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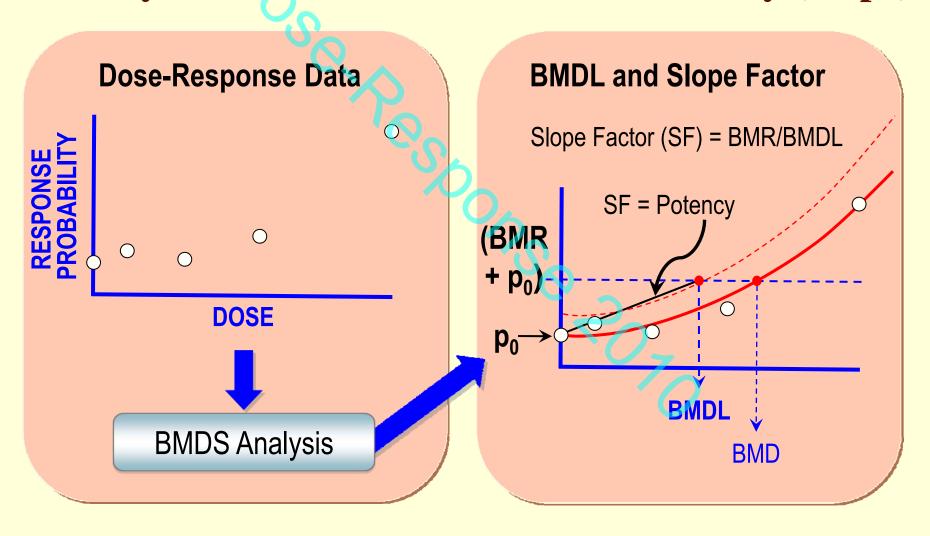
Generic Hockey-Stick Model for Estimating Benchmark Dose and Potency

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Medicine, and Risk Assessment

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U.S. EPA BMDS Modeling Approach is Now Widely Used to Estimate BMD and Potency (Slope)

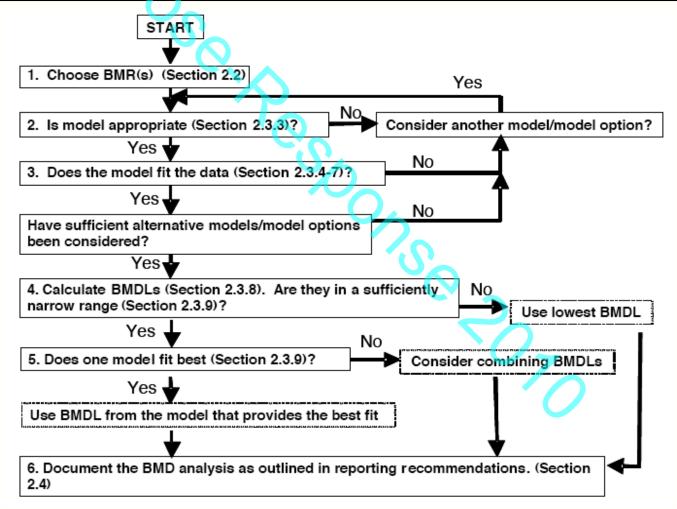


Some Quantal Models Used by BMDS v. 2.1.1

Risk Model Name ^a	Symbol	Risk Model Function, <i>P(d)</i> , of Dose <i>d</i>					
Linear (Quantal Linear)	(QL)	$1 - (1-p_0)\exp(-q_1d)$					
Linear-Quadratic (Multistage)	LQ (MS)	$1 - (1-p_0)\exp(-q_1d - q_2d^2)$					
Probit	PR	$1 - (1-p_0)\Phi[(d-\mu)/\sigma]$					
Logistic	LG	$p_0/[p_0 + (1-p_0)\exp(-q_1d)]$					
Weibull	WB	$p_0/[p_0 + (1-p_0)\exp(-q_1d^n)]$					
Gamma	GM	$1 - (1-p_0)[\Gamma(a, b) - \Gamma(a, d)]$					
Among BMDS models there is no hormetic model, such as:							
Hormetic	Н	LQ model with q₁ < 0					

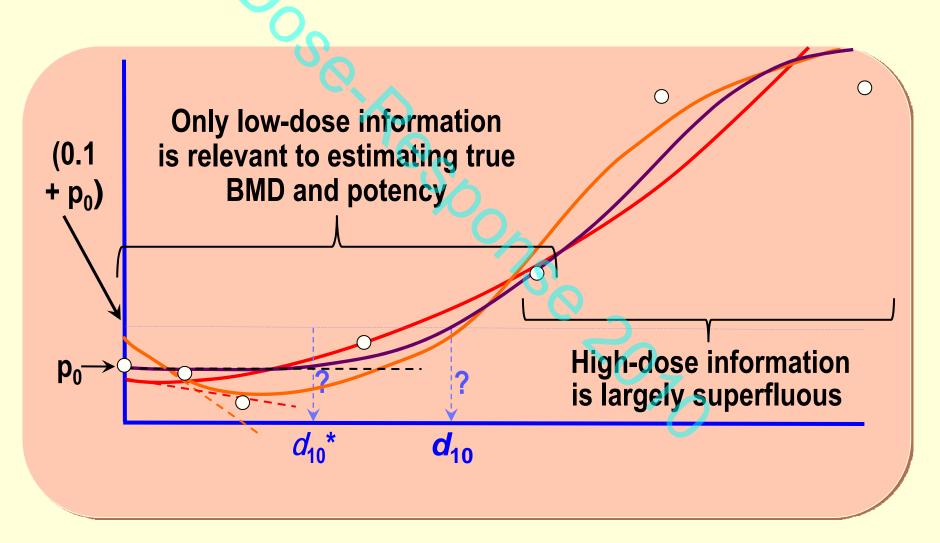
^a BMDS-equivalent names appear in parentheses

U.S. EPA BMD Decision Tree^a is Complex and May Impose Unquantified Bias or Error



^a EPA 2008 Benchmark Dose Technical Guidance

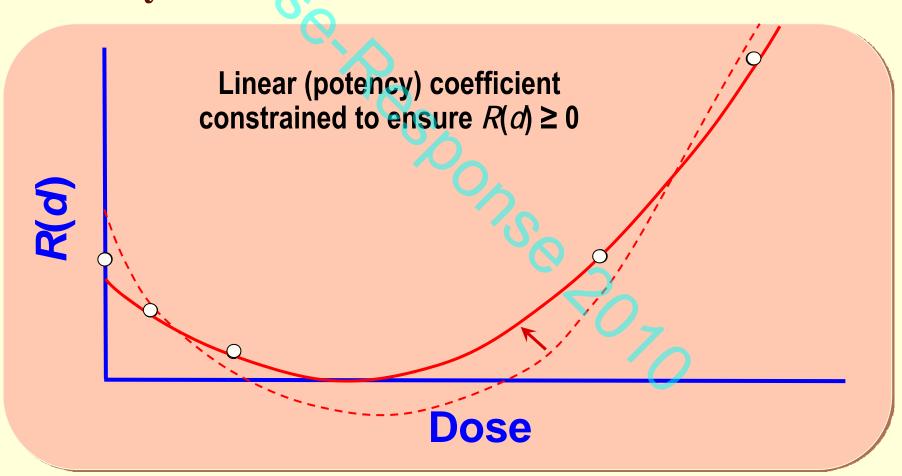
U.S. EPA BMDS Model Selection and Estimation Process has a Dubious Statistical Basis



A Single, "Generic Hockey-Stick" (GSH) Model Suffices to Estimate BMD and Potency

- Modified "linearized" multistage model:
 - $1 \exp[-\Sigma q_i d^i]$ for $i \in G(g)$ for g dose groups
 - G(g) = any subset of $\leq g$ elements of $G = \{0, 1, ..., g-1, g+1\}$
- All nonlinear coefficients $q_i(i \neq 1) \ge 0$
- Linear ("potency") coefficient q_1 is constrained only to ensure that $R(a) \ge 0$ over the experimental dose range

A GSH Model is Adequate to Estimate BMD and Potency (continued)



A GSH Model is Adequate to Estimate BMD and Potency (continued)

- All possible coefficient combinations are optimized analytically, by iterative, weighted, constrained linear regression on logit-transformed data
- Best-estimate coefficients are those that minimize chi-square using the observed data
- Confidence bounds on q_1 and BMD are calculated by the Monte Carlo bootstrap-percentile method

Simulated Quantal-Response Data were used to Compare the Reliability of BMDS versus GHS Estimates

Risk Model	Doses <i>d_j, j</i> = 1,,5 (mg/kg/day)	$P(d=0) = p_0$	Risk Model, <i>P</i> (d) Parameters	Expected Potency, q ₁ P(d) (mg/kg/day) ⁻¹	Expected BMD ^a d ₁₀ P(d) (mg/kg/day)
L			$q_1 = 0.04$	0.04	2.63
LQ	0, 1, 2, 4, 10	0.05	$q_1 = 0.02, q_2 = 0.005$	0.02	3.01
PR			μ = 7, $σ = 2.5$	0	3.80
LG			$q_1 = 0.25$	0.0225	2.99
WB	0, 1, 2, 4, 10	0.10	$q_1 = 0.075, n = 1.5$	0_0	4.63
GM			a = 1.1, b = 20	0	2.74
Н	0, 1, 3, 9, 27	0.10	$q_1 = -0.04$, $q_2 = 0.004$	-0.04	12.2

^a Benchmark dose (BMD) = d_{10} = d||(BMR = $P(d) - p_0$ = 0.10) BMR = Benchmark Response

BMD (d_{10}) and BMDL (d_{10}^{*}) Estimates from BMDS Fits to Simulated Data

Model Used to Generate Data	nª	Expected Value, Ed ₁₀	Average Simulated Value, Ad ₁₀	Bias, Ad ₁₀ –Ed ₁₀	Bias P- Value	95% LCL, Ad ₁₀ *	d ₁₀ * Coverage ^b
L	93	2.63	3.41	0.78	6×10 ⁻⁶	2.37	0.68
LQ	99	3.01	3.04	0.03	0.78	2.24	0.79
PR	96	3.80	3.59	-0.21	0.19	2.76	0.94
LG	96	2.99	2.83	-0.15	0.46	2.04	0.90
WB	96	4.63	4.09	-0.54	0.0046	2.85	0.98
GM	94	2.74	3.21	0.47	0.0028	2.19	0.72
Н	65	12.2	12.7	0.56	0.30	9.18	0.98

a n =# good fits to 100 simulated data sets

^b Coverage = $Pr(d_{10}^* \le Ed_{10})$



Model Used to Generate Data	n	Expected Value, Eq	Average Simulated Value, Aq	Bias, A <i>q</i> –E <i>q</i>	P- Value	Aq*	<i>q</i> * Coverage ^a
L	93	0.04	0.034	0.0063	2×10 ⁻⁶	0.048	0.66
LQ	99	0.02	0.037	0.017	0	0.051	1
PR	96	0	0.030	0.030	0	0.038	1
LG	96	0.0225	0.042	0.019	0	0.058	1
WB	96	0	0.028	0.028	0	0.039	1
GM	94	0	0.036	0.036	0	0.051	1
Н	65	-0.04	0.0082	0.048	0	0.011	1 (0)

^a Coverage = $Pr(q^* \ge Eq)$; in parentheses: $Pr(q^* < 0)$

BMDS Model Fits Tend to Mis-Specify the True Model used to Simulate Data that were Fit

Model Used to	_	Percent of BMDS Fits Indicating the Following "Best" BMDS Model (percent)						
Generate Data	n	QL	MS	PR	LG	WB	GM	
L	93	67.7	1.1	19.4	7.5	4.3	0	
LQ	99	19.2	20.2	23.2	19.2	18.2	8.1	
PR	96	0	51.0	2.1	30.2	11.5	5.2	
LG	96	29.2	20.8	18.8	27.1	_11.5	8.3	
WB	96	4.2	24.0	18.8	33.3	3.1	16.7	
GM	94	22.3	9.6	11.7	20.2	2.1	40.4	
Н	65	0	47.7	0	3.1	49.2	0	

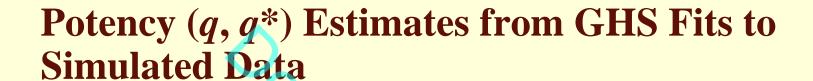


BMD (d_{10}) and BMDL (d_{10}^*) Estimates from GHS Fits to Simulated Data

Model Used to Generate Data ^a	Expected Value, Ed ₁₀	Average Simulated value, Ad ₁₀	Bias, Ad ₁₀ –Ed ₁₀	Bias P- Value	Ad ₁₀ *	d ₁₀ * Coverage ^b
L	2.63	3.41	0.78	6·10 ⁻⁵	1.28	0.98
L ₁	2.63	2.83	0.19	0.12	1.16	0.98
LQ	3.01	3.13	0.12	0.44	1.39	0.97
PR	3.80	3.96	0.16	0.28	2.02	1.00
LG	2.99	3.37	0.38	0.099	1.24	0.96
WB	4.63	4.76	0.13	0.44	1.67	0.98
GM	2.74	3.49	0.74	0.002	1.26	0.97
Н	12.2	13.0	0.84	9·10 ⁻⁵	7.75	0.98
H₁	12.2	11.9	-0.25	0.095	6.91	1.00

^a Model L₁ and H₁ fits were all conditioned on |q| > 0

^b Coverage = $Pr(d_{10}^* < Ed_{10})$

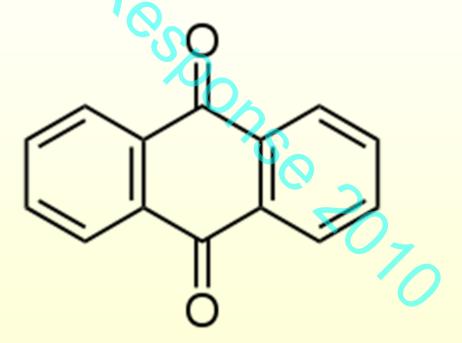


Model Used to Generate Data	Expected value, Eq	Average Simulated Value, Aq	Bias, A <i>q</i> –E <i>q</i>	P- Value	Aq*	<i>q</i> * Coverage ^a
L	0.04	0.032	-0.0085	0.001	0.092	0.97
L ₁	0.04	0.038	-0.0019	0.39	0.10	0.98
LQ	0.02	0.027	0.0068	0.13	0.085	0.97
PR	0	0.00051	0.00051	0.84	0.053	0.83
LG	0.0225	0.025	0.0024	0.84	0.10	0.96
WB	0	-0.0012	-0.0012	0.84	0.080	0.83
GM	0	0.028	0.028	0	0.11	1.00
н	-0.04	-0.026	0.014	0	0.025	1 (0.78)
H₁	-0.04	-0.038	0.0024	0.034	0.0176	1 (0.99)

^a Coverage = $Pr(q^* \ge Eq)$; in parentheses: $Pr(q^* < 0)$

Illustrative GHS Model Application:

Anthraquinone (AQ): A known rodent carcinogen and anti-carcinogen



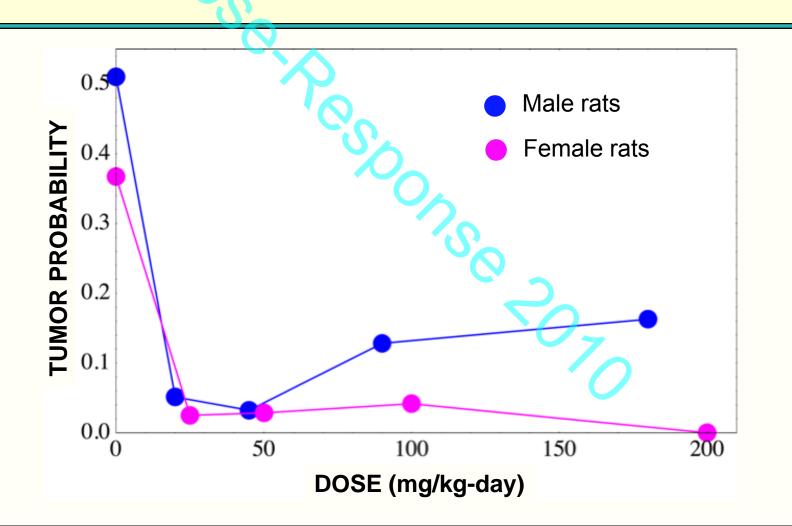
GHS Estimates of AQ Tumor Potency (100)

Species, Sex	Tumor Type ^a	q (mg/kg/day) ⁻¹	<i>q</i> * (mg/kg/day) ⁻¹	HE ^b q (mg/kg/day) ⁻¹	HE ^b q* (mg/kg/day) ⁻¹
Rat, M	MCL	-13	(-24, -5.0)	-68	(-130,-27)
Rat, F	MCL	-5.2	(-11,-1.0)	-33	(-67,-6.3)
Rat, F	RTAC	0.34	0.72	2.1	4.5
Mouse, M	HB	0.091	0.18	1.0	2.0
Mouse, M	HC or HB	0.22	0.34	2.5	3.8
Mouse, M	HAC or HB	0.48	0.90	5.4	10
Mouse, F	HC	0.015	0.059	0.16	0.63
Mouse, F	HAC or HB	1.1	1.7	12.	18.

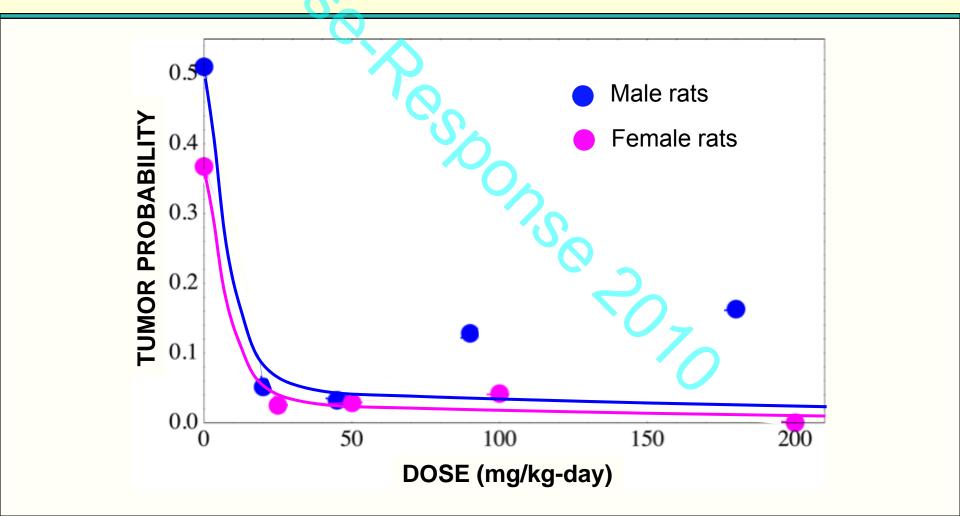
^a MCL = mononuclear cell leukemia, RTAC = renal cell adenoma or carcinoma, HB = hepatoblastoma (benign or malignant), HC = hepatocellular carcinoma, HAC = hepatocellular adenoma or carcinoma.

^b HE = human equivalent

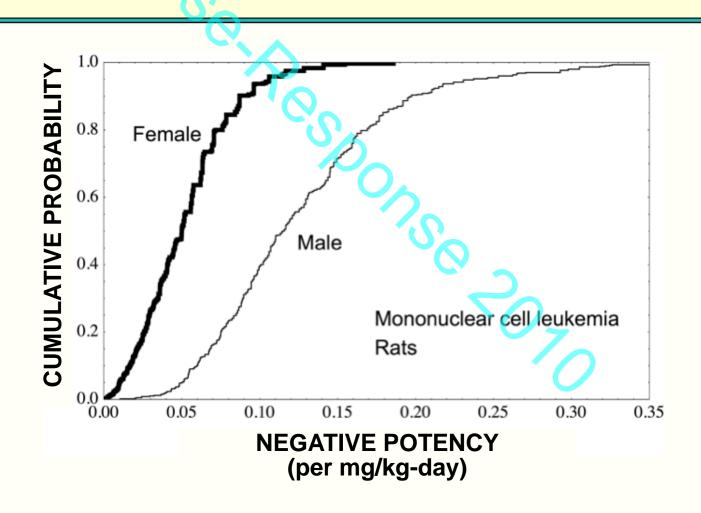
AQ Suppresses Mononuclear Cell Leukemia (MCL) in Male and Female F344/N Rats



AQ Effect on MCL in Rats Modeled as Pure Suppression (i.e., Exponential Loss)



GHS Estimates of AQ Potency for Suppressing Spontaneous MCL in Rats



Net Potency Calculation

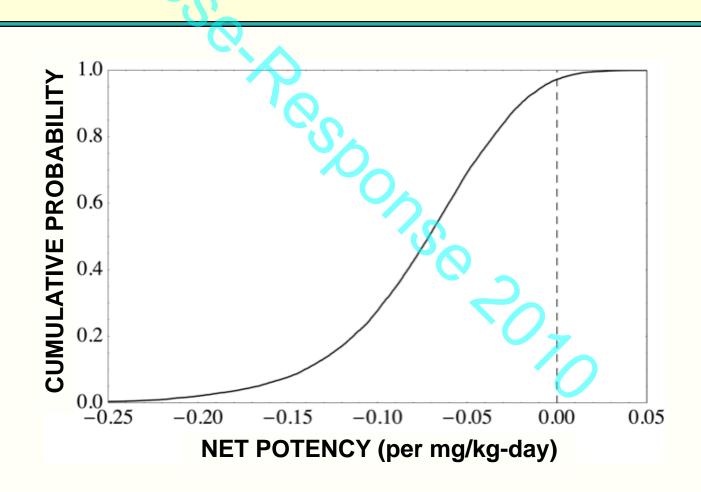
• Net potency Q of joint effects involving tumors induced at potencies q_i must adjust for estimated background rates r_j of any tumor types purely suppressed at rates a_i

$$Q = \sum_{i=1}^{n_i} q_i - \sum_{j=1}^{m_j} r_j a_j$$

Net Human-Equivalent AQ Potency: Approach

- Equal weights were used to aggregate estimated potencies for
 - MCL suppression in male vs. female rats
 - Tumor suppression vs. induction in rats
 - HAC or HB induction in male vs. female mice
 - Tumor induction in mice vs. rats
- Standard animal-to-human surface-area adjustment

Net Human-Equivalent AQ Potency: Result



Conclusions

- The USEPA BMDS procedure does not reliably identify dose-response relationships
- BMD & potency estimates are easier to obtain by the GHS than by the BMDS procedure
- GHS estimation performs as well or better than BMDS estimation (at least for quantal data)
- The GHS model can be used to test objectively for, and to characterize, negative dose-response patterns such as AQ-induced MCL suppression in rats