect Endpoint		Dichotomous Dose-Response Model (1)	POD (% Effect)	Goodness-of-Fit			Dose of B(a)P (µg)		Notes
		Animal	Tissue			p-value for Chi-Square Test (2)	AIC (3)	Scaled Residual of Interest (4)	BMD	BMDL	
Nesnow, 1983	B(a)P	Female SENCAR	Carcinomas	Gamma	10%	0.72	90	0.46	2.09	1.67	
Nesnow, 1983	B(a)P	Female SENCAR	Carcinomas	Logistic	10%	0.77	90	0.06	2.16	1.73	
Nesnow, 1983	B(a)P	Female SENCAR	Carcinomas	LogLogistic	10%	0.39	91	0.85	2.18	1.77	
Nesnow, 1983	B(a)P	Female SENCAR	Carcinomas	LogProbit	10%	0.38	91	0.76	2.11	1.75	
Nesnow, 1983	B(a)P	Female SENCAR	Carcinomas	Multistage 2	10%	0.31	92	-1.30	1.46	1.19	
Nesnow, 1983	B(a)P	Female SENCAR	Carcinomas	Multistage 3	10%	0.98	89	-0.12	1.97	1.27	
Nesnow, 1983	B(a)P	Female SENCAR	Carcinomas	Multistage-Cancer 2	10%	0.31	92	-1.30	1.46	1.19	
Nesnow, 1983	B(a)P	Female SENCAR	Carcinomas	Multistage-Cancer 3	10%	0.98	89	-0.12	1.97	1.27	
Nesnow, 1983	B(a)P	Female SENCAR	Carcinomas	Probit	10%	0.82	90	-0.07	2.05	1.61	
Nesnow, 1983	B(a)P	Female SENCAR	Carcinomas	Weibull	10%	1.00	89	-0.06	1.98	1.54	Best fit; lowest AIC, highest p-value, lowest scaled residual
Nesnow, 1983	B(a)P	Female SENCAR	Carcinomas	Quantal-Linear	10%	0.000	116	0.00	0.52	0.42	
										BMDL ratio = 1.48	

Abbreviations

AIC = Akaike's Information Criterion POD = point of departure B(a)P = Benzo (a) pyrene
 BMD = benchmark dose SD = standard deviation
 BMDL = 1-sided 95% lower confidence limit for the benchmark dose

Notes

- USEPA's BMDS v.2.4 (Build 4/1/2013) was used to determine dose-response dichotomous data. Multi-stage value indicates the degree of the polynomial.
- The chi-square test is a hypothesis test in which the null hypothesis states that the data fit the dose-response function. Higher p-values indicate better fits. Values in bold are less than 0.1 and indicate that the data do not fit the model at significance level $\alpha = 0.1$.
- For each dataset, models with relatively low AIC are indicative of better fits.
- A scaled residual is the difference between the observed and predicted effect (i.e., percent response) divided by the standard deviation. Scaled Residual of Interest is a summary output parameter of the BMDS model, and is the scaled residual for the data point closest to the BMR or POD. Absolute value less than 2.0 is indicative of a good fit. Values in bold are >2.0

References

Nesnow, 1983