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APPENDIX B: SUMMARY OF REVISIONS TO LEAD UPTAKE BIOKINETIC MODEL SOFTWARE VERSIONS

TABLE B-1. SUMMARY OF REVISIONS TO LEAD UPTAKE/BIOKINETIC MODEL SOFTWARE FROM LEAD 0.2 TO LEAD 0.4

Item	Lead 0.2 (September, 1989)	Lead 0.4 (September, 1990)
GI-tract absorption model	Default is linear "passive" model.	Default is non-linear "active-passive" model
Drinking water defaults	Composite = 9 µg/L First flush = 0 µg/L Flushed = 9 µg/L Fountain = 0 µg/L % First flush = 0 % Flushed = 0 % Fountain = 0	Composite = 4 µg/L First flush = 4 µg/L Flushed = 1 µg/L Fountain = 10 µg/L % First flush = 50 % Flushed = 35% % Fountain = 15% (New defaults were provided EPA/ODW)
Diet defaults	Dietary lead intakes are based on FDA surveys completed in 1986. Default values range from 22-34 µg/day for ages 0-7.	Dietary lead intakes are based on FDA surveys completed in 1988. Default values range from 5.8-7.5 µg/day for ages 0-7.
Probability density function	P(x) = (1/(2.51)(GSD))¡ exp((-1/2)((lnx-lnGM)/ lnGS D)2)	P(x) = (1/(2.51)(x)(lnGSD))¡ exp((-1/2)((lnx-lnGM)/ lnGSD)2)
Plot of probability density function	Ordinate of "Bell-shaped plot" labelled "probability".	Ordinate of "bell-shaped plot" labelled "probability density function f(blood lead)" numbers removed from ordinate. Probability is computed as the integral of this function over a specified ranged. This is graphically illustrated in the "S-shaped" probability percent plot.
Calculation of blood lead in newborn (BPbn)	Fixed at 6.4 µg/dL: BPbn = BPbm ¡ k, where BPbm is the maternal blood lead (7.5 µg/dL) and k is a constant (0.85).	User option: 1) As in Lead 0.2 and option to select maternal blood lead. 2) "Fetal" model, in which maternal blood lead is calculated based on user-defined exposure data and a maternal biokinetic model, and newborn blood lead is calculated from biokinetic model.
Soil/Dust primary data entry screen	Menu includes "Change GI Absorption Method"	Menu revised to "Change GI Method/Bioavailability". If "yes" is selected, a window containing the following message appears over the secondary data entry screen: "Bioavailability of soil lead may vary depending on the lead source. For example, lead from mine wastes may have a lower bioavailability than lead from smelters. Differences in bioavailability are thought to reflect differences in gastrointestinal absorption of specific lead species and particle sizes, which vary depending on the source. The following data entry screen allows the user to make adjustments in the gastrointestinal absorption coefficients to account for site-specific information on bioavailability.

TABLE B-2. SUMMARY OF REVISIONS TO LEAD UPTAKE BIOKINETIC MODEL SOFTWARE FROM LEAD 0.4 TO LEAD 0.5

Parameter or Feature	Lead 0.4 (September, 1990)	Lead 0.5 (December, 1990)
(Non-linear GI Absorption Model	Volume of GI-tract calculated, VGI = (VGI)/(GF); where VGI is the adult GI-tract volume (liters) and GF is the age-dependent allometric scaling factor (GF < 1 for children). Default value for Km, 100 µg/L.	Volume of GI-tract calculated, VGI = (VGI)(GF). Default value for Km, 100 mg/L.
Age Range Selection	Menu specified selection.	User designated option allows user to specify any designed age range from 1-7 years.
Multiple Runs	Multiple model runs are made manually; i.e., the user specifies input for each run, and saves output in Results Out file.	Allows user to input a range of lead values for one medium (air, diet, drinking water, dust or soil), and make a series of model runs in which lead levels in the specified medium are varied over the specified range.
X-axis Scaling	Set by program.	Allows user to set scaling of X-axis of probability density function and probability percent graphs manually.
Overlay Graph Files	Not available; graphs of individual model runs can be displayed and/or printed.	Allows user to save graph output (i.e., probability density function or probability percent graphs) from multiple runs to an file and print output of multiple runs on a single graph.
Text Files	Data from individual model runs can be saved to a file.	Allows user to save the data output of individual or multiple model runs, in user specified ASCI text files; these files can be reviewed and printed in Lead and/or imported into a word or processing program after exiting from Lead.
Blood vs. Media Concentration: Model Runs (Graph Output)	Not available.	Allows user to input a range of lead values for one primary medium (air, diet, drinking water, dust or soil), and produce a series of model runs in which lead levels in the specified medium are varied over the specified range. The output of each run is captured in an X-Y plot of mean blood lead vs. medium lead.
Blood vs. Media Concentration: Find	Not available.	Calculates a lead level in the user-specified medium that is associated with a specified mean blood lead.

TABLE B-3. SUMMARY OF REVISIONS TO LEAD UPTAKE BIOKINETIC MODEL SOFTWARE FROM LEAD 0.5 TO LEAD 0.99d

Parameter or Feature	Lead 0.5 (December, 1990)	Lead 0.99d (January, 1994)
Batch Mode Model Runs	Not available.	Accepts a properly formatted ASCII text file (*.DAT) containing data on lead exposure and blood lead levels for a sample population, and calculates predicted blood lead levels for each individual. The output is saved as a *.TXT file that can be viewed within Lead or imported into a text editor (e.g., word processor), and as a *.ASC file that can be imported into PBSTAT for selected statistical analysis and graphic display.
PBSTAT	Not available.	Accepts the output of batch mode operations (i.e., *.ASC files) and delivers statistical and graphic output selected by the user from a menu. PBSTAT can be accessed from the main menu of Lead, or externally with a DOS command (PBSTAT). The printer options in PBSTAT are the same as those in PBPLOT.
PBPLOT	Not available.	Produces graph prints from Lead. It is accessed with a DOS command (PBPLOT). PBPLOT performs the same functions as "Graphics Selection Menu" in Lead, however, it produces graph prints at much higher resolutions (e.g. HP Plotter and PostScript printer graphs). PBPLOT accepts *.LAY and *.PBM files produced with Lead.
Main Menu		Restructured.
Model Iteration Period	One month with no user option.	One day with user option.
"Fetal" Model	Maternal blood lead is calculated based on user-defined exposure data and a maternal biokinetic model, and newborn blood lead (BPbn) is calculated from a biokinetic model.	Not available.
Soil Intake	Default value is 100 mg/day for all ages.	Default values are: age (yr) — soil intake (mg/day) 0-1 — 85 1-2 — 135 2-3 — 135 3-4 — 135 4-5 — 100 5-6 — 90 6-7 — 85
View/Print Data File	User must exit Lead and import *.TXT data files into a text editor (e.g., word processor) to view or print data.	Allows the user to view and print *.TXT data files within Lead.

TABLE B-3 (cont'd). SUMMARY OF REVISIONS TO LEAD UPTAKE BIOKINETIC MODEL SOFTWARE FROM LEAD 0.5 TO LEAD 0.99d

Parameter or Feature	Lead 0.5 (December, 1990)	Lead 0.99d (January, 1994)
Contribution of soil lead to indoor dust lead	Default value function is 0.28 µg Pb/g dust per µg Pb/g of soil.	Default value function is 0.70 µg Pb/g dust per µg Pb/g of soil.
Outdoor air lead concentration	Default value is 0.2 $\mu g/m^3$.	Default value is 0.1 $\mu g/m^3$.
Dietary lead intake	Default values were based on a preliminary analysis of 1988 FDA survey data.	Default values are based on a more detailed analysis of FDA 1988-90 data.
Editing of default biokinetic parameters	Coding error resulted in changes to RECSUM time constants (e.g., TPLUR) not being accepted, as a result the UBM appeared to be insensitive to changes in TPLUR.	Coding error corrected.
Euler Algorithm	Forward Euler algorithm calculates the increase compartmental lead mass over the iteration interval as the total lead inflow to the compartment, minus the total lead outflow at the beginning of the interval.	Backward Euler algorithm calculates the increase compartmental lead mass over the iteration interval as the total lead inflow to the compartment, minus the total lead outflow at the end of the interval.
Tissue Pb and Excretory Transfer Coefficients		Revised.
Non-linear GI Absorption Model	"Non-integrated" approach: Saturable absorption coefficients are calculated for each medium (soil, diet, drinking water, etc.) based on intakes from each medium, and are used to calculate media-specific uptakes which are summed to yield total uptakes.	"Integrated" approach: Intakes from all media are considered in the calculation of the saturable absorption coefficients for each medium (via SATURATION(t).