INVERT

Version 4.103

USERS GUIDE

Date: 2008-12-16

INDEX

1. START-UP

Command line syntax

In the next sections „<name>“ stands for the name of the executable: usually „invert“.

<name>	equivalent to: <name> -P
<name> -P	writes keyboard input to standard protocol-file
<name> -P PFILE	writes keyboard input to protocol-file PFILE
<name> -p	reads keyboard input from standard protocol-file
<name> -p PFILE	reads keyboard input from protocol-file PFILE
<name> -s	shows the size of the reserved memory and (after the calculation) of the actually used memory for different data types
<name> -w	suppresses some warning messages.
<name> -C CFILE	writes example of array size hints to configuration-file CFILE
<name> -c CFILE	reads array size hints from configuration-file CFILE (namelist directed). The given sizes are minimal values, indicating how much memory will be allocated at program start. But these values will be automatically increased when more memory is required.
<name> -b	batch mode: deactivate interactive input during iterations.

Protocol file

1. When the program asks for the observations file (the first question), then typing one of the characters > or < instead of a file name has the same effect as the -p and -P options described above. Then the program asks again for the observations file, but without interpreting the result as -p or -P options.

>	is equivalent to	-P
>FILE	is equivalent to	-P FILE
<	is equivalent to	-p
<FILE	is equivalent to	-p FILE

2. The standard protocol-file is named '<name>.inp'.

3. Every third line in the protocol-file represents the last keyboard input. This input might be changed, ONLY if the preceding line does NOT start with '#', otherwise the input values will be read in the wrong order.

4. Input starting with '<' represents the default value. The input following this character is NOT read from this file, but the default value for the actual run will be used instead.

5. Input starting with '>' resumes input from keyboard.

6. Only every third line is used for input. The two preceding lines are never read, and may be changed or left blank.

Interaction with the shell

If the answer to any question begins with a $-sign, then some shell commands can be executed:

$	Invokes a new shell; then any shell commands can be used. The usual way to return to INVERT will be typing „exit“, but this depends on the actual shell.
$DIR	Changes the working directory of INVERT for reading and writing files.

After returning to INVERT, the program shows the actual working directory.

2. RUN-TIME INPUT PARAMETERS

After each numerical parameter, the units are indicated within parenthesis: [ ].
[σ] is a ratio relative to the a-priori standard deviation
[**parameter**] is a ratio relative to a previously defined run-time parameter
[number] is a counter
[none] is a unit less number without physical meaning

Erroneous previous input parameters can be corrected by entering one or more q's instead of the actually requested parameter:
q requests for the last parameter entered.
qq requests for the first parameter of the last connected block of parameters (implicating a bigger steps backwards than **q**).
qqq quits the program completely.

General

- Name of observations file

  Any file name is allowed, including drive and/or directory names.

  When no file name is defined (only the RETURN-key pressed), then a sample definition file is produced, named *def* if no file with this name exists.

  When a question mark is typed, then the maximum size of the model parameters is shown.

- Name of definitions file

  Any file name is allowed, including drive and/or directory names.

  When the file name consists of a prefix (p...p) before the period and a suffix (**.**sss) consisting of 3 characters behind the period (p...p**.**sss), then the output files will have the same prefix, while the suffix is replaced as defined in the *Output files* description part in this paper. When the file name doesn't meet these requirements, the suffix of the output files is simply appended to the complete file name of the definition file.

- Multiplier of standard deviation **msd** [σ]

  Changes the weight of the a-priori information with respect to the observations (computes **s' = msd** ∗ **s,** where **s** are the values in line '**s**' for independent variables).

  Special cases:

  msd = 0 (for **s** = 0 (fixed variables): no effect (**s'** = **s** = 0))

  The user will be asked, whether only bound variables have to be kept fixed:
  for **s** > 0 (bound variables): kept fixed (equivalent to **s** = 0)
  for **s** < 0 (free variables): no effect, stay free (**s'** = **s**)

  Or all variables have to be kept fixed:
  for **s** > 0 (bound variables): kept fixed (equivalent to **s** = 0)
  for **s** < 0 (free variables): kept fixed (equivalent to **s** = 0)

  msd < 0 (for **s** = 0 (fixed variables): no effect (**s'** = **s** = 0))

The user will be asked, whether bound variables have to be set free:

for **s** > 0 (bound variables):	set free (**s'** = **msd** * **s**)
for **s** < 0 (free variables):	no effect, stay free (**s'** = **s**)

Or free variables are to be bound:

for **s** > 0 (bound variables):	no effect, stay bound (**s'** = **s**)
for **s** < 0 (free variables):	get bound (**s'** = **msd** * **s**)

- Algorithm option defining the kind of algorithm to be used for optimisation.

  The **inversion algorithm** (Levenberg-Marquardt algorithm) is a direct or iterative inversion algorithm giving the least-squares solution for linearised observation equations.

  The **evolutionary algorithm** creates a number of models (population) at random, selects the best ones according to the least squares criterion, replaces the worse ones by copies of the best ones while making small changes on the variable values (mutations). The process of selecting, copying and mutation is iterated until no improvement is achieved any more. The genetic algorithm is a special case, where a new model is not a copy of *one* old model with mutations, but a mixture of variable values of *two* old models.

Inversion Algorithm

- Multiplier of data standard deviation **mdsd** [σ_d]

  Changes the weight of the observations with respect to the a-priori information (computes σ_d' = **mdsd** $*$ σ_d, where σ_d are the values in column '**s**' of the observations file). This parameter **mdsd** represents the parameter (usually called λ) of the Tikhonov L-curve, which depicts the fit of the a-priori information relative to the fit of the observations. Note that increasing the absolute value of this parameter has the inverse effect as decreasing the absolute value of the previously defined parameter **msd**: multiplier of standard deviation (of variables); except for some side effects of negative **msd**, they are each others reciprocals.

  Special cases:

  -1 < **mdsd** ≤ 0 not allowed

  mdsd > 0 Varying **mdsd** at subsequent runs of INVERT will provide the coordinates of the Tikhonov L-curve. The optimal value is reached when at a given change rate of **mdsd** the improvement of fit of a-priori information is equal to the deterioration rate of fit of the observations (the "corner" of the L-curve).

  mdsd <= -1 The initial value of |**mdsd**| will be adapted after each iteration to achieve a equal weighted squared sum of errors of the a-priori information and of the observations. This provides a means to reduce the assumed quality of the observations to be in equilibrium with the quality of the a-priori information, which is assumed to be given well by the a-priori (co-)variances. The quality of the observations will never be assumed to be better than their given standard deviation in the observations file.

- Differentiation distance **dd** [σ']

  Partial differentiations, which are necessary to compute the Jacobian of the observation equations y(x) are performed numerically by evaluating y(x) at the last variable estimate x^0, and at x^0 + |**dd**|∗σ'. Where σ' is the minimum of 1) the a-priori (or normalizing) standard deviation in line '**s**', 2) the criterion standard deviation in line '**c**', 3) the a-posteriori standard deviation (only when the Choleski-decomposition is performed, s. below).

  Special cases:

  dd = 0 not allowed

  dd < 0 extend normal matrix from $\sum_i \frac{\partial y_i(x^0)}{\partial x_k}\frac{\partial y_i(x^0)}{\partial x_l}$ in case of **dd** > 0, to complete Hessian of F-test criterion for extremely non-linear models:

$$\sum_i \left[\frac{\partial y_i(x^0)}{\partial x_k}\frac{\partial y_i(x^0)}{\partial x_l} - \left(\tilde{y}_i - y_i(x^0)\right)\frac{\partial^2 y_i(x^0)}{\partial x_k \partial x_l} \right]$$

- Adaptive damping factor **adf** [$1/\sigma^2$]

  For non-linear problems the solution is damped by imposing that the change of variables in each iteration is equal to zero, with a variance equal to 1/**adf** ∗ σ^2. Strong damping is achieved by large **adf**; decreasing **adf** reduces damping. During iteration **adf** will be decreased when the solution improves, and increased when the solution gets worse. For the computation of the (co)variances of variables, the damping is removed (**adf** = 0). When the solution is underdetermined at iteration **nit**, iteration will continue with increasing **adf** until a well-determined solution is found.

  Special cases:

  adf = 0 no damping; to be used for fast computation of linear problems
  adf < 0 damping will be kept constant at |**adf**| as long as solution improves. When the solution gets worse, **adf** will increase; when solution stagnates, **adf** will decrease as normal.

- F-test improvement limit **fil** [σ^2]

  Computation will stop when the change of F-test-value is smaller then **fil** *and* the mean weighted squared change of variables is smaller than $\mathbf{fil}^{½} * \sigma$, both being true for at least 4 iterations. Only when the F-test increases by less than **fil** with infinite variance limit, the iteration will stop immediately.

  Special cases:

  fil > 0 weights of the change of variables by the a-posteriori covariance matrix.
  (**fil** = 0) iteration will stop, when change of F-test and the change of variables is exactly zero.
  fil < 0 weighting of the change of variables by the criterion standard deviations.

- Number of iterations **nit** [number]

  Computation will stop after at most **nit** iterations. When the F-test improvement limit is reached before, computation may stop earlier.

  Special cases:

(**nit** = 0)	no optimisation; to be used for forward modelling of data in **.def**-file
nit < 0	Iteration will temporary halt after |**nit**| iterations and ask for a new number of iterations and/or change the other algorithm parameters.

- Inversion method is either a direct inversion algorithm of the triangular **Cholesky-decomposition** of the normal matrix, or an iterative **conjugate-gradients** minimization of the normal equations. The **regularized Cholesky-decomposition** and the conjugate-gradients method allow for regularization, and will give a (mathematical) solution of even singular problems.

- Cholesky: singularity limit **csl** [σ]

  The inverse a-posteriori covariance matrix will be assumed to be singular as soon as one pivot of the Cholesky decomposition is smaller than **csl** . The regularized Cholesky-decomposition will regularize this matrix by some diagonal matrix with a „small“ norm.

  Special cases:

(**csl** = 0)	regularization only if matrix is numerically singular to machine precision
csl < 0	not allowed

- CG: Convergence criterion **ccc** [σ]

  The iterations of the CG-algorithm will stop as soon the relative (to σ-weighted right side) error of the solution of the normal equations is smaller than **ccc**. This implies some kind of regularization.

  Special cases:

(**ccc** = 0)	iteration will stop when no improvement occurs
ccc < 0	not allowed

- CG: Number of iterations **cnit** [number]

  The iterations of the CG-algorithm will stop after at most **cnit** iterations. When the convergence criterion is fulfilled before, iteration may stop earlier. This implies some kind of regularization.

  Special cases:

cnit $\leq$ 0	not allowed

Evolutionary Algorithm (including genetic algorithm)

- Size of population **npop** [number (of models)]

  Total number of models to be sorted according to fitness (F-test value)

  Special cases:

npop < 2	not allowed
npop < 4	not allowed for genetic algorithm (**ir** > 0)

- Size of parents population **npar** [number (of models)]

  Number of best models (according to F-test), which are, by combining (crossing-over) and changing (mutation), the basis of a new generation of models.

  Special cases:

npar < 1	not allowed
npar < 2	not allowed for genetic algorithm (**ir** > 0)

- Life span **ls** [number (of iterations)]

  A model will be replaced by a random one, when it exists for more than **ls** iterations. When a model is the basis (parent) of a model with a smaller F-test value than its own, than its age is reduced by 1 iteration, and therefore its life span increased by 1 iteration.

  Special cases:

ls = 0	models will last forever, when no better ones are generated
ls < 0	not allowed

- Discrimination limit **dl** [σ]

  When root mean squared weighted (by σ) difference of the variables of two models is smaller than **dl**, than the worst one will be replaced by a random model (starting from model in line '**m**' and according to initial mutation rate **mr**).

  Special cases:

(**dl** = 0)	only when two models are exactly equal, one will be replaced
dl < 0	not allowed

- Initial scattering **is** [σ]

  The variable values of initial population will be created by scattering around the starting values (line '**M**') and, in case **is** > 0 around the a-priori values (line '**m**'). When the actual run is a restart with option '**b**' after a previous evolutionary algorithm, then the initial population equals the last population of the previous run, so **is** will not be used.

  Special cases:

is > 0	initial population from Gauss-distributed models over the model space around the starting and a-priori variable values with a standard deviation of σ∗**is**.
is = 0	not allowed
is < 0	initial population from uniformly distributed models over model space around the starting variable values (**M**-σ∗|**is**| < **M'** < **M**+σ∗|**is**|).

- Mutation rate **mr** [σ]

  Each variable of a newly generated model will be changed randomly starting from the values copied from its parent(s), with a standard deviation of **mr** ∗ σ for the first generation.

  Special cases:

mr = 0	no mutation will take place for genetic algorithm (0 ≤ **ir** ≤ 1), not allowed otherwise (**ir** < 0)
mr < 0	not allowed

- Change of mutation rate **cmr** [**mr**]

  The mutation rate of each variable of a model will change by a factor defined by **cmr**:

cmr > 1	random change of the parent models mutation rate $\mathbf{mr}_{par}$ between $\mathbf{mr}_{par}$/**cmr** and $\mathbf{mr}_{par}$∗**cmr** with expectation $\mathbf{mr}_{par}$ (only applied to new models)
cmr = 1	no change of mutation rate
0 < **cmr** < 1	decrease of mutation rate of all parent models at every iteration i from initial $\mathbf{mr}_{i-1}$ to $\mathbf{mr}_{i-1}$∗**cmr**
cmr ≤ 0	not allowed

- Inversion rate **ir** [**npop – npar**]

  In a genetic algorithm new models are created by combining the values of one part of one parent model with the values of variables of the complementary part of the other parent model. A 'part' is a set of subsequently numbered variables (random numbered for the first generation). The inversion rate determines the number of models for which the numbering of the variables will be (randomly) changed. A good inversion rate is high enough for a reasonable probability of appropriate variable values to come together, while being low enough not to split such combinations too often.

  Special cases:

ir > 1	not allowed
0 ≤ **ir** ≤ 1	apply genetic algorithm
ir < 0	apply non-genetic evolutionary algorithm

- Seed of random value generator **seed** [none]

  Only the same value for **seed** in different runs will reproduce same results, when all other data are left unchanged too. Other values will produce differing sample tests at random.

  Special cases:

seed < 0 not allowed

- F-test improvement limit **fil** [σ^2]

  Computation will stop when the change of the mean F-test-value over the whole parents population (**npar**) is smaller then **fil** for at least **nit**/4 iterations after the last improvement of the best model ever since.

  Special cases:

  (**fil** = 0) stops iteration if change of F-test is exactly 0
  fil < 0 not allowed

- Number of iterations **nit** [number]

  Computation will stop after at most **nit** iterations. When the F-test improvement limit is reached before, computation may stop earlier.

  (**nit** = 0) create population, sort according to fitness and stop
  nit < 0 Iteration will temporary halt after |**nit**| iterations and ask for a new number of iterations and/or change the other algorithm parameters.

- Number of output models **nom** [number]

  (**nom** = 0) only output of best model ever since, not of models of last population
  nom < 0 not allowed

General

- Output in definitions file:

  Next options control the amount of output items in the definitions file. Multiple selections are usually allowed, some options are only conditionally available:

  a output all items
  l linearity test
  R eigenvalues of resolution
  C eigenvalues of covariance
  r resolution matrix
  c correlation matrix
  s a-posteriori standard deviation
  M adjusted variables (compressed)
  m adjusted variables (extended)
  n no output of any of these items

  Special cases:

  M instead of **m** suppresses the output similar to the input of a definitions file, but lists in a compact way only the adjusted variable values of the model bodies; incompatible with option **m**.
  l can only be chosen in combination with **C**

a has priority over all other options
n is not allowed in combination with any other option.

- Output in separate file:

  Next options control the amount of output items in the separate files, which have been described above. Multiple selections are usually allowed, some options are only conditionally available:

  a output all items
  i iteration results (variable values and statistics per iteration step)
  V vectors and matrices (incl. 2nd derivative) in **.vec**-file
  v vectors and matrices (excl. 2nd derivative) in **.vec**-file
  e eigenvectors as definitions file with option **eC** in **.dfc**-file, with option **eR** in **.dfr**-file
  l linearity test in **.evc**-file
  R eigenvalues of resolution in **.evr**-file
  C eigenvalues of covariance in **.evc**-file
  r resolution matrix in **.rsl**-file
  c correlation matrix in **.cor**-file
  M model data (input & output) in **.plt**-file
  m model data (only output) in **.plt**-file
  n no output in any file

  Special cases:

  l can only be chosen in combination with **C**
  e only in combination with **C** or **R**: creates a eigenvectors-file like a definitions file.
  v returns the linearised model matrix (Jacobian) of the optimum iteration, the a-priori and a-posteriori observations, variables and their respective standard deviations, the inequality constraints, and, when explicitly defined, the a-priori correlation matrix
  V additionally to the output of **v** the second derivatives matrix will be returned; incompatible with **v**
  M incompatible with **m**
  a has priority over all other options
  n is not allowed in combination with any other option.

- Output of observations results

  R output residuals in **.res**-file and also the standard deviation of these residuals.
  r output residuals in **.res**-file but do not calculate their standard deviations.
  o output of model effect on the original point coordinates in **.mod**-file.
  p output of model effect on the horizontal point coordinates but at one constant elevation (which will be asked for) in **.mod**-file. This option removes influence of elevation differences on the model effect of disturbing bodies, which cannot be removed by Bouguer- and terrain reduction.
  g output of model effect at the coordinates of a rectangular grid and at the same elevation for all grid points in **.grd**-file. This option avoids irregular isolines, which usually arise when the model effect is interpolated over the irregular distributed data points.

  Special cases:

  o incompatible with **p**.

R incompatible with **r**.
n is not allowed in combination with any other option.

- Output elevation (when „output of observations results“-option **c** or **g** is chosen)

  Elevation for the computation of the model effect. Elevation above or below model bodies is also allowed.

- Grid corners **xmin**, **xmax**, **ymin**, **ymax** [coordinate-units]

  Only when „output of observations results“-option **g** is chosen:
  Minimum and maximum X - and Y coordinate.

  Special cases:

  Depending on the value if ny (s. below) these coordinates are the corners of a rectangular grid (ny>1) or the endpoints of a profile (ny=1).
  The smallest (largest) value will be automatically assigned to the minimum (maximum).
  Minimum and maximum coordinates in at least one direction must be different.

- Number of X grid lines **nx** [number]

  nx < 2 not allowed

- Number of Y grid lines **ny** [number]

  ny > 1 rectangular grid
  ny = 1 profile with **nx** points
  ny < 1 not allowed

- Data code **dc** [none]

  Data code to be assumed for the grid points, equivalent to the data code for observations.

- Interruption of iterations

  The iterations may be interrupted by pressing any key. When the key pressed matches one of the next option letters, then that option is selected directly, otherwise the option can be chosen from a shown menu. Then the next options are available:

  s stops the iterations immediately.
  p starts a dialogue to change the iteration parameters.
  a (only in case of the inversion algorithm) accepts the actual solution, also when it would be rejected by the algorithm otherwise.
  i requests the number of iterations still to be performed before stopping all iterations (by entering a positive number), or until the next automatic temporary halt or interruption (by entering a negative number).
  c continues the iterations.

- Restart options

  s stops the iterations immediately.
  n restarts computation while using the variable values as defined in line '**M**' in the input part of the definitions file as starting values. To be used when other algorithm parameters have to be tested.
  b restarts computation while using the adjusted variable of the last computation as starting values. Algorithm parameters can still be changed.
  B like **b**, but by changing the sign of values representing the standard deviation of the observation, when they are positive: the optimisation criterion is no longer a minimal least squares solution, but a minimal least absolute deviation (s. observations file).
  s stop program

3. FILE CONTENTS

_	indicates one or more blanks.
↵	indicates end of record, which is created by pressing the RETURN-key on most text editors. For MS-DOS/WINDOWS it is effectively a carriage-return (CR, ASCII 13 or ^M) and a line-feed (LF, ASCII 10, ^J) character, for Unix/Linux it is only a line-feed character.
→	indicates one or more blanks, tabs or ↵'s.
[**x** _] (1:n) ↵	indicates that some variable **x** delimited by one or more blanks will be repeated n times, after the n-th value **x** a ↵ follows.

Input files

Observations-file

Maximum number of character per line is 512.
All text starting with an exclamation mark and ending with an exclamation mark or the end-of-line is interpreted as blanks and might be used as comment text.
The name and all numbers have to be delimited by blanks, tabs or ↵'s and can be distributed over several lines.

[**n** → **x** → **y** → **d** → **s** → **z** → **c** ↵] (1:nd) — **n**=name (character), **x**=x-, **y**=y-coordinate, **d**=observation, **s**=standard deviation, **z**=z coordinate, **c**=data code

n may contain any characters but not more than 4, names need not be unique; they are not used.
x ,**y** ,**d** ,**s** and **z** may be floating point numbers or integers in free format; the decimal sign is a period or a comma; the scientific e- or E-format is allowed. The number of significant digits on input and during computation is 15 (double precision), but the output format is fixed; therefore, it may be necessary to change units of variables, to be able to see all significant digits on output.
c must be an integer.

If **s** = 0, then this observation is not used for adjustment, on output however, the model effect will be computed for this observation point.
If **s** < 0, then an L1-norm is minimized (least absolute values) for this observation, instead of an L2-norm (least squares) in case of **s** > 0, by iteratively changing the standard deviation according to the last computed residual. The initial standard deviation equals the absolute value of **s**.
The standard deviations should not only account for the observation accuracy, but also for the expected modelling accuracy!

Only observations and model bodies with matching data code **c** (ignoring the sign of c) will contribute to each other. In this way, different kinds of observations may be contained in one data file. If **c** < 0 then these observations are interpreted as a-priori information; so they contribute to the a-priori covariance matrix to compute the resolution matrix.

When for some kind of observations coordinates are meaningless, then the **x, y**, and **z**-values may have arbitrary values.

Definitions-file

General

Maximum number of character per line is 256.
All text starting with an exclamation mark and ending with an exclamation mark or the end-of-line is interpreted as blanks and might be used as comment text.

A keyword is the first word on a line (leading blanks and tabs are allowed), with 5 significant characters.

Input starts with keyword *START* and stops with keyword *STOP*.
Input may be repeatedly restarted with a subsequent *START* and *STOP* keywords, giving the ability to skip some input data. Nothing between *STOP* and *START* is read.

Input ends with either keyword *END*, or with the end-of-file.
Output of results overwrites everything following the keyword *END*.

Model body keyword

Model bodies are defined by keywords *EXTERNAL FUNCTION, OFFSET FUNCTION, BOUGUER REDUCTION, SPHERE, ROD, ELLIPSOID, CYLINDER, PLATE, PROFILE, DIGITAL TERRAIN MODEL and TRIANGULATION*.

After reading a model body keyword, the program searches in the following order for:
1. lines starting with keyword *t*,
2. lines starting with keyword *p*,
3. a line starting with keyword *n*, assuming that it is followed by lines starting with *s*, (*c*,*i*, *b*, (*i*, *b*,) *m*) and *M*,
4. repeating the search for a line starting with either *n* or a new model body keyword.

Line 't'

Contains text (usually a file name and/or command) required by some model bodies.

The file name is separated from the command by one or more blanks or tabs.

The text may be continued on subsequent lines following a line '**t**', by starting each line again with *t*; a blank will always be assumed at the end of each line.

When no line '**t**' is found, the text is assumed to consist of only blanks.

Line 'p'

Contains constant, non-adjustable parameters.

The minimum number of parameters is dependent on the kind of model body. More parameters are allowed, to be used as special parameters for an external program, when in line '**t**' a **command** is defined.

The list of parameters may be continued on subsequent lines following a line '**p**', by starting each line again with *p*. The parameters are delimited by one or more blanks or tabs (not ↵'s). The decimal sign is a period or comma. Parameters are read as floating point numbers but will be rounded to integers for some model bodies.

When no line '**p**' is found, the number of parameters is assumed zero.

Line 'n'

Contains names (positive numbers) to reference independent variables. Negative numbers define a linear dependency of the actual variable on the independent variable with a name equal to the absolute value of this number.

The number of names in this *single* line defines how many variables will be read in the following lines '**s**', ('**c**', '**i**', '**b**', ('**i**', '**b**',) '**m**') and '**M**'. More variables than can be contained in one line '**n**' can be defined by repeating several blocks of lines '**n**', '**s**', ('**c**', '**i**', '**b**', ('**i**', '**b**',) '**m**') and '**M**'

This line cannot be continued.

Names are delimited by one or more blanks or tabs (not ↵'s).

The names of independent variables must be integers between 0 and 99999. A variable with name 0 is allowed, but cannot be referenced.

The names of independent variables need not be unique, as long as no references to the non-unique names are made in any line '**n**' (by negative names), any correlation matrix or any condition matrix. Otherwise, a warning will be produced.

The adjusted value of a dependent variable d, which depends on independent variable i is equal to $\mathbf{M}_d = \mathbf{m}_d + \mathbf{s}_d * (\mathbf{M}_i - \mathbf{m}_i)$

Where $\mathbf{s}_j$, $\mathbf{m}_j$ and $\mathbf{M}_j$ are '**s**'-, '**m**'- and '**M**'-values of variable j. So a change of $\mathbf{dm}_i = (\mathbf{M}_i - \mathbf{m}_i)$ of independent variable i with respect to its '**m**'-value implies a change of $\mathbf{s}_d * \mathbf{dm}_i$ of dependent variable d with respect to its own '**m**'-value.

If **s** = 1 the dependent variable changes „parallel" to the independent variable, but separated by a „distance" ($\mathbf{m}_d - \mathbf{m}_i$).
If **s** = 1 and $\mathbf{m}_d = \mathbf{m}_i$ then the dependent variable will stay equal to the independent variable, whatever its adjusted value may be.

Lines 's', 'c', 'i', 'b', 'm' and 'M'

The first continuous set of characters (which should be one of the characters *s*, *c*, *i*, *b*, *m*, or *M*), delimited by blanks, tabs or ↵'s is skipped; then as many values as found in line '**n**' will be read.

These values have to be delimited by blanks, tabs or ↵'s and may be distributed over several lines.

All lines may contain floating-point numbers or integers in free format; the decimal sign is a period or a comma; the scientific e- or E-format is allowed. The number of significant digits on input and during computation is 15 (double precision), but the output format is fixed; therefore,

it may be necessary to change units of variables, to be able to see all significant digits on output.

When line '**n**' contains N names (numbers), then all values following the N-th value on the same line will be skipped. Then reading will continue on the next line with the next input-item.

Line 's'

Contains the standard deviations and/or normalizing factors of independent variables ('**n**'-value positive or zero), or linear multipliers for dependent variables.

- If the '**s**'-value > 0 and the '**n**'-value ≥ 0, than it is the standard deviation of a *bound* variable with a-priori-value equal to the '**m**'-value.
- If the '**s**'-value = 0 and the '**n**'-value ≥ 0, than this variable is *fixed* to its '**m**'-value.
- If the '**s**'-value < 0 and the '**n**'-value ≥ 0, than the standard deviation is equal to infinity; it is a *free* variable. The '**s**'-value (ignoring the sign) is in this case a normalizing factor, defining the range of 'reasonable' values for this variable: If the a-posteriori standard deviation is much larger than this value, the program defines the result as underdetermined.
- If the '**n**'-value < 0, than it defines the linear multiplier of the independent variable for calculating the dependent variable (s. „Line '**n**').
- The status *bound*, *fixed* or *free* of a dependent variable is equal to the status of the variable it depends on: it is essentially the same variable, with only possibly another constant offset ('**m**'**-**value).

Line 'c' (optional)

Contains criterion standard deviations of variables for comparison purposes. These standard deviations are not used for the adjustment, but only for normalizing the a-posteriori correlation- and resolution matrix.

This line is optional and defaults to the values of line '**s**'.

The '**c**'-values of fixed and dependent variables are not used, negative '**c**'-values are interpreted as positive values.

When line '**c**' is omitted but the run-time input parameter 'Multiplier of standard deviation' is not equal one, than on output a line '**c**' will be created, containing the original '**s**'-values. When all '**c**'-values equal all '**s**'-values in one output line, then line '**c**' is not printed.

Line 'i' and line 'b' (optional)

Contains together with line '**b**' inequality constraints on the actual variable. If the '**i**'-value is positive then the corresponding '**b**'-value is an upper limit, a negative '**i**'-value defines the '**b**'-value as a lower limit. If the '**i**'-value equals zero, no inequality constraint is implied.
The inequality constraint is achieved by an exponential penalty- or weighting function:

$$p_{b,i}(x) = \frac{1}{2}\left(\left(\frac{x-b}{i}\right)\left(1+erf\left(\frac{x-b}{i}\right)\right)+\frac{1}{\sqrt{\pi}}exp\left(-\left(\frac{x-b}{i}\right)^2\right)\right) \quad ,$$

so that on the acceptable side $\lim_{\left(\frac{x-b}{i}\right)\to-\infty} p_{b,i}(x)=0$, but $\lim_{\left(\frac{x-b}{i}\right)\to\infty} p_{b,i}(x)=\left(\frac{x-b}{i}\right)$ on the forbidden side.

If variable value *x* equals '**b**'-value *b*, then the penalty function $p_{b,i}(b)$ equals 0.2821. This means that it is in equilibrium with exceeding the a-priori variable values or observations with about a quarter standard deviation. The norm of the '**i**'-value defines the distance from the '**b**'-value, where the weight of the penalty function is reduced (on the acceptable side) to $p_{b,i}(-i)$ = 0.0251 or is increased (on the forbidden side) to $p_{b,i}(i)$ = 1.0251. In this way the '**i**'-value defines the range, where the penalty function is perceptible. Moving the '**b**'-value slightly towards the acceptable side might increase the weight at the limiting value, when too strong other data push the variable value across the '**b**'-value.

Line '**i**' and line '**b**' are optional and default to zeros, which implies absence of inequality constraints. These two lines must occur in combination.

Line '**i**' and line '**b**' may be defined twice, once for an lower limit and once for an upper limit. The order of these lines is in this case:

Line '**i**' of constraint 1
Line '**b**' of constraint 1
Line '**i**' of constraint 2
Line '**b**' of constraint 2

The order of lower and upper constraints is not important. The '**b**'-value of the lower limit must be smaller than the '**b**'-value of the upper limit. Two lower or two upper limits are not allowed.

When all '**i**'-values are zero in one output line, then line '**i**' and line '**b**' are not printed.

Line 'm' (optional)

Contains the a-priori value of bound variables ('**s**'-value > 0). For fixed variables ('**s**'-value = 0) and free variables ('**s**'-value < 0) this value is usually meaningless, except for calculating dependencies (s. line '**n**').

If this line is omitted, then all '**m**'-values default to their respective '**M**'-values: starting values will be equal to a-priori values.

On output '**m**'-values may be changed, when a condition matrix with non-zero residuals is defined (s. Condition Matrix).

Line 'M'

Contains the starting values for the iterative adjustment of *bound* and *free* variables. For extremely non-linear problems, with several local minima, it can be useful to choose a starting value at the 'safe' side of the a-priori value in line '**m**'.

On output line '**M**' contains the adjusted values of the variables, which may be used as starting values for subsequent iterations by moving the keyword *START* to the top of the output section, and the keywords *STOP* and *END* to the end of the output section.

Line ‘R’

This line is created on output and contains the difference between the a-priori values in line ‘**m**’ and the adjusted values in line ‘**M**’.

Line ‘S’

This line is created on output for „output in definitions file“-option **s** and contains the a-posteriori standard deviation of the adjusted values in line ‘**M**’.

For the inversion algorithm, it is computed by propagation of a-priori (co)variances; for the evolutionary algorithm, it is estimated from all models in the last parents population.

Matrix-keyword

Matrices are defined by keywords *CORRELATION MATRIX, CONDITION MATRIX*.

No model bodies must follow matrices.

Correlation matrix

ncv → **ex** ↵	**ncv**=number of correlated variables, **ex**=zero or power of relative distances in the natural exponent function
[**n** → [**c** →] (1:i) ↵] (i=1:ncv)	**n**=name of variable, **c**=elements of correlation matrix or distance matrix

If **ex** = 0, then the variables are correlated according to the correlation matrix defined by the lower triangular part. The diagonal elements must be equal to one.

If **ex** ≠ 0, then the correlation matrix is computed by: $exp\left(-\left|\frac{c_{ij}}{\sqrt{c_{ii}c_{jj}}}\right|^{|ex|}\right)$.

where $\mathbf{c}_{ij}$ is the distance between variable i and variable j, $\mathbf{c}_{ii}$ and $\mathbf{c}_{jj}$ are the correlation lengths for variable i and variable j.

If **ncv** < 0 and **ex** = 0, then it is assumed that the correlation matrix is already inverted.

The i-th variable name **n** defines what variable is referenced in row and column i. The order of variables may be freely chosen.

Several correlation matrices may be defined.

No variable may be referenced twice in one matrix, or in different correlation- or condition matrices.

Dependent variables cannot occur in the correlation matrix; use the independent variable instead.

Condition matrix

ncv → **ncnd** ↵	**ncv**=number of related variables, **ncnd**=number of conditions

[**n** → [**c** →] (1:ncnd) ↵] (1:ncv)	**n**=name of variable, **c**=elements of condition coefficient matrix
r → [**r** →] (1:ncnd) ↵	(line starts with keyword *r*) **r**=residual of condition (optional)
s → [**s** →] (1:ncnd) ↵	(line starts with keyword *s*) **s**=standard deviation of condition

The variables should fulfil the conditions defined by $C^t(M-m)=0+e$, where **M** is a vector with adjusted variable values, **m** is a vector with a-priori variable values. The standard deviation of misfit e_i of condition i equals s_i. This means that satisfying of the conditions is weighted against the fitting of the observations and the a-priori information. Exact fulfilling of the conditions cannot be enforced, because the standard deviation must be greater than zero. If **r** ≠ 0, then the '**m**'-values are changed by a factor **dm,** before adjustment starts, to satisfy the conditions: $C^t(m+dm)=r+e$, where **r** is a vector of residuals, i.e. deviations from fulfilling the condition, such that $C^tM=r+e$ throughout the computation. If **r** = 0, or when line '**r**' is omitted, it is *assumed* that the '**m**'-values already satisfy the conditions, only the differences of adjusted values with respect to the a-priori values are influenced by the conditions.

The i-th variable name **n** defines what variable is referenced in row i of matrix **c** (column i of C^t). The order of variables may be freely chosen. The j-th column represents the j-th condition in matrix **c** and vectors **r** and **s**.

Several condition matrices may be defined.

No variable may be referenced twice in one matrix, or in different correlation- or condition matrices.

Dependent variables cannot occur in the condition matrix; use the independent variable instead.
On output line '**r**' is will be 'commented' by an exclamation mark, because the a-priori values in line '**m**' are changed, such that the residuals are minimized already. In this way, the output is equivalent to the input.

Results in definition file

- On output the first few items show some **statistics of the observations**. All kinds of data are put together, so there is no statistical significance for the numbers: they are only for purposes of identification of the input data.

- The **development of the iterations** is shown in the same table as during run-time.

  For the inversion algorithm for each iteration the **actual** and **optimal** (minimal) **F-test** values is shown. When the F-test increases, than that solution is discarded, and the variance limit is decreased as will be shown in the next iteration. The **χ^2-improvement** shows how the overall fit changes from one iteration to the other; negative values indicate deterioration, positive values improvement. (Note that the F-test only depends on the number of degrees of freedom, i.e. the number of variables minus number of observations, while χ^2 directly depends on the number of variables and number of observations.) The **weighted RMSE** shows the fit of the observations. The standard deviation of the observations have been modified by the **multiplier** in the next column to get the solution of the actual iteration. When the parameter "multiplier of data standard deviation" is set negative, this multiplier is optimised in each iteration. The **model difference** is the root mean squared weighted difference between the variables in the last iteration and in the actual iteration. Weighting is performed in one column by the **a-priori standard deviation** in the other column by the **a-posteriori standard**

deviation. Small values (<< 1) indicate a stable, large values (>1) an unstable solution. The last column shows the **adaptive variance limit**, the damping of the actual solution. Good solutions should be achieved without any damping. The last line starting with a „-“, indicates the calculation of the a-posteriori covariance matrix. This matrix will always be calculated without damping, except when the matrix is singular, but in that case, the covariance matrix will be too optimistic; the **adaptive variance limit** in this line shows whether inversion without damping was possible.

For the evolutionary algorithm the F-test value of the best solution over all iterations is shown in the first column, the mean and improvement since the last iteration over the actual parents population in column 2 and 3. The weighted RMSE and the model difference is the same as for the inversion algorithm, but they are only computed when the best model over all iterations improves.

- For both algorithms, some **algorithm parameters** are shown.

- Then the output equivalent to the input of the definitions file follows, with the **adjustment results** in line '**M**', the residuals in line '**R**' and, in case of „output in definitions file“-option **s**, the a-posteriori standard deviations in line '**S**'.

- For the evolutionary algorithm, the best models found during all iterations is shown in line '**M**', if the „number of output models“ is not equal zero, than the **best models** the last iteration are also shown in order of decreasing F-test values.

- When an a-priori correlation or condition matrix is defined, it will be shown.

- When a **correlation matrix** of the independent variables should be shown (for „output in definitions file“-option **c** or **r**), then its lower triangular part is shown. When the matrix is too wide, it might be splitted horizontally in blocks of 22 columns.

  The count of the variables and the variable names are listed in the first two columns (probably truncated to the last digits). Only *bound* and *free* variables are contained in this matrix. *Free* variables are indicated by an asterisk behind the diagonal element. A count of variables is also shown over each column.

  Matrix values are coded by single characters:

code	0	1	2	…	8	9	a	b	…	y	z	A	B	…	Y	Z	#
meaning	0.0	0.1	0.2	…	0.8	0.9	1.0	1.1	…	3.4	3.5	3.6	3.7	…	6.0	6.1	≥6.15

The minus sign has the usual meaning. The values are rounded to the nearest code.

The diagonal elements are the quotient of the a-posteriori standard deviation and '**s**' value, i.e. the a-priori standard deviation (for *bound* variables) or the normalizing factor (for *free* variables).

The off-diagonal elements are the a-posteriori correlation coefficients.

For the inversion algorithm, this a-posteriori correlation matrix is computed by propagation of a-priori (co)variances; for the evolutionary algorithm, it is estimated from all models in the last parents population.

- When a **resolution matrix** should be calculated (output for „output in definitions file“-option **r**, then it is shown as second and third numbers below the elements of the correlation matrix. The rows of the upper triangular part are folded onto the columns of the lower triangular part, as a third number per element.

The matrix values are coded in the same way as the correlation matrix.

In this way the second element in row i and column j represents the influence of a change of 1 normalizing standard deviation of „real-world“ variable j on the adjusted value of variable i, expressed in units of 1 normalizing standard deviation, as a result of a-priori information. This a-priori information can be defined by bound variables, inequality constraints, correlation - and condition matrices and observations with negative data code. The third element expresses the influence of „real-world“ variable i on adjusted variable j.

The resolution matrix is normalized by either the a-priori standard deviations, or the criterion standard deviations if a line '**c**' is defined, which corresponds to a similarity transformation.

- When **eigenvalues/-vectors** of the a-posteriori covariance and/or resolution matrix should be computed (output for „output in definitions file“-option **C** or **R**), then the eigenvectors are shown as the columns of a matrix, with the eigenvalues (and for output for „output in definitions file“-option **IC**: the non-linearity ratio) on top of this matrix.

  The matrix is preceded by two columns containing the variable count and the variable names. On top of the eigenvalues, a count of eigenvectors is shown. The ratios/eigenvalues of odd eigenvectors are listed in the upper line(s); the ratios/eigenvalues of even eigenvectors are listed in the lower line(s), such that they are centred over their respective eigenvectors.

  The components of the eigenvectors are normalized and coded. The normalization scales the absolute values of the largest component of each eigenvector to one, while leaving zero components unchanged. The coding shows simply the first two decimal digits, except for the largest component, which is coded by ±a_. All values are rounded toward the nearest code.

  The components of eigenvectors are computed relative to the a-priori standard deviations or to the criterion standard deviations if a line '**c**' is defined.

  The eigenvalues/-vectors of the covariance matrix are actually the result of the generalized eigenvalue problem $\mathbf{C}_{post}\,\mathbf{x} = \lambda\,\mathbf{C}_{crit}\,\mathbf{x}$ where $\mathbf{C}_{post}$ is the a-posteriori covariance matrix and $\mathbf{C}_{crit}$ is the criterion matrix with the squared a-priori standard deviations, or the squared criterion standard deviations if a line '**c**' is defined, on the diagonal. Eigenvalues < 1 express a better result than expected by the criterion values, values > 1 a worse result.

  The linearity ratio is the increase of summed squared errors (F-statistic times degrees of freedom, s. below) by adding (upper value) or subtracting (lower value) one eigenvector times the corresponding eigenvalue to the optimum model. For a linear model, all ratios are equal one. The calculated a-posteriori standard deviations and eigenvalues of non-linear models are only valid, for ratios ≅ 1. Values larger than one indicate underestimation of the eigenvalues, values smaller than one indicate an overestimate of the a-posteriori standard deviation (eigenvalue) for this eigenvector. If the linearity ratio is smaller than zero, then a better model than the actual optimum is found for this combination of eigenvector and eigenvalue, which means that the coefficients cannot be interpreted correctly.

  The eigenvalues/-vectors of the resolution matrix are computed as the result of the generalized eigenvalue problem $\mathbf{C}_{post}\,\mathbf{x} = \lambda\,\mathbf{C}_{prior}\,\mathbf{x}$ where $\mathbf{C}_{post}$ is the a-posteriori covariance matrix and $\mathbf{C}_{prior}$ is the a-priori covariance matrix with the squared a-priori

standard deviations („**s**“-values > 0) on the diagonal. If some data codes of observations are negative, then the influence of the observations is also interpreted as a-priori information. Eigenvalues ≈ 1 express that the linear combination of variables as defined by the corresponding eigenvector is mainly determined by the observations, values ≈ 0 indicate that the corresponding eigenvector is a copy of the a-priori information.

- At the end of the output the **resulting statistics** are shown:

  If a variable is inside or beyond the range of the penalty function (< b+i for lower bounds or > b-i for upper bounds), then the number of variables inside or beyond the range, exceeding the boundary and exceeding the range is listed.

  If a-posteriori standard deviations of the observations are calculated (“output of observations results”-option **R**), then the minimal, mean and maximal relative a-posteriori standard deviations of the observations (per data code) are listed. This is the quotient of the a-posteriori to the a-priori standard deviation. From this value the equivalent redundancy is calculated as the number of additional observations (with the same a-priori standard deviation) that are necessary to reduce the a-posteriori standard deviation to the same amount by averaging.

  In the same way the minimal, mean and maximum relative a-posteriori standard deviation of the variables is listed, as well as the similarly calculated equivalent redundancy.

  The RMSE of the observations: the root mean squared weighted difference between the model effect (adjusted observations) and the (a-priori) observations. Weighting is performed by the a-priori standard deviation. If observations with different data codes are defined, also RMSE values per data code are listed.

  The RMSE of the (*bound*) variables: the root mean squared weighted difference between the adjusted variable values and the a-priori variable values. Weighting is performed by the a-priori standard deviation.

  The F-statistic: the sum of the squared weighted differences between adjusted and a-priori observations *and* variables, divided by the degrees of freedom (number of observations minus number of *free* variables).

  The 5% F-criterion is the value, which will be exceeded by the F-statistic with a probability of less than 5%, when all assumptions (no errors in observations, a-priori variable values, a-priori (co)variances and modelling theory) are valid.

  The 5% t-criterion is the value, which will be exceeded by a one single weighted (with respect to the a-priori standard deviation) residual of an observation or (bound) variable, with a probability of less than 5%, when all assumptions (no errors in observations, a-priori variable values, a-priori (co)variances and modelling theory) are valid.

  The coordinates of the Tikhonov L-curve are shown as a function of the actual parameter λ, which might have been improved by the algorithm or given by the user as a multiplier of the standard deviation of the observations.

  When the evolutionary algorithm was used, then for the chosen number of output models the resulting statistics are shown.

Export and import files for model bodies (in line 't' of the definitions file)

External function / Bouguer reduction

From INVERT **to** external routine when '**command**' is present in line '**t**'; i.e. only for 'external function':

1. **ib**	index of actual model "body".
2. **init** ↵	–1 during first call, 0 when computing observation, 1 when computing first derivative, 2 when computing second derivative
3. **np** ↵	number of constant parameters
4. [**par** ↵] (1:np)	constant parameters
5. **nv** ↵	number of variables
6. [**var** ↵] (1:nv)	variables
7. **nd** ↵	number of observations
8. [**n** ↵ **x** ↵ **y** ↵ **d** ↵ **s** ↵ **z** ↵ **c** ↵] (1:nd)	**n**=name (4 characters), **x**=X-, **y**=Y-coordinate, **d**=observation, **s**=standard deviation, **z**=Z-coordinate, **c**=data code (which is always equal to **par**(1))

From external routine **to** INVERT:

[[**rd** ↵] (1:nc)] (1:nd)	returned data (**nc**=1 when '**command**' is present in line '**t**'; **nc**=number of variables otherwise. **nd**=number of observations) only for data points with same data code as the model body!

Sphere / Rod / Plate / Profile / DTM / Triangulation

From INVERT **to** external routine when '**command**' present in line '**t**':

1. **ib**	index of actual model body.
2. **init** ↵	–1 during first call, 0 when computing observation, 1 when computing first derivative, 2 when computing second derivative
3. **np** ↵	number of constant parameters
4. [**par** ↵] (1:np)	constant parameters
5. **nv** ↵	number of variables
6. [**var** ↵] (1:nv)	variables

From external routine **to** INVERT:

1. **nb** ↵	number of bodies
2. [[**p** →] (1:k) **nd** ↵ [[**d** →] (1:l) ↵] (1:nd)] (1:nb)	(**nd**=number of body points (spheres, rods, dtm-grid points, prims-grid points+layers, vertices of plate, profile or triangulated body and s. table below)

Sphere	Rod	Plate	Profile	DTM
k = 3	K = 5	k = 5	k = 5	k = 9
p(1) = data code **p**(2) = exchange R/D **p**(3) = radius	**p**(1) = data code **p**(2) = exchange R/D **p**(3) = radius **p**(4) = x0 **p**(5) = y0	**p**(1) = data code **p**(2) = max. aperture **p**(3) = density **p**(4) = zmin **p**(5) = zmax	**p**(1) = data code **p**(2) = X0 **p**(3) = Y0 **p**(4) = density **p**(5) = azimuth	**p**(1) = data code **p**(2) = approx. distance **p**(3) = max.distance **p**(4) = xmin **p**(5) = xmax **p**(6) = nx **p**(7) = ymin **p**(8) = ymax **p**(9) = ny
l = 4	l = 3	l = 2	l = 2	l = 3
d(1) = density **d**(2) = x **d**(3) = y **d**(4) = Z	**d**(1) = density **d**(2) = d **d**(3) = z	**d**(1) = x **d**(2) = y	**d**(1) = d **d**(2) = z	**d**(1) = density **d**(2) = zmin **d**(3) = zmax (nd=nx+ny)

Triangulation
k=2
p(1) = data code **p**(2) = density
l=3
(2*nd-4)/3 times: **d**(1) = index vertex 1 **d**(2) = index vertex 2 **d**(3) = index vertex 3 (nd+4)/3 times: **d**(1) = x **d**(2) = y **d**(3) = z

Output files

Plot file (.plt)

Created for „output in separate file“-option **m**.

Contains the input and results of the parameters and variables of the model bodies.

io ↵	(character) **io** equals INPUT when following data are a-priori values (line '**m**'), and **io** equals OUTPUT when following data are adjusted values (line '**M**' computed in last iteration).
nb ↵	order number of model body
keyword ↵	one of the model body keywords in the definitions file.

Depending on the kind of model body, the next data are:

EXTERNAL FUNCTION:

np ↵	number of constant parameters
c ↵ [**par** ↵] (1:np-1)	**c**=data code, **par**=other constant parameters
nv ↵	number of variables
[**var** ↵] (1:nv)	variable values
nod ↵	number of data points
[**n _ x _ y** ↵ [**f** →] (1:nv)] (1:nod)	**n**=name (4 characters), **x**=X-, **y**=Y-coordinate, **f**= value of constant multiplier at data point read from external file

OFFSET FUNCTION

c _ kof _ xmin _ xmax _ ymin _ ymax ↵	**c**=data code, **kof**=kind of function, **xmin**=minimal, **xmax**=maximal X-coordinate, **ymin**=minimal, **ymax**=maximal Y-coordinate
nod ↵	**nod**=number of data points (always 1 for **kof** = 0)
[**n _x _ y _ f** ↵] (1:nod)	**n**=name (4 characters), **x**=X-, **y**=Y-coordinate of data point, **f**=offset function value at data point (**x** = **xmin** and **y** = **ymin** for **kof** = 0)

BOUGUER REDUCTION

c _ rz_ bd _ td _ d ↵	**c**=data code, **rz**=Z-coordinate of reduction level, **bd**=prior Bouguer density, **td**=prior terrain density, **d**=Bouguer density
nod ↵	**nod**=number of data points
[**n _x _ y _ z _ t** ↵] (1:nod)	**n**=name (4 characters), **x**=X-, **y**=Y-, **z**=Z-coordinate of data point, **t**=terrain effect at data point with prior terrain density

SPHERE

nob ↵	number of bodies
c _ erd _ r ↵	**c**=data code, **erd**=exchange rad./dens., **r**=radius
ns ↵	**ns**=number of spheres
[**d _ x _ y _ z** ↵] (1:ns)	**d**=density, **x**=X-, **y**=Y-, **z**=Z-coordinate of sphere

ROD

nob ↵	number of bodies
c _ erd _ r _ x0 _ y0 _ a ↵	**c**=data code, **erd**=exchange rad./dens., **r**=radius, **x0**=x-, **y0**=y-coordinate of origin, **a**=azimuth of **dc**
nr ↵	**nr**=number of rods
[**d _ dc _ zc** ↵] (1:ns)	**d**=density, **dc**=distance-, **zc**=z-coordinate of rod

ELLIPSOID

c _ kob _ d _x _ y _ z ↵	**c**=data code, **kob**=kind of body, **d**=density, **x** =x-, **y**=y-, **z**=z-coordinate of centre
ab _ dc _ rb _ ra _ rc ↵	**ab**=azimuth of rb, **dc**=dip of rc, **rb** =radius b, **ra**=radius a, **rc**=radius c

CYLINDER : Same as PLATE

PLATE

nob ↵	number of bodies
c _ ma _ d _ zmin _ zmax ↵	**c**=data code, **ma**=maximum aperture, **d**=density, **zmin**=lower, **zmax**=upper Y-coordinate
nv ↵	**nv**=number of vertices
[**x _ y** ↵] (1:nv)	**x**=X-, **y**=Y-coordinate of vertex

PROFILE

nob ↵	number of bodies
c _ x0 _ y0 _ d _ a ↵	**c**=data code, **x0**=X-, **y0**=Y-coordinate of origin, **d**=density, **a**=azimuth of **d**
nv ↵	**nv**=number of vertices
[**d _ z** ↵] (1:nv)	**d**=distance, **z**=Z-coordinate of vertex

DIGITAL TERRAIN MODEL

nob ↵	number of bodies
c _ ra _ rm ↵	**c**=data code, **ra**=approximation -, **rm**=maximum distance
xmin _ xmax _ nx _ ymin _ ymax - ny ↵	**xmin**=minimal, **xmin**=maximal X-coordinate, **nx=** number of X-grid lines, **ymin**=minimal, **ymin**=maximal Y-coordinate, **ny=** number of Y-grid lines
ng ↵	**ng**=number of grid points

[**d** _ **zmin** _ **zmax** ↵] (1:ng)	**d**=density, **zmin**=lower, **zmax**=upper Z-coordinate of grid point

TRIANGULATION

nob ↵	number of bodies
c _ **d** ↵	**c**=data code, **d**=density
nfv _ **nf** _ **nv** ↵	**nfp**=number of faces+points, **nf**=number of faces, **nv**=number of vertices
[**i1** _ **i2** _ **i3** ↵] (1:nf)	**i1**=index vertex 1, **i2=** - 2, **i3=** - 3
[**x** _ **y** _ **z** ↵] (1:nv)	**x**=X-, **y**=Y-, **z**=Z-coordinate of vertex

Residuals file (.res)

Created for „output of observations results“-option **r** or **R**.

Contains difference between original observations and model effect of adjusted variables and the a-posteriori standard deviation of the model effect.

[**n** _ **x** _ **y** _ **r** _ **s** _ **z** _ **c** _ **p** ↵] (1:nd)	**n**=name (character), **x**=X-, **y**=Y-coordinate, **r**=residual, **s**=a-priori standard deviation, **z**=Z-coordinate, **c**=data code, **p**=a-posteriori standard deviation of the model effect (always equal 0 for option **r**), **nd**=number of data points

Model-effect file (.mod)

Created for „output of observations results“-option **v** or **c**.

Contains model effect of adjusted variables at chosen elevation.

[**n** _ **x** _ **y** _ **m** _ **s** _ **z** _ **c** _ **p** ↵] (1:nd)	**n**=name (character), **x**=X-, **y**=Y-coordinate, **m**=model effect, **s**=a priori standard deviation, **z**=Z-coordinate, **c**=data code, **nd**=number of data points

Grid file (.grd)

Created for „output of observations results“-option **g**.

Contains model effect of adjusted variables at chosen elevation on defined grid points.

xmin _ **xmax** _ **nx** _ **ymin** _ **ymax** _ **ny** ↵	**xmin**=minimal, **xmax**=maximal X-coordinate, **nx**=number of X-grid-lines, **ymin**=minimal, **ymax**=maximal Y-coordinate, **ny**=number of Y-grid-lines (a profile is defined by **ny**=1, extending from (**xmin, ymin**) to (**xmax, ymax**) with **nx** equidistant profile points
[[**g** _] (1:nx) ↵ **]** (1:ny)	grid point values, where 1:nx/ny starts with x/y minimum and ends with x/y maximum.

Correlation file (.cor)

Created for „output in separate file“-option **c**.

For the inversion algorithm, this a-posteriori correlation matrix is computed by propagation of a-priori (co)variances; for the evolutionary algorithm, it is estimated from all models in the last parents population.

nv ↵	number of variables
[**cov** ↵] (1:nv)	a-posteriori variances
[[**cor** ↵] (1:i) **]** (i=1:nv)	correlation coefficients, the diagonal elements contain the quotient (a-posteriori / a-priori) standard deviation. Only the lower triangular part is returned, the inner loop switches between columns, the outer loop between rows.

Resolution file (.rsl)

Created for „output in separate file“-option **r**.

Contains the normalized resolution matrix indicating the influence of a change of 1 standard deviation in a „real-world“ column-variable on an adjusted row-variable, because of a-priori information, expressed again in units of 1 (criterion) standard deviation (s. „Results in definitions file“).

nv ↵	number of variables
[[**res** ↵] (1:nv) **]** (1:nv)	resolution coefficients, normalized by the a-priori standard deviations or with the criterion standard deviations when line ‘**c**’ is defined in the definitions file. The inner loop switches between columns, and the outer loop switches between rows.

Eigenvalue/-vector file (.evc and .evr)

.evc :
Created for „output in separate file“-option **C**.
Contains the standard deviation, resolution and residuals of the eigenvectors and eigenvectors of the a-posteriori covariance matrix, and for „output in separate file“-option **IC**, the values of the linearity ratios for solutions in distance of + 1 and −1 times the standard deviation of the eigenvector.

.evr :
Created for „output in separate file“-option **R**.
Contains the eigenvalues/-vectors of the resolution matrix

(s. „Results in definitions file“)

nd ↵	number of dimensions
nvl ↵	number of values per eigenvector
[[**val** ↵] (1:nd) **]** (1:nvl)	values (standard deviation, resolution, (unsigned) residual and (with option **IC**) +1 and -1 linearity ratios in **.evc**, eigenvalues in **.evr**)
[[**vec** ↵] (1:nd) **]** (1:nd)	eigenvectors, normalized such that the largest component equals one. The inner loop switches between components, and the outer loop switches between eigenvectors

Eigenvalue/-vector model file (.dfc and .dfr)

.dfc :
Created for „output in separate file“-option **eC**.
Contains the eigenvectors of the a-posteriori covariance matrix multiplied by the eigenvalue, in form of a definitions file, showing in line ‘**M**’ a model, which causes an increase of ±1 (criterion) standard deviation in the observations, compared with the optimal model (line ‘**M**’ of last iteration).

.dfr
Created for „output in separate file“-option **eR**.
Contains the eigenvectors of the resolution matrix in form of a definitions file, showing in line ‘**M**’ a model, that has a resolution of the difference with the optimal model (line ‘**M**’ of last iteration), equal to ±1 times the eigenvalue on top this file.

On top of each eigenvector model the corresponding sign of the eigenvector and eigenvalue is listed. All eigenvector models are initially ‘commented’ by an exclamation mark in front of the keyword *START.*

Vectors - and - matrices - file (.vec)

Created for „output in separate file“-option **v** or **V**.

Contains vectors and matrices as used during the last iteration of the non-linear model.

no ↵	number of observations
nv ↵	number of independent variables
nap ↵	number of independent a-priori variables
nic ↵	number of inequality constraints
[[**jac** ↵] (1:nv)] (1:no+nap+nic)	Jacobian normalized by the a-priori standard deviations of the observations and the a-priori (criterion) standard deviations of the variables.
[**b0** ↵] (1:no+nap+nic)	observations + a-priori variables + inequality constraints.
[**ba** ↵] (1:no+nap+nic)	adjusted obs. + a-priori var. + ineq. constr.
[**sb0** ↵] (1:no+nap+nic)	a-priori st.dev. of obs. + a-priori var. + ineq. constr.
[**sba** ↵] (1:no+nap+nic)	a-posteriori st.dev of obs. + a-priori var. + ineq. constr. (only non-zero for „output of observations results“-option **R**, or when a-posteriori (co)variances are calculated for other output options).
[**v0** ↵] (1:nv)	a-priori variable estimates.
[**va** ↵] (1:nv)	adjusted variables.
[**sv0** ↵] (1:nv)	a-priori st.dev. of variables.
[**sva** ↵] (1:nv)	a-posteriori st.dev. of variables (only non-zero when a-posteriori (co)variances are calculated for some output options).
[**iv1** ↵] (1:nv)	“**i**”-value of inequality constraint 1 of variables.
[**bv1** ↵] (1:nv)	“**b**”-value of inequality constraint 1 of variables.
[**iv2** ↵] (1:nv)	“**i**”-value of inequality constraint 2 of variables.
[**bv2** ↵] (1:nv)	“**b**”-value of inequality constraint 2 of variables.
nc ↵	number of rows/columns in following covariance matrix. (only non-zero when matrix defined in definitions file)
[[**cor** ↵] (1:i)] (i=1:nc)	inverse of a-priori covariance matrix of variables, normalized by the a-priori (criterion) standard deviations. Columns and rows representing free parameters have zero valued diagonal elements. Only the lower triangular

	part is returned, the inner loop switches between columns, the outer loop between rows.
ns ↵	number of rows/columns in following second derivatives matrix (only non-zero for option **V**)
[[**scd** ↵] (1:i)] (i=1:ns)	second derivatives matrix of optimising criterion summed over all observations, normalized by the a-priori (criterion) standard deviations. Only the lower triangular part is returned, the inner loop switches between columns, the outer loop between rows.

Label file (.lbl)

Created for „output in separate file“-options **c**,**r**,**C**,**R**,**v**,**V** and **l**.

Contains a translation table between index and “name” (line ‘**n**’) of all independent variables.

nv ↵	number of (independent) variables
[**idx** ↵	index of (independent) variable among all variables
lnn ↵] (1:nv)	“name” of variable as contained in line ‘**n**’

Iteration file (.itr)

Created for „output in separate file“-options **i**.

Contains variable values and statistical information for each iteration step.

nit ↵	number of iterations
nv ↵	number of values per iteration
[[**val** ↵] (1:nv)] (1:nit)	**val** (1): damping factor, (2): χ^2-improvement, (3): RMS model difference weighted by a-priori covariance, (4): RMS model difference weighted by a-posteriori covariance, (5:nv): values if (independent) variables. For the 0-th iteration the first 4 values will be zero.

4. MODEL BODIES

Model bodies define how to compute the model effect at an observation point.

Line **t** must be commented out (exclamation mark), when the model is not defined externally on file or using some external program.

A model body only contributes to an observation point, when their data code is the same (ignoring the sign). The data code is the first parameter in line **p**.

The number of parameters may be extended beyond the number explained below, this may be useful to parse some additional information to the external program when in line **t** a **command** is defined.

The number of variables is usually strictly bound to certain multiples, depending on the model body. Variables in excess may be commented out, by deleting or commenting the line **n** or inserting the keyword *STOP*.

Units are mgal (gravity), gr/cm^3 (density) and meter (coordinates, distances),
or equivalently mgal (gravity), kg/m^3 (density) and kilometre (coordinates, distances).

External function

Flexible kind of defining some special model effects.

t

Two kinds of input are possible:

1.

file

INVERT reads from **file** N constants per observation (in the same order as in the data file!), which are multiplied by N variables and summed to give the model effect at that observation point. The number of constants in **file** should match the number of variables.

2.

file command

INVERT writes parameters, variables and observations to **file**, executes **command** in the local shell environment (a user-defined program that reads **file**, computes the model effect at all observation points and overwrites **file** with these values), and reads the externally computed model effect from **file**.

If **command** equals „userfunc“, then the internal subroutine „userfunc“ is used and **file** is only a keyword telling userfunc what kind of computation to do. No data are written to **file** in this case, all data exchange in done in working space.

p

1. data code
2. optional user-defined parameters for computing the model effect

v

user-defined variables

Offset function

Model effect with only geometrical meaning.

p

1. data code
2. kind of offset function:
   - 0 constant
   - +/- 1 Chebyshev polynomials (range: [-1,1])
   - +/- 2 Fourier series (range [0,2π])
   - (<1 = 1-dimensional, >1 = 2-dimensional)
3. X-coordinate to be mapped to the minimum of range
4. X-coordinate to be mapped to the maximum of range
5. Y-coordinate to be mapped to the minimum of range
6. Y-coordinate to be mapped to the maximum of range

If **p**(2) = 0 then **p**(3,4,5,6) are meaningless and may have arbitrary values, they are only used as output coordinates of the offset function in **.plt**-file.
If **p**(2) < 0 the coordinates are the starting and end points of a profile, if **p**(2) > 0 the coordinates define a rectangular area.

v

Coefficients for the next base functions:

If **p**(2) = -1: $\left[C_n(x)\right](n=0:N)$ N+1 variables

If **p**(2) = +1: $\left[\left[C_{n-m}(x)\cdot C_m(y)\right](m=0:n)\right](n=0:N)$ (N+1)(N+2)/2 variables

with $C_0(x)=1$; $C_1(x)=x$ and $C_{n+1}(x)=2xC_n(x)-C_{n-1}(x)$, $n\geq 1$

If **p**(2) = -2: $\left[1 \quad \left[\cos nx \quad \sin nx\right](n=1:N)\right]$ (1+2N) variables

If **p**(2) = +2:

$$\left[\begin{array}{c} 1 \\ \left[\begin{array}{c} \cos nx \quad \sin nx \\ \left[\cos nx\cos my \quad \cos nx\sin my \quad \sin nx\cos my \quad \sin nx\sin my\right](m=1:n-1) \\ \cos nx\cos ny \quad \cos nx\sin ny \quad \sin nx\cos ny \quad \sin nx\sin ny \\ \left[\cos(n-m)x\cos ny \quad \cos(n-m)x\sin ny \quad \sin(n-m)x\cos ny \quad \sin(n-m)x\sin ny\right](m=1:n-1) \\ \cos ny \quad \sin ny \end{array}\right](n=1:N) \end{array}\right]$$ $(2N+1)^2$ variables

Bouguer reduction

This model body changes assumed density of the Bouguer- and terrain reduction applied to the observations.

t

If in this line contains a file name, this file should contain the terrain effect at each observation point (in the same order as in the data file!), calculated with some arbitrary (non-zero) density. The terrain reduction included in the observations will be recalculated for the same density as the Bouguer reduction. No line **t** should be defined if no terrain reduction should be performed

p

1. data code
2. Z-coordinate of the reduction level for the Bouguer reduction.
3. density used for the Bouguer and terrain reduction of the observations, if **p**(3) = 0 then no Bouguer and terrain reduction is included in the observation data.
4. density used for the calculation of the terrain effect in **file** (this parameter should not be defined if line **t** is missing).

v

1. new density for Bouguer- and terrain reduction

Sphere / Rod / Plate / Profile / DTM / Triangulation

Two kinds of input are possible if line **t** is defined:

1.

t

file

Density and geometrical parameters describing the model body are read from **file,** only the relative density change (relative to the density read from file) is a variable.

p

1. data code

v

1. relative density change

2.

t

file command

INVERT writes parameters and variables to **file**, executes **command** in the local shell environment (a user-defined program that reads **file**, computes the density and geometrical parameters and overwrites **file** with these values), reads the density and geometrical parameters from **file** and computes the model effect for this model body.

If **command** equals „userfunc“, then the internal subroutine „userfunc“ is used and **file** is only a keyword telling userfunc what kind of model body to compute. No data are written to **file** in this case, all data exchange in done in working space.

p

1. data code
2. The standard parameters as defined below for the Sphere / Rod / Plate / Profile / DTM and Triangulation and optional user-defined parameters for computing the density and geometrical body parameters.

v

user-defined variables

Otherwise line **t** should not be defined or commented out

Sphere

Gravity effect of a point mass or sphere with variable mass, and coordinates. The mass is derived from the assumed volume density and radius.

p

1. data code
2. 0 or 1
   0 = radius is constant (**p**(3)), density is variable (**v**(1))
   1 = density is constant (**p**(3)), radius is variable (**v**(1))
3. radius if **p**(2)=0 or density if **p**(2)=1

v

1. density if **p**(2)=0 or radius if **p**(2)=1
2. X-coordinate of centre
3. Y-coordinate of centre
4. Z-coordinate of centre

Rod

Gravity effect of a horizontal rod (line) or cylinder with variable line density, coordinates and azimuth. The line density is derived from the assumed volume density and radius. The coordinates are defined within a vertical plane. The origin of the horizontal coordinates, which is equal centre of rotation for the azimuth of the vertical plane, is fixed, but may be freely chosen.

p

1. data code
2. 0 or 1
   0 = radius is constant (**p**(3)), density is variable (**v**(1))
   1 = density is constant (**p**(3)), radius is variable (**v**(1))
3. radius if **p**(2)=0 or density if **p**(2)=1
4. X-coordinate of origin for D-coordinates and centre of rotation for azimuth
5. Y-coordinate of origin for D-coordinates and centre of rotation for azimuth

v

1. density if **p**(2)=0 or radius if **p**(2)=1
2. azimuth of positive D-direction, perpendicular to rod extension

3. D-coordinate of centre relative to (**p**(4), **p**(5))
4. Z-coordinate of centre

Ellipsoid

Gravity effect of an ellipsoid, an elliptical cylinder or rectangular prism, with variable centre coordinates, variable declination and inclination and variable radii of all 3 body axes. The model effect is approximated with 3 spherical harmonics coefficients according to Grand and West (1966). This approximation is only usable if the body axes are almost of equal length and, especially for the cylinder and the prism, if the body is far away from the observation point.

p

1. data code
2. kind of body
   0 = ellipsoid
   1 = elliptical cylinder
   2 = rectangular prism

v

1. density
2. X-coordinate of centre
3. Y-coordinate of centre
4. Z-coordinate of centre
5. azimuth of axis **v**(7)
6. dip angle of axis **v**(7)
7. radius of the axis, in direction **v**(5) and **v**(6))
8. radius of a horizontal axis, perpendicular to **v**(7)
9. radius of the axis, perpendicular to **v**(7) and **v**(8)

Cylinder

Gravity effect of a vertical cylinder with variable density, lower and upper plane and centre coordinates and shape of the constructing horizontal curve. This curve is approximated by a polygon. The gravity effect of the constituting triangular prisms is approximated by vertical cylinders centred at the observation points. The shape of the curve may be a circle (no modes defined, 6 variables) or by a trochoid, which is a curve created by endpoint of a (satellite) bar with length r_i, which is rotating at the end of another rotating (base) bar with length R. The angle velocity of the satellite bar is i=1,2,3,... times the angle velocity of the base bar. The integer i defines the mode of the trochoid. Several modes (satellite bars) can be accumulated to complex bodies. When the sum of the lengths of the bars becomes to big, loops may occur with an effective density, which is a multiple of the defined density. Hypotrochoids are created with positive r_i, epitrochoids are created by negative r_i (unlike the mathematical definition of trochoids, where the change from hypo- to epitrochoid is achieved by changing the sign of the angle velocity and where the sign of radius is equivalent to an angle offset of 180°)
When the upper plane is lower than the lower one, the effective density changes sign.
When the observation point lies on or within the cylinder, the model effect is correctly calculated

p

1. data code
2. number of segments and vertices.
3. maximum angle at observation points for subdividing a vertex into smaller ones, for better approximation of model effect. Angle 0 defaults to 20°. If **p**(2) is positive the coordinates of the first vertex, relative to the centre coordinates, are at azimuth zero if no modes are defined, or at azimuth **v**(8), if at least one mode is defined. If **p**(2) is negative, the

connection between the first and second vertex is perpendicular to azimuth zero, if no modes are defined, or the connection is perpendicular to azimuth **v**(8), if at least one mode is defined

4,5,6,...
modes of trochoids. Number of maxima (and minima) of departure from base circle (2=ellipse, 3-triangle, etc.).All radii defined by these modes are added to the radius of the base circle.

v

1. density
2. Z-coordinate of lower plane on cylinder
3. Z-coordinate of upper plane on cylinder
4. X-coordinate of centre
5. Y-coordinate of centre
6. radius of base circle

7,9,11,...
radius of departure from base circle for each mode. A positive radius defines a hypotrochoid, a negative radius an epitrochoid

8,10,12,...
azimuth [degrees] of a maximum of departure from base circle for each mode

Plate

Gravity effect of a plate with variable density, horizontal lower and upper plane and a polygon with variable coordinates of the vertices. The gravity effect of the constituting triangular prisms is approximated by vertical cylinders centred at the observation points.
The order of the vertices should be in clockwise direction when looking towards the negative Z-direction (elevation).
The first and the last vertex are always connected, even when a polygon is not closed.
When the upper plane is lower than the lower one, or when the vertices are defined in counter clockwise direction, the effective density changes sign. Multiple loops imply an effective density, which is a multiple of the defined density.
When the observation point lies on or within the plate, the model effect is correctly calculated.

p

1. data code
2. maximum angle at observation points for subdividing a side of the polygon into smaller ones, for better approximation of model effect. Angle 0 defaults to 20°.

v

1. density
2. Z-coordinate of lower plane on cylinder
3. Z-coordinate of upper plane on cylinder

4,6,8,...
X-coordinate of vertex

5,7,9,...
Y-coordinate of vertex

Profile

Gravity effect of a so-called 2½-dimensional profile, defined by a polygon of vertices in the vertical plane and reaching from minus to plus infinity horizontally and perpendicular to the profile direction. The density, azimuth of the vertical plane and the coordinates of the vertices are variable. The origin of

the horizontal coordinates of the polygon, which is equal to the centre of rotation for the azimuth of the vertical plane, is fixed, but may be freely chosen.
The order of the vertices should be in clockwise direction the positive D-direction (azimuth of the vertical plane) is taken towards the right, and the positive Z-direction (elevation) is taken positive upward.

When the last and first vertices have different elevations, the polygon is implicitly augmented with two vertices. The last vertex is connected to an additional vertex at the same elevation, but horizontally at minus infinity (D-coordinate). The next vertex has the same elevation as the first vertex of the polygon, and is also located horizontally at minus infinity, this vertex is connected with the first vertex of the polygon. These additional vertices define a horizontal slab which is connected to the first and last vertices and which is extending toward minus infinity.

When a closed loop of vertices is defined in counter clockwise direction, the effective density changes sign. Multiple loops imply an effective density that is a multiple of the defined density.
When the observation point lies on or within the profile, the model effect is correctly calculated.

p

1. data code
2. X-coordinate of origin for D-coordinates and centre of rotation for azimuth
3. Y-coordinate of origin for D-coordinates and centre of rotation for azimuth

v

1. density
2. azimuth [degrees] of positive D-direction

3,5,7,...
D-coordinate of vertex relative to (**p**(2), **p**(3))

4,6,8,...
Z-coordinate of vertex

Digital Terrain Model (DTM)

Gravity effect of a rectangular grid of quadratic vertical prisms, with fixed coordinates in the horizontal plane, but with variable density and variable lower and upper boundary. For each prism these 3 values are mean values of at least 4 neighbouring points. Approximations may reduce the computation time. When the grid cells are not quadratic, then the mean of the sizes is used, while keeping the centre of the grid at the same place.
The order of the grid points is from the lower left corner with minimal X- and minimal Y-coordinate row-wise, i.e. inner loop over X-direction, outer loop over Y-direction, to upper left corner with maximal X- and maximal Y-coordinate.
When the upper plane is lower than the lower one, the effective density changes sign.
When the observation point lies on or within the prisms, the model effect is correctly calculated.

At the moment line **t** must be present, with the next contents:

t

dtm userfunc

p

1. data code
2. minimum x/y-distance from the observation point for approximation of the gravity effect of each prism by that of a vertical line mass. The effective distance is calculated like the maximum distance below. If positive, than outside *two* times this distance, prisms are additionally averaged in blocks with a side length equal to this doubled distance, and for every next concentric layer around the observation point the side length is doubled again.

When an averaging block lies partially outside the original grid, only the available values are considered for the averaging of the Z-coordinates; so the mean of the available data is "extrapolated" outside the given grid. For the density the data outside the given grid are interpreted as zero values, so the averaged density is reduced proportionally to the number of failing data. When an averaging block lies completely outside the given grid, it is discarded. If the distance is negative, than no block averaging is performed, but all prisms outside this distance are computed individually with the line mass approximation. If the radius is zero, no averaging and no approximation is performed.

3. maximum x/y-distance from the observation point for including prisms into the gravity effect. The most distant grid point, which is still considered for a given observation point is calculated as follows: The effective maximum distance is given by the given maximum distance rounded to the nearest multiple of the grid size plus 1. This effective radius is added to or subtracted from the observation position rounded to the nearest grid lines.
4. minimum X-coordinate of grid
5. maximum X-coordinate of grid
6. number of X grid points
7. minimum Y-coordinate of grid
8. maximum Y-coordinate of grid
9. number of Y grid points

v

1,4,7,...
density
2,5,8,...
Z-coordinate of lower plane
3,6,9,...
Z-coordinate of upper plane

Triangulation

Gravity effect of body of arbitrary shape, delimited by plane triangular faces. The density and the coordinates of the vertices are variable.
Each face is defined by the 3 indices of the vertices. An index i refers to the i-th triple of coordinates in the list of variables. The order of the indices of the vertices of each face should be in clockwise direction when looking from an outer position onto the each face of the body. The order of the vertices in the list of variables is insignificant. A body with *n* vertices, where the tree edges of a face are indicated by pairs of indices (i_r, i_s), (i_s, i_t), (i_t, i_r), is a *closed* body only if:
1. the number of faces equals *2n-4*
2. each pair of indices is defined once in forward order (i_r, i_s) and once in reverse order (i_s, i_r)

When vertices of a face are defined in counter clockwise direction, the effective density changes sign. When the observation point lies on or within the body, the model effect is correctly calculated.

p

1. data code
2,5,8,...
index of first vertex of a face
3,6,9,...
index of second vertex of a face
4,7,10,...
index of third vertex of a face

v

1. density

2,5,8,...
    X-coordinate of vertex
3,6,9,...
    Y-coordinate of vertex
4,7,10,...
    Z-coordinate of vertex