Note: Bolded text in the Errata/Notes below indicate the edits that were made to the BMDS Slides; bolded strikethroughs indicate text that was removed from the BMDS Slides.

Introduction

Slide 3 – Added the following acknowledgement to the Contributors: John Fox, Ph.D., and Battelle for development of the alternative BMDS models

Dichotomous Models

Slide 8 – Second bullet edited to read "Extra risk is recommended by the IRIS **Program**, and is used in IRIS risk assessments"

Slide 94 – Second sub-bullet edited to correct proper file directory where EPA users need to locate their BMDS 250 folder: **C:\Users\name\BMDS250**

Continuous Models

Slide 3 – Graphic corrected to read that "**Error bars are calculated by the software (based on reported standard deviations) and are model-independent**"

Slide 13 – Third bullet edited to read: ~~**As**~~ When using the **RD** as the base for the BMR, the user must check that the model-estimated control mean approximates the observed control means; if not, the BMD could be misspecified.

Slide 25 – Second bullet with no accompanying text was removed.

Slide 84 – Sub-bullet edited to read: Deselect the option to run with constant variance, **but retain all other default options.**

Slide 86 – Sub-bullet edited to read: Run with non-constant variance, **retain all other default options.**

Nested Dichotomous Models

Slide 9 – Second bullet edited to read "Extra risk is recommended by the IRIS **Program**, and is used in IRIS risk assessments"

Slide 21 – Corrected the four recommended iterations of nested dichotomous model runs as follows:

- Litter specific covariate/intra-litter correlation: -/-

- Litter specific covariate/intra-litter correlation: +/-

- Litter specific covariate/intra-litter correlation: -/+

- Litter specific covariate/intra-litter correlation: +/+

Slides 61, 64, 66, 68 - Second sub-bullet under instructions on what data to record (second main bullet) edited to read: p-value, AIC and Scaled Residual of Interest (1. find "mean litter specific covariate **for all the data**"; 2. look at **litter** data and dose group closest to BMD; 3. find individual rows for which reported ~~mean~~ litter specific covariate is **closest** to the value for all data; 4. **Find the maximum scaled residual value**)

Slides 63, 65, 67, 69 – Row for scaled residual values corrected to read: **Litter** Scaled residual (max value)

Slide 70 – Row for scaled residual values corrected to read: **Litter** Scaled residual (max value) and scaled residual values updated to reflect the correct values

Cancer Models

Slide 74 – Second bullet edited to read: Models differing in the maximum number of **stages** should be evaluated by comparing the AICs, the log-likelihood, and graphical comparison of data to the fitted models

Time Models

Slide 14 – First bullet edited to read: In order to profile the BMD with respect to time **(i.e., $BMD_\gamma(t)$)**, a sequence of points $\{t\}$ is chosen and the corresponding $\{BMD_\gamma(t)\}$ values are calculated

Slide 49 – Third sub-bullet edited to read: However, due to its simplicity, Haber's Law **is** extensively used **in** toxicological dose-response research