Chemical Mass Balance Model: EPA-CMB8.2

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ABSTRACT

The Chemical Mass Balance (CMB) method has been a popular approach for receptor modeling of ambient air pollutants for over two decades. For the past few years the U.S. Environmental Protection Agency's Office of Research and Development (ORD) and Office of Air Quality Planning and Standards (OAQPS) have collaborated to develop a new generation of CMB software, CMB8. Developmental work was initiated under EPA contract by the Desert Research Institute and is being continued by Pacific Environmental Services. The current version, EPA-CMB8.2, incorporates the upgrade features that CMB8 has over CMB7, but also addresses problems identified with CMB8 and adds enhancements for a more robust and user-friendly system. EPA-CMB8.2 features include: (1) full use of Windows (32-bit) capability for file access/management, (2) a *tabbed-page interface* that facilitates the sequence of steps for doing a CMB calculation, (3) multiple indexed arrays for selecting fitting species and sources, (4) versatile display capability for ambient data and source profiles, (5) mouse-overs and on-line help screens, (6) increased attention to volatile organic compounds (VOC) applications, (7) correction of some CMB7 and CMB8 flaws, (8) more options for input and output data formats, (9) addition of a more accurate least squares computational algorithm, (10) a new treatment of source collinearity, and (11) choice of criteria for determining *best fit*.

INTRODUCTION

The Chemical Mass Balance (CMB) air quality model is one of several receptor models that have been applied to air resources management for over two decades. Receptor models use the chemical and physical characteristics of gases and particles measured at source and receptor to both identify the presence of and to quantify source contributions to receptor concentrations. Receptor models are generally contrasted with dispersion models that use pollutant emissions rate estimates, meteorological dispersion and transport, and chemical transformation mechanisms to estimate the contribution of each source to receptor concentrations. CMB helps explain observations that have been made; it does not predict ambient impacts from sources as do dispersion models. The two types of models are thus complementary, with each type having strengths that compensate for the weaknesses of the other.

The U.S. Environmental Protection Agency (EPA) has tacitly approved CMB as a regulatory planning tool through the Agency's approval of numerous State Implementation Plans (SIPs) which have had a CMB component. CMB has proven to be a useful tool in applications where steady-state Gaussian plume models are inappropriate (e.g., stagnant wind regimes), as well as for confirming and or adjusting emission inventories. Since about 1990 EPA has supported and freely distributed the current version of the CMB software (CMB7). CMB8 was originally developed in 1998 by Desert Research Institute, Reno, NV under contract with EPA's

ORD and OAQPS. In September 1999, Pacific Environmental Services began work under contract with ORD/OAQPS to repair, reconfigure and enhance CMB8. This joint contractual venture resulted in a *beta* test version of this new generation of CMB model: EPA-CMB8.2, which is the subject of this paper. Associated documentation and guidance will be released when a fully functional and tested model is complete.

THE CMB APPROACH

The CMB modeling procedure requires: 1) identification of the contributing source types; 2) selection of chemical species or other properties to be included in the calculation; 3) knowledge of the fraction of each of the chemical species which is contained in each source type (source profiles); 4) estimation of the uncertainty in both ambient concentrations and source profiles; and 5) solution of the chemical mass balance equations. The CMB approach is implicit in all factor analysis and multiple linear regression models that intend to quantitatively estimate source contributions.[1] These models attempt to derive source profiles from the covariation in space and/or time of many different samples of atmospheric constituents that originate in different sources. These profiles are then used in a CMB solution to quantify source contributions to each ambient sample.

CMB quantifies contributions from chemically distinct source-types rather than contributions from individual emitters. Sources with similar chemical and physical properties cannot be distinguished from each other by CMB.

The effective variance weighted solution[2] is generally applied because it: 1) theoretically yields the most likely solutions to the CMB equations, providing model assumptions are met; 2) uses all available chemical measurements, not just so-called "tracer" species; 3) analytically estimates the uncertainty of the source contributions based on precision of both the ambient concentrations and source profiles; and 4) gives greater influence to chemical species with higher precision in both the source and receptor measurements than to species with lower precision. The effective variance is a simplification of a more exact, but less practical, generalized least squares solution proposed by Britt and Luecke.[3]

The CMB model can be written as:

$$C_i = \sum_{j=1}^{p} a_{ij} S_j, \quad i = 1, n \tag{1}$$

where C_i is the ambient concentration of specie i, a_{ij} is the fractional concentration of specie i in the emissions from source j, S_j is the total mass concentration contributed by source j, p is the number of sources, and n is the number of species, with $n > p$. The C_i and a_{ij} are known and the S_j are found by a least squares solution of the overdetermined system of equations (1). While the system is simple in appearance its solution is not, because of the need to take account of uncertainties in both the C_i's and the a_{ij}'s. These uncertainties are introduced through "effective variance" weighting of the terms in Eq. (1).

EPA-CMB8.2 FEATURES

EPA-CMB8.2 is intended to replace CMB7[4] as a more convenient method of estimating contributions from different sources to ambient chemical concentrations. EPA-CMB8.2 returns the same results as CMB7, but it operates in a Windows-based environment and accepts inputs

and creates outputs in a wider variety of formats than CMB7. The major EPA-CMB8.2 enhancements are:

Windows-based, Event-driven Operations

EPA-CMB8.2 makes full use of Windows (32-bit) features, including a *tabbed interface* that facilitates the necessary progression for doing a CMB calculation. Commands may be executed with hot-keys or toolbar buttons, and features are described via *mouse-overs* and on-line help screens. EPA-CMB8.2 also offers flexible options for input/output data formats. Input formats are compatible with output files from EPA's source profile library SPECIATE (*www.epa.gov/ttn/chief/*).

Multiple Arrays for Fitting Species and Fitting Sources

Up to ten indexed arrays of fitting species and fitting source profiles may be specified in input data selection files. Different arrays can be selected during EPA-CMB8.2 operation. Upon exit from any selection windows for fitting species or fitting sources, an option is provided to conveniently save (update) or rename selection files to reflect arrays that are added, modified or deleted during the session.

Britt-Luecke Algorithm

A general solution to the least squares estimation problem that includes uncertainty in all the variables (i.e., the source compositions as well as the ambient concentrations) is available. While an approximation[5] to the Britt-Luecke iteration scheme[3] was used in CMB7, exercise of Britt-Luecke algorithm option in EPA-CMB8.2 allows solution without approximation.

Improved Collinearity Diagnostics

Collinearity in a CMB context refers to a situation in which the compositions of two or more source profiles are so similar that it is difficult to infer the separate impact of each. Collinearity is a form of mathematical *ill conditioning*, and its presence is associated with additional serious problems beyond the one just noted. The basis for detecting and handling collinearity in EPA-CMB8.2 is the same as that used in CMB7: the analysis and formulation given by Henry.[6,7] However the "packaging" is very different versus CMB7: the "uncertainty/similarity clusters" description used in CMB7 has been replaced in EPA-CMB8.2 by "maximum source uncertainty", " minimum source projection", and "estimable sources" terminology. User experience will be needed however before the new freedom to select collinearity parameter values can be exercised confidently.

The approach in EPA-CMB8.2 more directly mirrors Henry's treatment of the collinearity problem and exploits its potential more quantitatively. It gives the user access to collinearity parameters which in CMB7 are "hard-wired" and not necessarily optimum for every application. Values for these parameters were chosen in CMB7 to be compatible with characteristics of particulate mass measurements, but they may not be as well suited to the CMB volatile organic compounds (VOC) applications which have become of increasing interest.

Search for Best Fit

Using a user-selected best fit criteria, EPA-CMB8.2 can systematically check up to 10 possible paired combinations of fitting species and sources arrays. The best fit pair of arrays are then indicated in their respective windows.

User-set Preferences

In EPA-CMB8.2, the user may set options for maximum iterations for convergence, eligible space tolerances, positions of decimal points in output, receptor concentration units, special calculation alternatives, and performance measure weights for use in Best Fit mode.

Negative Source Contributions

EPA-CMB8.2 calculations can be set to eliminate negative contributions.

Improved Memory Management

EPA-CMB8.2 memory is limited only by the available RAM on the computer, not by pre-set memory limitations.

Flexible Input and Output Formats

Comma-separated value (CSV), xBASE (DBF), and worksheet (WKS) formats are supported as input and output files, in addition to the blank-delimited ASCII text files (TXT) supported by CMB7.

File Handling

EPA-CMB8.2 differs from CMB7 in several ways with regard to the files used by each. EPA-CMB8.2 does not support CMB6 style ambient data and source profile data files. Control file (formerly filenames file), source profile, ambient data, and sample selection file formats differ slightly from CMB7. CMB7 source profile and ambient concentration data files can be read directly by EPA-CMB8.2, however, so backward compatibility is assured. Text output can be directed to the printer, the clipboard, or a report file. A feature of EPA-CMB8.2 is that the computational machinery files (*.exe, *.dll, etc.) need not reside in the same folder as either the input or output files. This facilitates file management.

Miscellaneous Changes

The following items are differences between CMB7 and EPA-CMB8.2 that are not as fundamental as the "featured" ones described above, but which are useful to list.

- An indexing error present in the CMB7 "Autofit" option has been corrected. The error caused a mismatch between sample label and computed source contributions, when VOC data were analyzed.

- The user can define a customized 'Fit Measure' more inclusive than either χ^2 or r^2 alone.

RUNNING EPA-CMB8.2

EPA-CMB8.2 employs an event-driven approach that features a logically organized menu, a system tool bar containing buttons for frequently used functions such as opening files and printing reports, a tabbed page interface, and a status bar. This type of presentation is clear and eliminates the confusion associated with multiple buttons for the same functions. A tabbed interface provides users with visual clues regarding the logical progression of steps necessary to run the model. EPA-CMB8.2 also features robust, context-sensitive Windows-style help, including keyword search. These improvements provide a Windows look-and-feel to the CMB software that is familiar to most users.

Input Files

Figure 1 shows the screen that first appears when EPA-CMB8.2 is launched. Most users will have prepared a *Control File* for a particular CMB application. Control Files are commonly used in air quality models to specify input files that will be invoked during runtime. In EPA-CMB8.2, the Control File would contain the names of the *required* ambient data and source profile data input files, as well as three *optional* selection files for ambient data samples, fitting species, and fitting source profiles. Selection of this mode brings up a Windows browse box for selecting a Control File. If a Control File has not been prepared and the user simply wants to run CMB with particular (freely associated) input files, the other mode should be selected. If *Use Control File* was selected, a browse box appears as shown in Figure 2.

Figure 1. Launching EPA-CMB8.2

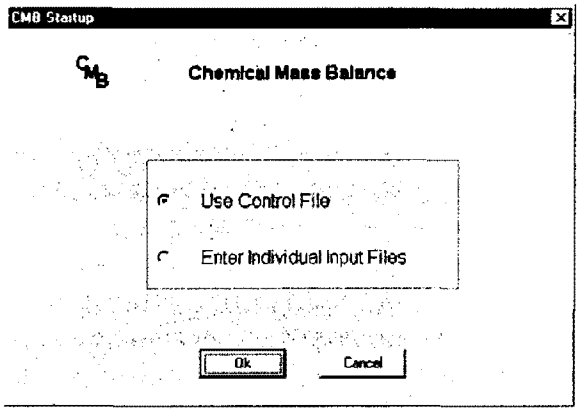
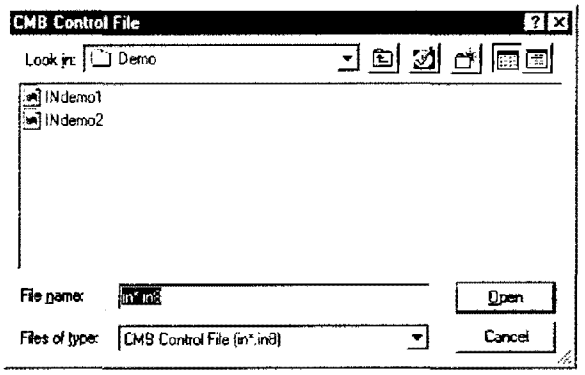


Figure 2. Browse Box for Selecting a Control File



Once a Control File is chosen, the Input Files window appears, as depicted in Figure 3. In the Input Files window, the name of the Control File is prominently displayed across the top, and the various input files it directs appear below. The Control File in use during any session also appears on all screens in the task bar at the top. Even though a Control File has been selected at this point, another one can easily be chosen via its browse box. This is also true for any of the input files (they may be changed or removed via respective browse functions). EPA-CMB8.2 also gives the user the option from this screen to create a new Control File (with the new input file(s)) by using the File/Save function in the upper left-hand corner. If at start-up (Fig. 1) a Control File is not used, an Input Files screen appears as illustrated in Figure 3, except that the Control File name is absent. Files are selected via their respective browse boxes.

EPA-CMB8.2 Options

Several options are available in EPA-CMB8.2 that are selected from the Options tab (Figure 4), where various values and selections may be changed from their default values.

Figure 3. Input Files Screen

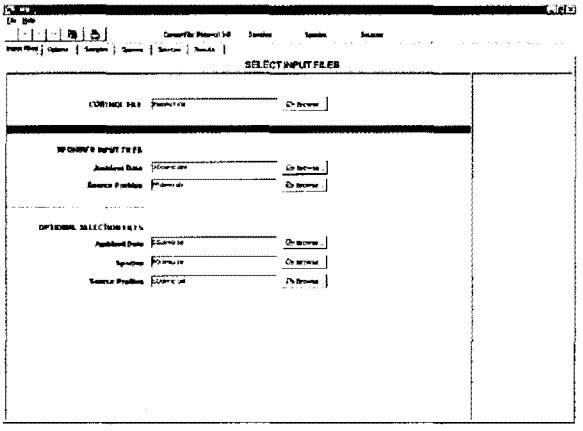
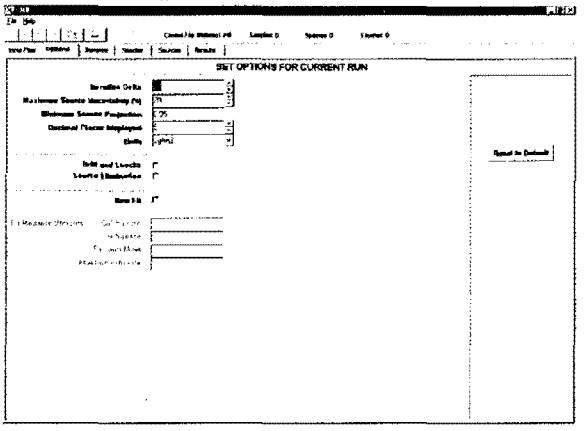


Figure 4. Options for Current Run



Iteration Delta

This parameter sets the maximum number of iterations EPA-CMB8.2 will attempt to arrive at a solution. If no convergence can be achieved, there is probably excessive collinearity for this sample and combination of fitting sources. Its value (default = 20) is adjusted via the scrolling arrows.

Maximum Source Uncertainty / Minium Source Projection

These parameters allow the eligible space collinearity evaluation method of Henry[7] to be implemented with each CMB calculation. The eligible space method uses: 1) maximum source uncertainty; and 2) minimum source projection on the eligible space. The maximum source uncertainty is expressed as a percentage of the total measured mass and is adjustable via the scrolling arrows (default = 20%). The minimum source projection is set to a default value of 0.95, but can be changed in the display field.

Decimal Places Displayed

This parameter sets the number of decimal places displayed in the output window and output files, and depends on the units used in the input data files. This parameter may be adjusted by using the scrolling arrows. The default value is 5 and the maximum value is 6.

Units

The units used for reporting results may be changed via a pull-down menu. Other typical units are available, or one may be created (the number of characters is limited to 5 or less).

Britt and Luecke

Checking this box applies the Britt and Luecke[3] linear least squares solution that is explained by Watson *et al.*[5] when applied to CMB calculations. This option enables a general

solution to the least squares estimation that includes uncertainty in all the variables (i.e., the source compositions as well as the ambient concentrations), whereas the default is the same approximation to the Britt-Luecke algorithm used in CMB7. Note that while the exact Britt-Luecke algorithm must generate a fit whose χ^2 value is equal to or better (i.e., smaller) than that from the approximation algorithm, there is no guarantee that the solution with the better χ^2 will be superior in terms of its physical meaning. Invocation of this option does affect the fit obtained and, as in the case of EPA-CMB8.2's new treatment of collinearity, user experience is necessary to judge the utility in exercising the new Britt-Luecke algorithm.

Source Elimination

Checking this box eliminates *negative* source contributions from the calculation, one at a time. After each fit attempt, if any sources have negative contributions, the source with the largest negative contribution is eliminated and another fit is attempted. This process is repeated until EPA-CMB8.2 finds no sources with negative contributions. Invocation of this option affects the fit obtained by effectively removing collinear sources.

Best Fit

Checking this box causes the program to cycle through the corresponding pairs of fitting species and source profile arrays specified in the source and species selection input windows until the best composite Fit Measure has been achieved. When Best Fit is invoked, EPA-CMB8.2 ignores any arrays of species and sources that may have been selected. The first fitting species array is paired with the first fitting sources array, and so on. EPA-CMB8.2 only attempts a search for a best fit among available corresponding pairs. After a Best Fit has been made the fitting species and fitting sources arrays will be tagged (highlighted) in their respective windows.

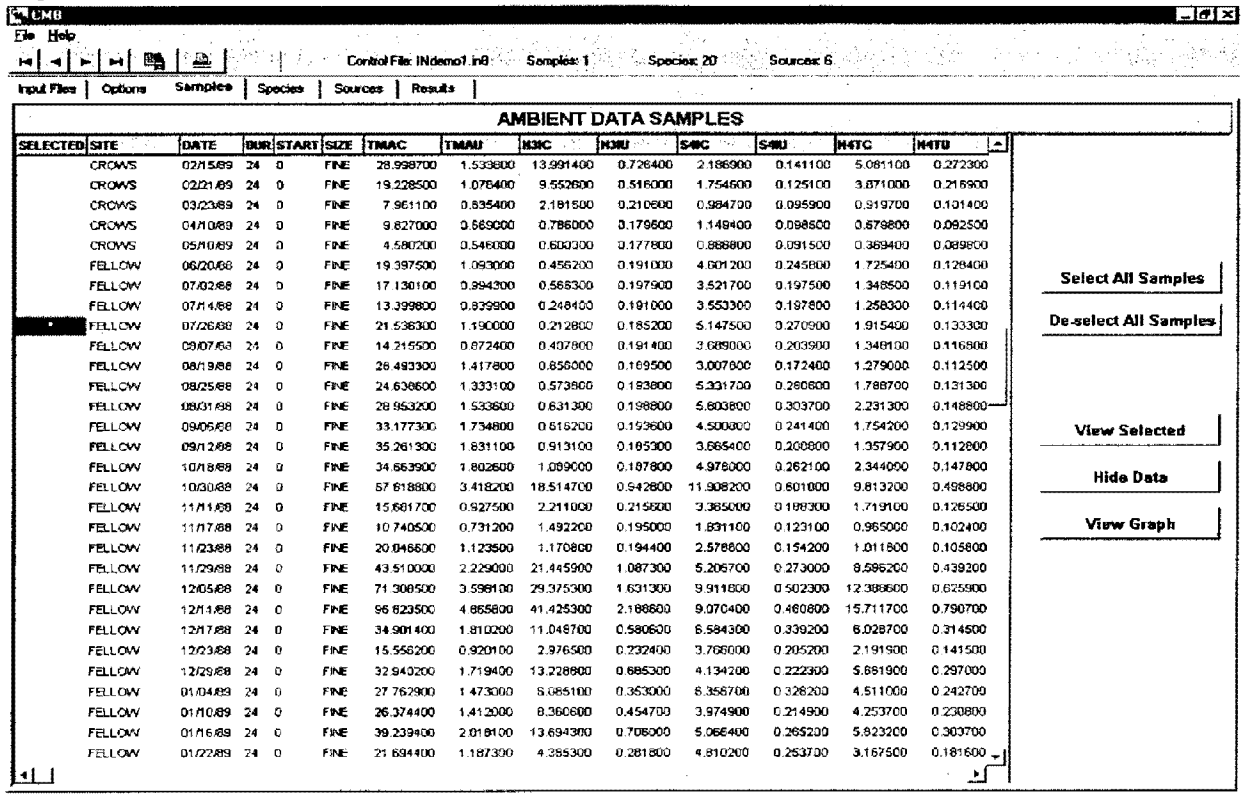
Fit Measure Weight

These are the weights (coefficients) applied to each of the performance measures χ^2, r^2, percent mass, and fraction of eligible sources (number in eligible space divided by number of fitting sources). Adjustment of these weights is not enabled in EPA-CMB8.2 unless Best Fit is invoked. Positive values between 0 and 10,000 may be entered by typing into the appropriate display fields. Defaults are 1.0 for each performance measure weight.

Selecting Ambient Data Samples

The screen for selecting a subset of samples on which source apportionment will be performed is shown in Figure 5. If an (optional) DS*.SEL file is being directed from the Control File, one or more samples may appear selected initially. Otherwise, individual samples are "tagged" by clicking in the respective fields under "SELECTED". Clicking again deselects the sample. Use of Select /Clear All Samples may be also be used to help establish the desired list of samples. A counter displays on the top task bar the number of samples selected at any given time. As indicated, for each sample, the collection date, duration, start hour, and size fraction (particles) are displayed. Show/Hide Data toggle between modes in which speciated data (alternating concentration and uncertainty) for the samples are either shown or masked. Toggling between View Selected/View All determines whether data will be displayed for all selected (tagged) samples only, or for all samples. Use of the "VCR" control buttons on the top task bar can help navigate down a long list of samples.

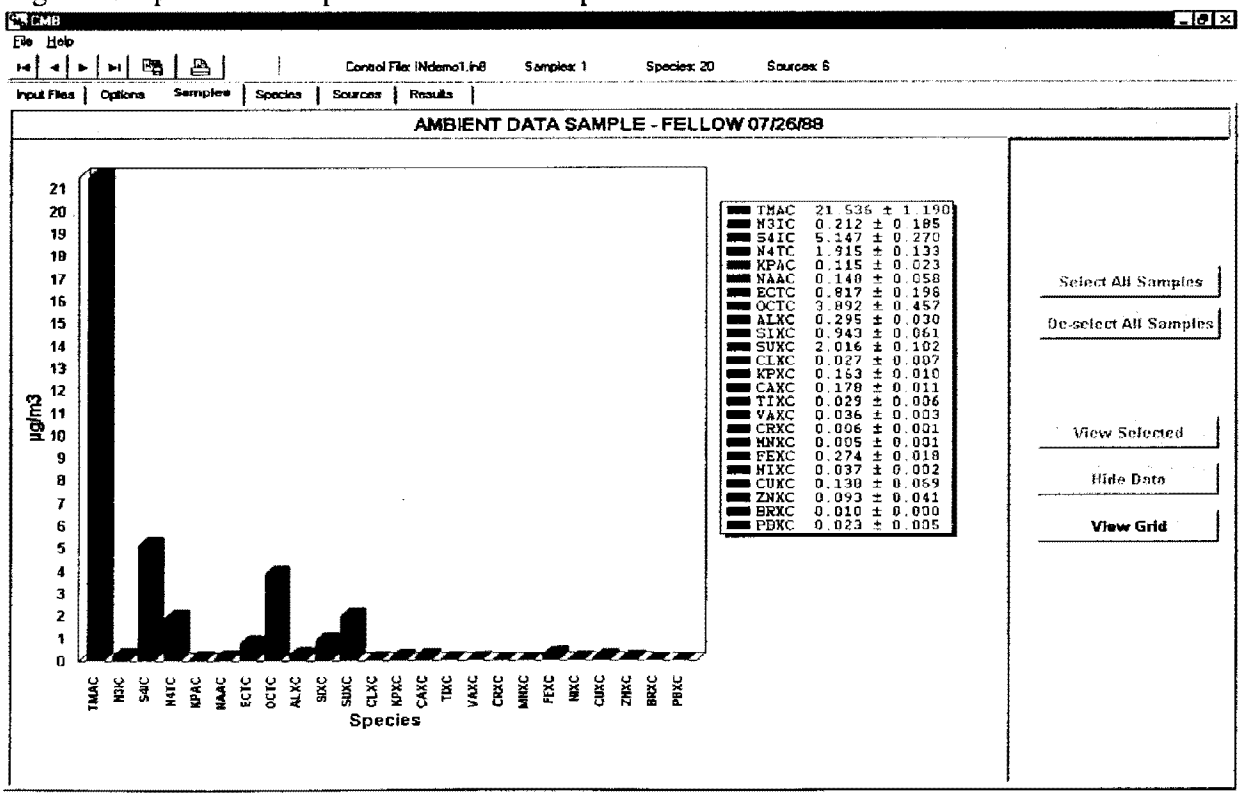
Figure 5. Ambient Data Selection



SELECTED	SITE	DATE	DUR	START	SIZE	TMAC	TMAU	N3C	N3U	S4C	S4U	N4TC	N4TU
	CROWS	02/15/89	24	0	FINE	28.998700	1.533800	13.991400	0.726400	2.186900	0.141100	5.081100	0.272300
	CROWS	02/21/89	24	0	FINE	19.228500	1.076400	9.552600	0.516000	1.754600	0.125100	3.671000	0.216900
	CROWS	03/23/89	24	0	FINE	7.961100	0.835400	2.181500	0.210600	0.984700	0.095900	0.919700	0.101400
	CROWS	04/10/89	24	0	FINE	9.827000	0.569000	0.786000	0.179600	1.148400	0.098600	0.679800	0.092500
	CROWS	05/10/89	24	0	FINE	4.580200	0.546000	0.600300	0.177800	0.888800	0.091500	0.369400	0.089800
	FELLOW	06/20/88	24	0	FINE	19.397500	1.093000	0.456200	0.191000	4.601200	0.245800	1.725400	0.128400
	FELLOW	07/02/88	24	0	FINE	17.130100	0.994300	0.565300	0.197900	3.521700	0.197500	1.348500	0.119100
	FELLOW	07/14/88	24	0	FINE	13.399800	0.939900	0.248400	0.191000	3.553300	0.197600	1.258300	0.114400
	FELLOW	07/26/88	24	0	FINE	21.536300	1.190000	0.212800	0.185200	5.147500	0.270900	1.915400	0.133300
	FELLOW	08/07/88	24	0	FINE	14.215500	0.872400	0.407800	0.191400	3.689000	0.203900	1.346100	0.116800
	FELLOW	08/19/88	24	0	FINE	26.493300	1.417800	0.856000	0.169500	3.007800	0.172400	1.279000	0.112500
	FELLOW	08/25/88	24	0	FINE	24.638600	1.333100	0.573800	0.193800	5.331700	0.260800	1.788700	0.131300
	FELLOW	08/31/88	24	0	FINE	28.953200	1.533800	0.631300	0.198800	5.803800	0.303700	2.231300	0.148800
	FELLOW	09/06/88	24	0	FINE	33.177300	1.734800	0.815200	0.193600	4.500800	0.241400	1.754200	0.129900
	FELLOW	09/12/88	24	0	FINE	35.261300	1.831100	0.913100	0.185300	3.665400	0.208800	1.357900	0.112800
	FELLOW	10/18/88	24	0	FINE	34.663900	1.802600	1.089000	0.187800	4.978000	0.262100	2.344000	0.147800
	FELLOW	10/30/88	24	0	FINE	57.618800	3.418200	18.514700	0.942800	11.908200	0.601000	9.813200	0.498800
	FELLOW	11/11/88	24	0	FINE	15.681700	0.927500	2.211000	0.215600	3.365000	0.188300	1.719100	0.126500
	FELLOW	11/17/88	24	0	FINE	10.740500	0.731200	1.492200	0.195000	1.891100	0.123100	0.965000	0.102400
	FELLOW	11/23/88	24	0	FINE	20.046800	1.123500	1.170800	0.194400	2.578600	0.154200	1.011800	0.105800
	FELLOW	11/29/88	24	0	FINE	43.510000	2.229000	21.445900	1.087300	5.206700	0.273000	8.596200	0.439200
	FELLOW	12/05/88	24	0	FINE	71.308500	3.598100	29.375300	1.631300	9.911800	0.502300	12.388600	0.625900
	FELLOW	12/11/88	24	0	FINE	96.823500	4.865600	41.425300	2.188600	9.070400	0.460800	15.711700	0.790700
	FELLOW	12/17/88	24	0	FINE	34.901400	1.810200	11.048700	0.580600	6.584300	0.339200	6.028700	0.314500
	FELLOW	12/23/88	24	0	FINE	15.556200	0.920100	2.976500	0.232400	3.766000	0.205200	2.191900	0.141500
	FELLOW	12/29/88	24	0	FINE	32.940200	1.719400	13.228800	0.685300	4.134200	0.222300	5.661900	0.297000
	FELLOW	01/04/89	24	0	FINE	27.762900	1.473000	8.085100	0.353000	6.358700	0.328200	4.511000	0.242700
	FELLOW	01/10/89	24	0	FINE	26.374400	1.412000	8.360600	0.454700	3.974900	0.214900	4.253700	0.230800
	FELLOW	01/16/89	24	0	FINE	39.239400	2.018100	13.694300	0.706000	5.066400	0.265200	5.823200	0.303700
	FELLOW	01/22/89	24	0	FINE	21.694400	1.187300	4.385300	0.281800	4.810200	0.263700	3.167500	0.181600

For any sample displayed, clicking View Graph will provide a bar chart such as shown in Figure 6. This graph is useful to verify that input data files have been properly read. View Grid returns to the ambient data selection screen.

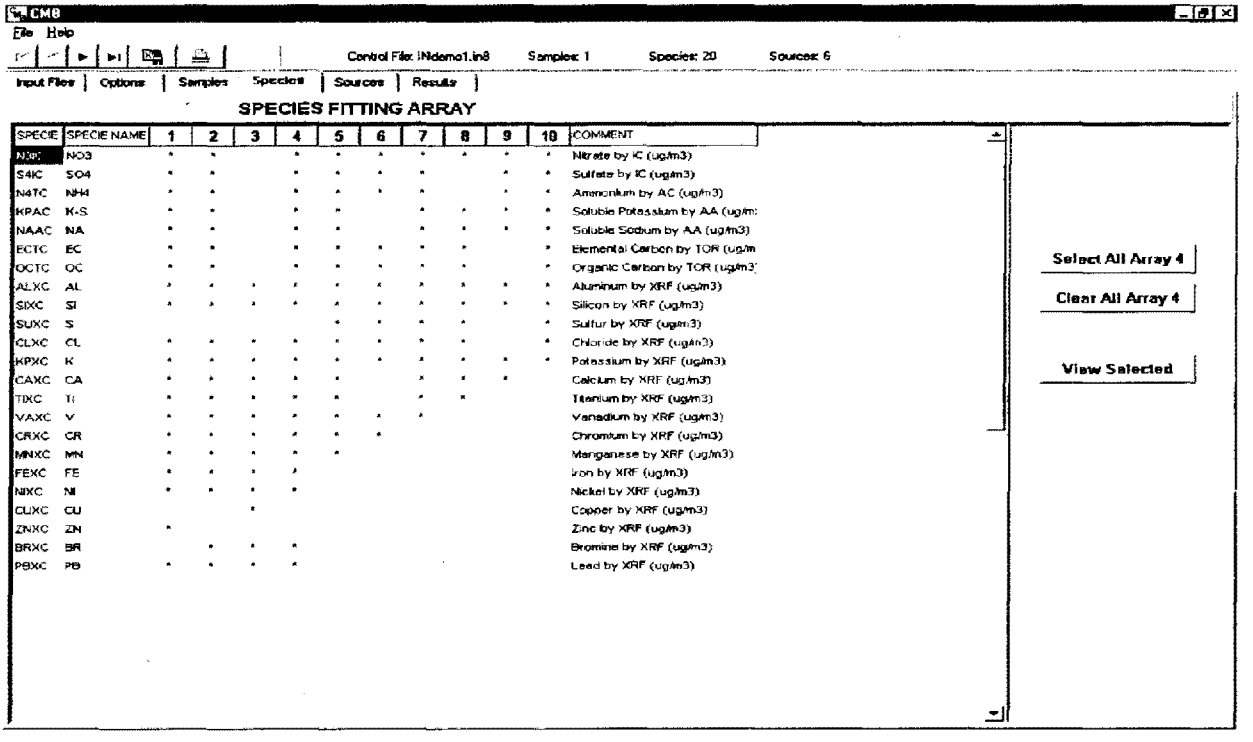
Figure 6. Speciation Graph for Ambient Sample



Selecting Fitting Species

Fitting species are used in the calculation of source contribution estimates. Species not included in this calculation are termed *floating* species. The comparison of calculated and measured values for floating species is part of the model validation process. Fitting species should be selected that are major or unique components of the source types influencing the receptor concentrations. The screen for selecting fitting species is shown in Figure 7. This screen is initiated by data read from the (optional) species selection file (PO*.SEL). Species contained in the selection file are listed down the left-hand side and a field of up to 10 arrays is provided. At start-up, the first array (in a series) will always be initially selected as a default. Other arrays may be selected by clicking on the array index (1 - 10). Within a given array, species may be added or removed by clicking in the appropriate field. Select/Clear All Array X may also help in configuring a selection array. Use of the "VCR" control buttons can help navigate down a long list of species, and a counter displays on the top task bar the number of species tagged for any selected array. For a selected array, toggling between View Selected/View All determines which species will be displayed. This can be handy for a long list of species that would be impossible to display on the screen. If comments are provided in the selection file, they will be displayed on the right-hand side.

Figure 7. Fitting Species Arrays



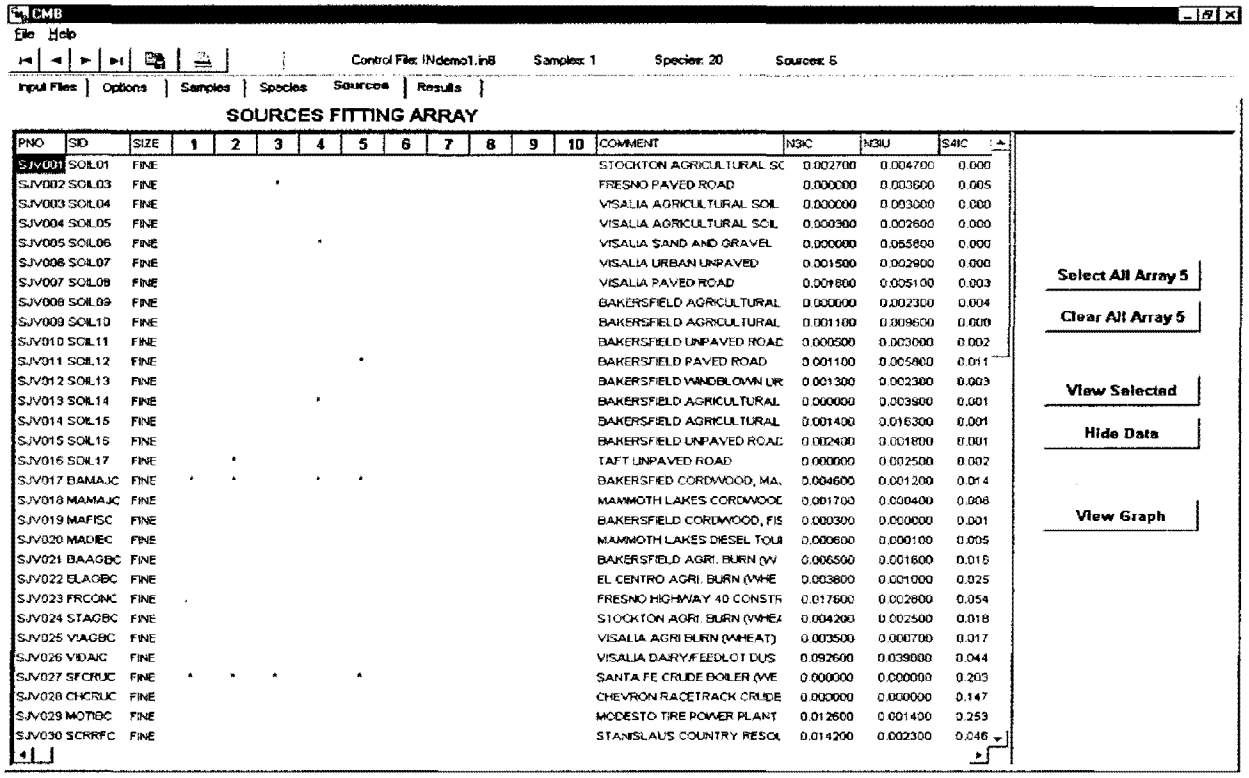
Multiple arrays for fitting species are useful when CMB calculations are performed on samples from several locations or during different times of the year that have different contributors. They are also used by the Best Fit option to cycle through different source combinations until the weighted Fit Measure is optimized.

Selecting Fitting Sources

For fitting sources the user should select profiles that represent the emissions most likely to influence receptor concentrations. The screen for selecting fitting sources is shown in Figure 8. This screen is initiated with data read from the (optional) species selection file (SO*.SEL).

Source profiles contained in the selection file are listed down the left-hand side and a field of up to 10 arrays is provided. As with fitting species, arrays are selected by clicking on the array index (1 - 10). Select/Clear All Array X, "VCR" control buttons, and View Selected/View All buttons function as described above for fitting species. Note that a counter displays on the top task bar the number of source profiles tagged for any selected array.

Figure 8. Fitting Sources Arrays



As for ambient samples, clicking View Graph will provide a bar chart for any source profile (selected or not) for which any field is filled with blue. This graph, similar to the one shown in Figure 6 for ambient samples, is useful for exploratory work. The graph helps to verify that input data files have been properly read and to identify abundant components in each profile.

Results

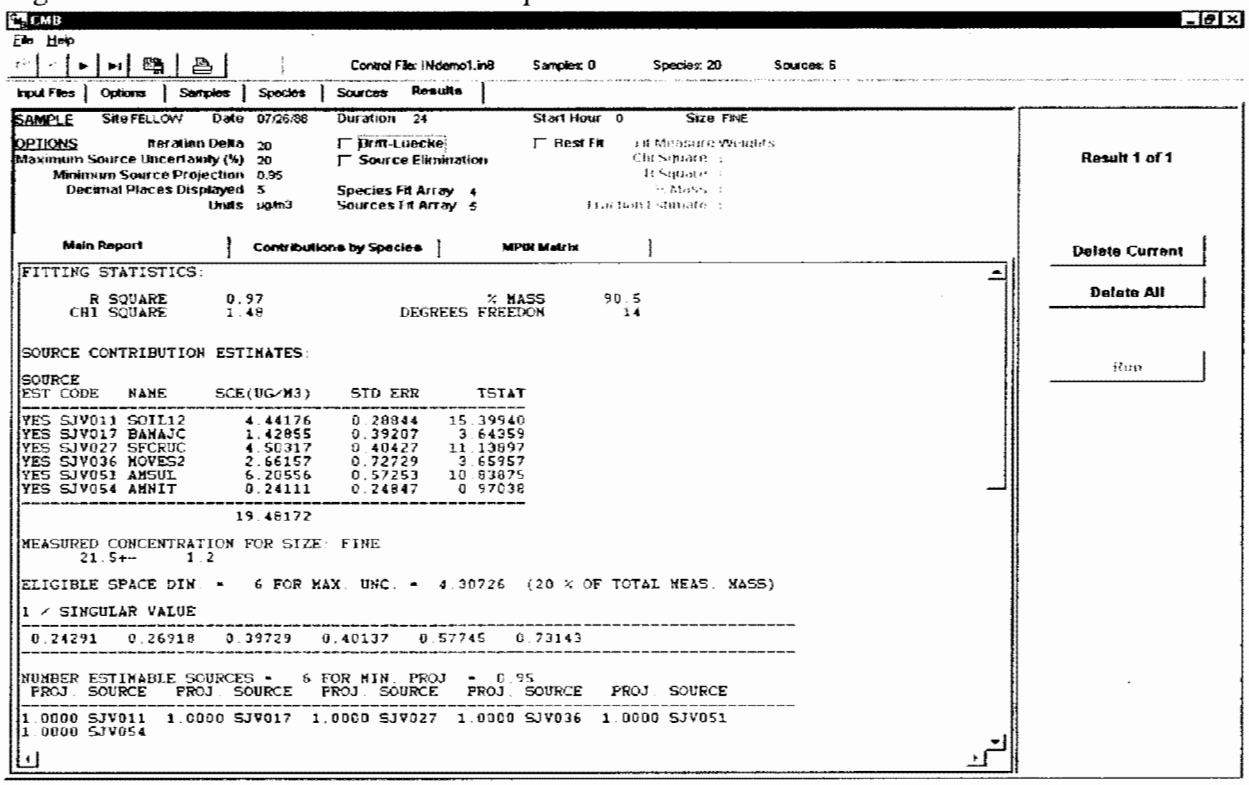
Calculations are initiated from the Results screen, where fitting results and statistics are also reported for examination. When Run is invoked, EPA-CMB8.2 performs the least-squares estimation of source contribution estimates and performance measures on the selected sample data using the designated fitting species and source profiles. If more fitting sources than fitting species have been selected, a warning appears and the user is forced to reconfigure before calculation will proceed.

Main Report

EPA-CMB8.2 attempts fits of all samples selected. If multiple samples were selected (*batch mode*), as each sample is apportioned, results are successively written to the output window as part of the Main Report (Figure 9). For any (*current*) result displayed in the output window, the header at the top reflects basic identifying information pertaining to the sample that has been apportioned and an echo of the options settings. The species and source profile fitting array indices are also indicated. For multiple samples, the number will be reflected in the box in

the upper right-hand corner. Viewing any sample result in a series is quite easy with the use of the VCR buttons on the task bar. Using appropriate buttons, the current or all results may be deleted from the output window. A report may be printed for any/all sample results via the *print* button on the task bar.

Figure 9. Calculation Results - Main Report

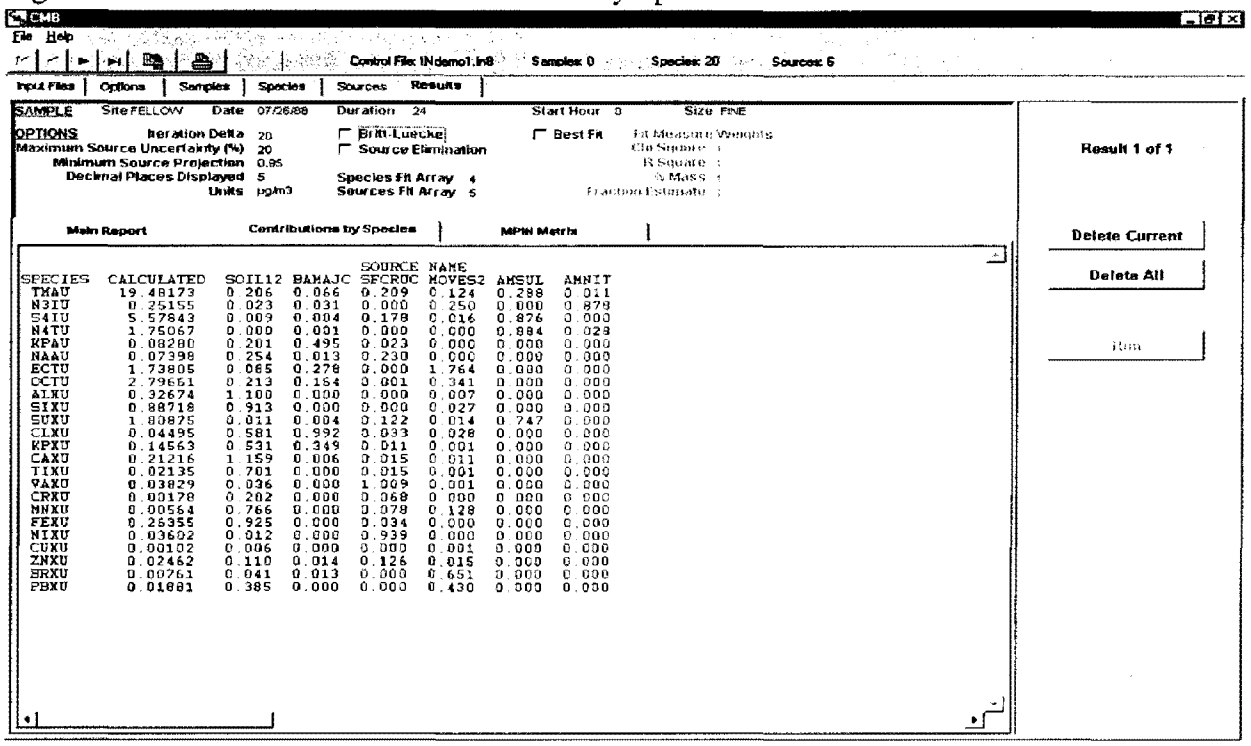


In the Main report are several information blocks which present performance measures. First are fitting statistics: r^2, χ^2, percent mass explained, and degrees of freedom. Next is a block that presents the most basic results from EPA-CMB8.2: source contribution estimates. For each source selected is presented a source contribution estimate (SCE) in user-chosen units, standard errors, and values for T-stat. The field 'EST' under 'SOURCE' indicates (YES or NO) whether a source's contribution was estimable by EPA-CMB8.2. The next block is the eligible space display: an echo of the measured concentration and error for the sample, eligible space dimension for the chosen maximum uncertainty, inverse singular values, the number of estimable sources for the chosen minimum source projection, and estimable linear combinations of inestimable sources. Finally (not shown), there is a block listing species concentrations. Shown for each species (fitting species are tagged with asterisks) is its measured and calculated mass and uncertainty, the ratio of calculated/measured mass (± uncertainty factor), and the ratio of the residual (calculated - measured mass) to the uncertainty.

Contributions by Species

It is also of interest to analyze the way in which pollutant mass is distributed among sources by species. This distribution is presented in the report Contributions by Species (Figure 10). This report provides one more dimension to the Species Concentrations block in the Main Report. These results are useful when source contributions to species other than total mass are of interest. The report also indicates which sources are the major and minor contributors to each species. As with the Main Report, a print-out of Contributions by Species may be obtained for the current sample result via the *print* button on the task bar.

Figure 10. Calculation Results - Contribution by Species



SPECIES	CALCULATED	SOIL12	BAMAJC	SOURCE NAME SECROC	MOVES2	AMSUL	AMNIT
TMAU	19.48173	0.206	0.066	0.209	0.124	0.288	0.011
N3IU	0.25155	0.023	0.031	0.000	0.250	0.000	0.878
S4IU	5.57843	0.009	0.004	0.178	0.016	0.876	0.000
N4TU	1.75067	0.000	0.001	0.000	0.000	0.884	0.028
KPAU	0.08280	0.201	0.495	0.023	0.000	0.000	0.000
NAAU	0.07398	0.254	0.013	0.230	0.000	0.000	0.000
ECTU	1.73805	0.065	0.278	0.000	1.764	0.000	0.000
OCTU	2.79661	0.213	0.154	0.001	0.341	0.000	0.000
ALKU	0.32674	1.100	0.000	0.000	0.007	0.000	0.000
SIXU	0.88718	0.913	0.000	0.000	0.027	0.000	0.000
SUXU	1.80875	0.011	0.004	0.122	0.014	0.747	0.000
CLXU	0.04495	0.581	0.992	0.033	0.028	0.000	0.000
KPXU	0.14563	0.531	0.349	0.011	0.001	0.000	0.000
CAXU	0.21216	1.159	0.006	0.015	0.011	0.000	0.000
TIXU	0.02135	0.701	0.000	0.015	0.001	0.000	0.000
VAXU	0.03829	0.036	0.000	1.009	0.001	0.000	0.000
CRXU	0.00178	0.202	0.000	0.068	0.000	0.000	0.000
MNXU	0.00564	0.766	0.000	0.078	0.128	0.000	0.000
FEXU	0.26355	0.925	0.000	0.034	0.000	0.000	0.000
NIXU	0.03602	0.012	0.000	0.939	0.000	0.000	0.000
CUXU	0.00102	0.006	0.000	0.000	0.001	0.000	0.000
ZNXU	0.02462	0.110	0.014	0.126	0.015	0.000	0.000
SRXU	0.00761	0.041	0.013	0.000	0.651	0.000	0.000
PBXU	0.01081	0.385	0.000	0.000	0.430	0.000	0.000

Modified Pseudo-Inverse Normalized (MPIN) Matrix

Another report that may be of interest is the Modified Pseudo-Inverse Normalized (MPIN) matrix (not shown). The MPIN matrix identifies which fitting species have the largest influence on the source contribution estimates from each profile. Examining these weights suggests sensitivity tests to determine the extent to which source contributions vary with changes in profile abundances or the selection of fitting species. As with the Main Report and Contributions by Species, a printout of the MPIN matrix may be obtained.

CONCLUSION

Features of the new version of CMB software (EPA-CMB8.2) have been described. The model requires additional *beta* testing to reveal and resolve problems before a final version can be released by EPA. It is anticipated that EPA-CMB8.2 will significantly increase the convenience, efficiency and accuracy of performing receptor modeling by the CMB method.

DISCLAIMER

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7. Author(s) C. Thomas Coulter, Robert A. Wagoner, Charles W. Lewis	8. Performing Organization Report No.
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16. Abstract

The Chemical Mass Balance (CMB) method has been a popular approach for receptor modeling of ambient air pollutants for over two decades. For the past few years the U.S. Environmental Protection Agency's Office of Research and Development (ORD) and Office of Air Quality Planning and Standards (OAQPS) have collaborated to develop a new generation of CMB software, CMB8. Developmental work was initiated under EPA contract by the Desert Research Institute and is being continued by Pacific Environmental Services. The current version, EPA-CMB8.2, incorporates the upgrade features that CMB8 has over CMB7, but also addresses problems identified with CMB8 and has been reconfigured and enhanced for a more robust and user-friendly system.

17. KEY WORDS AND DOCUMENT ANALYSIS

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