

# Genevestigator Export Formats

Revision: 2.0

## 1 Export Formats

### 1.1 Convention

We use the following convention in the file format descriptions:

- [x.y] represents the value attribute y of entity x.
- "x" is a string constant.
- ... indicates that the example output was shortend.

### 1.2 Exported Files

The following files are exported and calculated for a given platform identified by the short name of the platform [platform.short\_caption] using the dataexport script prepackaged with the export tools:

Filename	Description
platforms.csv	Platforms descriptions.
experiments_[platform.short_caption].csv	Experiment descriptions.
experimenttree_[platform.short_caption].csv	File containing the experiment-replica-chip relations
anatomytree_[platform.short_caption].csv	File containing the anatomy annotations
cellinetree_[platform.short_caption].csv	File containing the cell line annotations
neoplasmtree_[platform.short_caption].csv	File containing the neoplasm annotations
developmenttree_[platform.short_caption].csv	File containing the development annotations
statevariabletree_[platform.short_caption].csv	File containing the state variable annotations
stimulustree_[platform.short_caption].csv	File containing the stimulus annotations and comparisons
mutationtree_[platform.short_caption].csv	File containing the mutation annotations and comparisons
expressionmatrix_[platform.short_caption].csv	Expression matrix file for measure/chip combinations
orthologpairs_[platform1]_[platform2].csv	Ortholog pair file for this platform combination
comparisons_[experiment].csv	File containing comparison definition for an experiment
diffexpression_[nr]_[experiment].csv	Differential expression file for a comparison of an experiment

Table 1: Exported Files

### 1.3 Platform Descriptions

All export files reference the platform by a short description [platform.short\_caption]. This platform-export defines all available platforms of the database and maps the short caption with a readable caption.

Following attributes will be exported:

Fieldname	Description
platform.short_caption	Short name of the platform
platform.caption	Long name of the platform
organism.short_caption	Short name of the organism of this platform
technology.caption	Name of the technology of this platform
datatype.captions	Comma separated list of datatypes supported in this platform

Table 2: Field values exported for platforms

### 1.3.1 File Name

platforms.csv

### 1.3.2 File Format

The file format uses a CVS format as defined in [2] with two header rows and the delimiter comma (,) to separate the fields of a row.

1. Row. Header indicating the type of the export

```
"@@@platforms"
```

2. Row. Header defining the fields of each data row

```
"platform.short_caption","platform.caption","organism.short_caption","organism.caption",  
"technology.caption","datatype.captions"
```

- N. Each data row containing

```
[platform.short_caption]","[platform.caption]","[organism.short_caption]","  
[organism.caption]","[technology.caption]","[datatype.captions]"
```

### 1.3.3 Example

The export of the platforms files would result in the following file content:

```
"@@@platforms"  
"platform.short_caption","platform.caption","organism..."..."technology.caption","datatype.captions"  
"AT_AFFY_AG","Affymetrix Arabidopsis Genome Array","AT","Arabidopsis thaliana","MicroArray","RMA,RMA_LOG"  
"AT_AFFY_ATH1","Affymetrix Arabidopsis ATH1 Genome Array","AT","Arabidopsis..."..."MicroArray","RMA,RMA_LOG"  
"AT_mRNASeq_TAIR10_GL","mRNA-Seq Gene Level..."..."AT","Arabidopsis..."..."NGS","EXPECTED_COUNT,TPM,TPM_LOG"  
...
```

## 1.4 Experiment Descriptions

This section specifies the attributes exported for experiments of a given platform. The following experiment attributes will be exported:

Fieldname	Description
experiment.nbr	A unique string to identify an experiment. Defined by our curators.
experiment.caption	Name of experiment.
repository.caption	Repository name.
experiment.link	URL address of the experiment in the experiment repository. Empty string indicates the information is not known.
experiment.experimenter	Authors of the experiment.

Table 3: Field values exported for experiments

### 1.4.1 File Name

experiments\_[platform.short\_caption].csv

### 1.4.2 File Format

The file format uses a CVS format as defined in [2] with two header rows and the delimiter comma (,) to separate the fields of a row.

1. Row. Header indicating the type of the export

```
"@@@@@experiments"
```

2. Row. Header defining the fields of each data row

```
"experiment.nbr","experiment.caption","repository.caption","experiment.link","experiment.experimenter"
```

- N. Each data row containing

```
"[experiment.nbr]","[experiment.caption]","[repository.caption]","[experiment.link]","[experiment.experimenter]"
```

### 1.4.3 Example

As an example the export of the experiment attributes of a Mus musculus array (MM\_AFFY\_430.2) would result in the following file content. (Output shortened for formatting reasons):

```
"@@@@@experiments"
"experiment.nbr","experiment.caption","repository.caption","experiment.link","experiment.experimenter"
"MM-00001","GSE1479: C57BL/6 Benchmark Set for Early...","GEO","http:...","Schinke M et al. / Izumo S"
"MM-00002","GSE1871: Lung samples treated with...","GEO","http:...","Jacobson J et al. / Garcia JG"
"MM-00004","GSE2372: Aortae of 32 weeks old apoE mice","GEO","http:...","Habenicht AJ"
"MM-00006","GSE2463: Targets of FGFR2-IIIb signalling in the hair follicle","GEO","http:...","Schlake T"
...
```

## 1.5 Experiment-Replica-Chip Relations

This section specifies the exported relation between Experiment, Replica and its chips for a given platform. The following attributes will be exported:

### 1.5.1 File Name

experimenttree\_[platform.short\_caption].csv

Fieldname	Description
experiment.nbr	Name of experiment.
replica.caption	The name of this replica according to our curators naming scheme.
chip.id	A unique key identifying the chip in the database.
chip.caption	The original name of this chip defined by the experimenters or the repository.

Table 4: Field values exported for the experiment replica chip tree

### 1.5.2 File Format

The file format represents a tree of the relation between experiments, its replicas and its chips:

1. Row. Header indicating the type of the export:

```
"@@@@experiment"
```

2. Row. Definition of the experiment:

```
[experiment.nbr]
```

3. Row. Definition of the replica of the previous defined experiment intended by one comma:

```
, [replica.caption]
```

4. Row. Identification of the chip of the previous defined replica intended by two commas and the original name of the chip (separated by a comma from the identification)

```
,, [chip.id], [chip.caption]
```

5. Row. The next replica of the previous defined experiment

```
, [replica.caption]
```

6. Row. Identification of the chip of the previous defined replica intended by two commas and the original name of the chip (separated by a comma from the identification)

```
,, [chip.id], [chip.caption]
```

7. Row. The next experiment

```
[experiment.nbr]
```

...

### 1.5.3 Example

The export of the relation experiment-replica-chips of an Arabidopsis thaliana array (AT\_AFFY\_ATH1) results in the file (excerpt):

```
"@@@@experiment"
"AT-00087"
,"Dev. base._wt_cot_7d"
,,"AT-00087;ATGE_1_A", "ATGE_1_A"
,,"AT-00087;ATGE_1_B", "ATGE_1_B"
,,"AT-00087;ATGE_1_C", "ATGE_1_C"
,"Dev. base._wt_hyp_7d"
,,"AT-00087;ATGE_2_A", "ATGE_2_A"
```

```

,,"AT-00087;ATGE_2_B", "ATGE_2_B"
,,"AT-00087;ATGE_2_C", "ATGE_2_C"
...
AT-00088"
,,"Dev. base. 2_wt_inf_shoa_14d"
,,"AT-00088;ATGE_8_A", "ATGE_8_A"
,,"AT-00088;ATGE_8_B", "ATGE_8_B"
,,"AT-00088;ATGE_8_C", "ATGE_8_C"
,,"Dev. base. 2_wt_roo_17d"
,,"AT-00088;ATGE_9_A", "ATGE_9_A"
,,"AT-00088;ATGE_9_B", "ATGE_9_B"
,,"AT-00088;ATGE_9_C", "ATGE_9_C"
...

```

## 1.6 Experiment Ontologies

This section specifies the exported experiment ontology tree and its relation to the annotated experiments. The entries for this tree represent the ontology categories. The three experiment ontologies "Research Area", "Global Study Type" and "Study Design" are available. The following attributes of this relation will be exported:

Fieldname	Description
ontologyClass.externalname	The name of the ontology class: applicationarea, globalstudytype, studydesign
factor.caption	The name of this ontology category.
factor.notes	The notes/description for this category.
experiment.nbr	A unique key identifying the experiment in the database

Table 5: Field values exported for experiment ontology tree

### 1.6.1 File Name

```

applicationarea_[platform.short_caption].csv
globalstudytype_[platform.short_caption].csv
neoplasmtree_[platform.short_caption].csv

```

### 1.6.2 File Format

The file format represents a tree of the relation between experiment ontology categories and the experiments:

1. Row. Header indicating the type of the export:

```
"@@@[@ontologyClass.externalname]"
```

2. Row. Definition of the category (and optional value for notes):

```
"[factor.caption]", "[factor.notes]"
```

- N. N rows. Each row identifying the experiment related to the previous defined category. The experiment.nbr is intended by a number of commas equally to the current hierarchylevel of the current category:

```
,"[experiment.nbr]"
```

3. Row. Definition of the containing category (and optional value for notes) of the previous defined category:

```

,, "[factor.caption] ", "[factor.notes] "

```

M. M rows. Each row identifying the experiment of the previous defined category. The experiment.nbr is intended by a number of commas equally to the current hierarchy level of the current category:

```

,,, "[experiment.nbr] "

```

...

### 1.6.3 Example

The export of the experiment ontology "Research Area" without notes results in the file (excerpt):

```

"@@@applicationarea"
"Cardiology and angiology"
,"Basic research (cardiology and angiology)"
,, "MM-00001"
,, "MM-00148"
...
,"Arrhythmia"
,, "Atrial fibrillation"
,,, "MM-00348"
,,, "MM-00427"
,,, "HS-00120"
,, "Tachycardia"
,,, "RN-00095"
...

```

## 1.7 Anatomy, Cell Line, Neoplasm, Development and State Variable Annotations

This section specifies the exported ontology tree and the annotated chips for a given platform and ontology. The entries for this tree represent the ontology categories. Note: The entries of an anatomy tree represent anatomical categories and are also known as otc (Organ-Tissue-Cells). The entries of a state variable tree represent clinical parameters.

The following attributes of this relation will be exported:

Fieldname	Description
ontologyClass.externalname	The name of the ontology class: anatomy, cellline, neoplasm development, statevariable
factor.caption	The name of this category.
factor.notes	The notes/description for this category.
chip.id	A unique key identifying the chip in the database

Table 6: Field values exported for exported ontology trees

### 1.7.1 File Name

```

anatomytree_[platform.short.caption].csv
celllinetree_[platform.short.caption].csv
neoplasmtree_[platform.short.caption].csv
developmenttree_[platform.short.caption].csv
statevariabletree_[platform.short.caption].csv

```

### 1.7.2 File Format

The file format represents a tree of the relation between ontology categories and the chips:

1. Row. Header indicating the type of the export:

```
"@@@ontologyClass.externalname"
```

2. Row. Definition of the ontology category (and optional value for notes):

```
"[factor.caption]", "[factor.notes]"
```

- N. N rows. Each row identifying the chip of the previous defined ontology category. The chip.id is intended by a number of commas equally to the current hierarchy level of the current ontology category:

```
,"[chip.id]"
```

3. Row. Definition of the containing ontology category (and optional value for notes) of the previous defined ontology category:

```
,"[factor.caption]", "[factor.notes]"
```

- M. M rows. Each row identifying the chip of the previous defined ontology category. The chip.id is intended by a number of commas equally to the current hierarchy level of the current ontology category:

```
,,,"[chip.id]"
```

...

### 1.7.3 Example

The export of the anatomy-chip-relation of an Arabidopsis thaliana array (AT\_AFFY\_ATH1) without notes results in the file (excerpt):

```
"@@@anatomy"  
"callus"  
,"AT-00265;GSM227609"  
,"AT-00265;GSM227610"  
,"AT-00078;GSM142591"  
,"AT-00078;GSM142592"  
,"AT-00078;GSM142593"  
...  
"cell culture / primary cell"  
,"AT-00005;T0_APH"  
,"AT-00005;T2_APH"  
,"AT-00005;T4_APH"  
,"AT-00005;T6_APH"  
,"AT-00005;T8_APH"  
...
```

## 1.8 Stimulus and Mutation Annotations

This section specifies the exported relation between Stimulus (resp. Mutation), the treatment and control comparison sets and its chips for a given platform. The following attributes will be exported:

Fieldname	Description
ontologyClass.externalname	The name of the ontology class: stimulus, mutation
factor.caption	The name of the stimulus/mutation category.
factor.notes	The notes/description of this stimulus/mutation category.
chip.id	A unique key identifying the chip in the database.

Table 7: Field values exported for stimulus/mutation chip tree

### 1.8.1 File Name

stimulustree\_[platform.short\_caption].csv  
 mutationtree\_[platform.short\_caption].csv

### 1.8.2 File Format

The file format represents a tree of the relation between stimulus (mutation), its optional contained stimulus (mutation), the chips annotated to the stimulus (mutation) and the comparison set in which the stimulus (mutation) participates defined as a treatment and control group of chips:

1. Row. Header indicating the type of the export:

```
"@@@ontologyClass.externalname"
```

2. Row. Definition of the category (and optional value for notes) :

```
"[factor.caption]","[factor.notes]"
```

- N. N rows. Each row identifying the annotated chip of the previous defined category (Intended by the a number of commas equal to the current hierarchy level).

```
,"[chip.id]"
```

3. Row. Keyword to indicate the start of a treatment and control group (Intended by the a number of commas equal to the current hierarchy level).

```
,"COMPARISONSET"
```

4. Row. Definition of the categories for the treatment group (each separated by comma):

```
,"[factor.caption]"
```

- N. N rows. Each row identifying the chip of the previously defined treatment group.

```
,"[chip.id]"
```

5. Row. Definition of the categories for the control group (each separated by comma):

```
,"[factor.caption]"
```

- N. N rows. Each row identifying the chip of the previously defined control group.

```
,"[chip.id]"
```

6. Row. Optionally an category contained in the previously defined category (and optional value for notes). (Intended by the a number of commas equal to the current hierarchy level).

...



Note: Each COMPARISONSET entry with the same treatment and control group is written once only to the file to reduce redundancy. During the depth-first traversal of the tree the COMPARISONSET entry is written to the first category participating in the control or treatment group. If the tree traversal encounters another stimulus category to the same COMPARISONSET entry the output is suppressed.

```

"@@@ontologyClass.externalname"
"factor1.caption","factor1.notes"
,"chip1.id"
,"chip2.id"
...
,"chipN.id"
,"COMPARISONSET"
,,"factor2.caption" of treatment replica set
,,,"chip1.id"
,,,"chip2.id"
...
,,,"chipN.id"
,,"factor3.caption" of control replica set
,,,"chip1.id"
,,,"chip2.id"
...
,,,"chipN.id"
...
"factor6.caption","factor6.notes"
,"chip1.id"
,"chip2.id"
...
,"chipN.id"
,"factor7.caption","factor7.notes"
,,"chip1.id"
,,"chip2.id"
...
,,,"chipN.id"
,,,"COMPARISONSET"
,,,"factor8.caption" of treatment replica set
,,,"chip1.id"
,,,"chip2.id"
...
,,,"chipN.id"
,,,"factor9.caption" of control replica set
,,,"chip1.id"
,,,"chip2.id"
...
,,,"chipN.id"

```

### 1.8.3 Example

The export of the stimulus-chip-relation of an Arabidopsis thaliana array (AT\_AFFY\_ATH1) without notes results in the file (excerpt):

```

"@@@stimulus"
"Biotic"
,"B. cinerea"
,,"AT-00147;GSM133025"
,,"AT-00147;GSM133026"
,,"AT-00147;GSM133027"
,,"AT-00147;GSM133028"

```

```

,, "AT-00147;GSM133029"
,, "AT-00147;GSM133030"
,, "COMPARISONSET"
,, "B. cinerea"
,,, "AT-00147;GSM133028"
,,, "AT-00147;GSM133029"
,,, "AT-00147;GSM133030"
,,, "AT-00147;GSM133025"
,,, "AT-00147;GSM133026"
,,, "AT-00147;GSM133027"
,, "non-infected rosette leaf samples"
,,, "AT-00147;GSM133034"
,,, "AT-00147;GSM133035"
,,, "AT-00147;GSM133036"
,,, "AT-00147;GSM133031"
,,, "AT-00147;GSM133032"
,,, "AT-00147;GSM133033"
, "P. syringae pv. tomato study 4 (DC3000 avrRpm1)"
,, "AT-00238;GSM157375"
,, "AT-00238;GSM157378"
,, "AT-00238;GSM157381"
,, "COMPARISONSET"
,,, "P. syringae pv. tomato study 4 (DC3000 avrRpm1)"
,,, "AT-00238;GSM157375"
,,, "AT-00238;GSM157378"
,,, "AT-00238;GSM157381"
,, "P. syringae pv. tomato study 4 (DC3000)"
,,, "AT-00238;GSM157373"
,,, "AT-00238;GSM157376"
,,, "AT-00238;GSM157379"
, "P. syringae pv. tomato study 4 (DC3000 hrpA-)"
,, "AT-00238;GSM157374"
,, "AT-00238;GSM157377"
,, "AT-00238;GSM157380"
...

```

## 1.9 Expression Matrix

This section specifies the files of exported expression values (RMA-normalized signal values for MicroArrays, TPM or expected counts for mRNASeq) for a given platform. The following fields will be exported:

Fieldname	Description
measure.captio	Identification of transcript
chip.id	A unique key identifying the chip in the database.

Table 8: Field values exported for expression matrix

### 1.9.1 File Name

expressionmatrix\_[platform.short\_captio].csv

### 1.9.2 File Format

The file format is a matrix containing the chip.ids in the first row and the measure captions in the first column. The upper left corner contains the datatype of the expression values. The comma is used as a

delimiter. Each expression value is formatted according to the *Float.toString(float f)* method. See [1].

```
[datatype.caption],chip1.id,chip2.id,chip3.id, ...
measure1.caption,#.#####,#.#####,#.#####, ...
measure2.caption,#.#####,#.#####,#.#####, ...
measure3.caption,#.#####,#.#####,#.#####, ...
...
```

### 1.9.3 Example

The export of the expression values of the mRNA-Seq Gene Level Arabidopsis thaliana platform (platform.short.caption AT\_mRNASeq\_TAIR10-GL) results in the file (excerpt):

```
"TPM", "AT-00699;SRR515335", "AT-00699;SRR515336", "AT-00699;SRR515337", "AT-00699;SRR515338", ...
"AT1G01010", "6.831336", "5.1100297", "4.6547737", "5.411358", ...
"AT1G01020", "19.085173", "18.716497", "18.911911", "17.526339", ...
"AT1G01030", "6.436051", "6.9451795", "5.311087", "6.461323", ...
"AT1G01040", "12.0511265", "11.710485", "11.278486", "12.226034", ...
...
```

## 1.10 Ortholog File

This section specifies the exported ortholog information. The following attributes will be exported:

Fieldname	Description
organism.short.caption	Short name of the organism
gene.caption	Name of the gene
alias.caption	Name of the alias(es) of the gene in different naming schemes
platform.short.caption	Short name of the platform of the measure
measure.caption	Name of the measure
numTissues	Number of tissues
sequenceScore	Sequence score, currently PAM
expressionScore	Expression score based on tissues and measure of the specified gene

Table 9: Field values exported in ortholog file

### 1.10.1 File Name

orthologs.csv

### 1.10.2 File Format

The file format is a csv file containing on each row a pair of orthologus genes from two different organisms including the number of tissues and measure used two compute expression score and the sequence score (PAM).

1. Row. Comment line indicating the type of the export:

```
# organism1, gene1, alias1, platform1, measure1, numTissues1,
organism2, gene2, alias2, platform2, measure2, numTissues2,
sequenceScore, expressionScore
```

- N. N rows. Definition of the orthologous gene pair :

```
"[organism1.short\_caption.caption]", "[gene1.caption]", "[alias1.caption]",
"[platform1.short\_caption.caption]", "[measure1.caption]", "[numTissues1]",
"[organism2.short\_caption.caption]", "[gene2.caption]", "[alias2.caption]",
"[platform2.short\_caption.caption]", "[measure2.caption]", "[numTissues2]",
"[sequenceScore]", "[expressionScore]"
```

### 1.10.3 Example

The export of the orthologous gene between Arabidopsis thaliana and Glycine max results in the file (excerpt):

```
# organism1, gene1, alias1, platform1, measure1, numTissues1, organism2, gene2, alias2, platform2, ...
AT, AT1G01050, PPA1, AT_AFFY_ATH1, 261579_at, 105, GM, Glyma.07G048300, Glyma.07G048300, GM_AFFY_...
AT, AT1G01060, LHY, AT_AFFY_ATH1, 261569_at, 105, GM, Glyma.07G048500, Glyma.07G048500, GM_AFFY_...
AT, AT1G01060, LHY, AT_AFFY_ATH1, 261569_at, 105, GM, Glyma.16G017400, Glyma.16G017400, GM_AFFY_...
AT, AT1G01080, , AT_AFFY_ATH1, 261577_at, 105, GM, Glyma.07G049500, Glyma.07G049500, GM_AFFY_...
AT, AT1G01100, RPP1A, AT_AFFY_ATH1, 261578_at, 105, GM, Glyma.04G229000, Glyma.04G229000, GM_AFFY_...
AT, AT1G01110, IQD18, AT_AFFY_ATH1, 261580_at, 105, GM, Glyma.16G019700, Glyma.16G019700, GM_AFFY_...
AT, AT1G01120, KCS1, AT_AFFY_ATH1, 261570_at, 105, GM, Glyma.03G260300, Glyma.03G260300, GM_AFFY_...
```

## 1.11 Comparison File

This section specifies the comparison file format. The following attributes are used:

Fieldname	Description
experiment.nbr	A unique key identifying the experiment in the database
chip.name	Sample name as shown in the Genvestigator system
chip.caption	Sample caption, original sample name
treatment.caption	Caption of the treatment group of a comparison
control.caption	Caption of the control group of a comparison
(t,c)	Sample membership in comparison, t = treatment, c = control

Table 10: Field values of a comparison file

### 1.11.1 File Name

comparisons\_[experiment.nbr].csv

### 1.11.2 File Format

The file format is a csv file containing for an experiment on each row the sample at its membership in a comparison of this experiment.

1. Row. Header line defining comparison names:

```
experiment number, chip name, chip caption org, [treatment.caption]" / "[control.caption],...
```

- N. N rows. Definition of the membership of the sample in the listed comparisons of the header :

```
"[experiment.nbr]", "[chip.name]", "[chip.caption]", (t|c|"),...
```

### 1.11.3 Example

The export of all comparisons of a human experiment results in a file (excerpt):

```
experiment number,chip name,chip caption org,prostate cancer study 8 (p. canc) / prostate cancer...
HS-00739,Prostate cancer 9_stro._pro_CD90+ ptasc_m#2_rep_1,GSM447178,c,,t
HS-00739,Prostate cancer 9_stro._pro_CD90+ ptasc_m#1_rep_1,GSM447176,c,,t
HS-00739,Prostate cancer 9_stro._bla_CD13+ btasc_m_rep_1,GSM447174,,,
HS-00739,Prostate cancer 9_prim._pro_p. can_m#4_rep_1,GSM447169,,t,,
...
```

## 1.12 Differential Expression File

This section specifies the differential expression file format used to show the differentially expressed of a comparison. The following attributes are used:

Fieldname	Description
gene.caption	Name of the gene
measure.caption	Name of the measure
treatment.caption	Caption of the samples in the treatment group of a comparison
control.caption	Caption of the samples in the control group of a comparison
chip.name	Sample name as shown in the Genvestigator system
alias.description	Description of the alias of current gene

Table 11: Field values of a differential expression file

### 1.12.1 File Name

diffexpression\_[nr]\_[experiment.nbr].csv

### 1.12.2 File Format

The file format is a csv file containing on each row a pair of orthologus genes from two different organisms including the number of tissues and measure used two compute expression score and the sequence score (PAM).

1. Row. Comment line indicating the experiment:

```
# experiment number: [experiment.nbr]
```

2. Row. Comment line indicating the comparison:

```
# comparison name: [treatment.caption]" / "[control.caption]
```

3. Row. Comment line indicating the samples of the treatment group:

```
# treatment chip names: (chip.name)+
```

4. Row. Comment line indicating the samples of the control group:

```
# control chip names: (chip.name)+
```

5. Row. Header line defining the exported data for differentially expressed genes:

```
"treatmentMeanExpression","controlMeanExpression","Log-ratio","p-value","minFDR",
"Gene","Measure","Description"
```

N. N rows. The exported data values, Floating point values are formatted according to the *Float.toString(float f)* method. See [1]:

```
[#.#####], [#.#####] ", "[#.#####]",  
"[#.#####]", "[#.#####]", "[gene.caption]", "[measure.caption]", [(alias.description)+]
```

### 1.12.3 Example

The export of the differentially expressed genes of a comparison of a human experiments results in a file like (excerpt):

```
"# experiment number: HS-00739"  
"# comparison name: prostate cancer study 8 (p. canc) / prostate cancer study 8 (ptasc)"  
"# treatment chip names: Prostate cancer 9_prim._pro_CD26+ p. canc_m#3_rep_1, Prostate ...  
"# control chip names: Prostate cancer 9_stro._pro_CD90+ ptasc_m#2_rep_1, Prostate ...  
"treatmentMeanExpression", "controlMeanExpression", "Log-ratio", "p-value", "minFDR", "Gene", "M...  
15.897747993469238,9.259182929992676,6.6385650634765625,2.892487585162697E-8,2.6950458005851977E-4,...  
16.8458251953125,9.435758590698242,7.410066604614258,2.9516181758604798E-8,2.6950458005851977E-4,...  
15.628425598144531,7.960296630859375,7.668128967285156,3.4487021846765027E-8,2.6950458005851977E-4,...  
...
```

### 1.13 Geo Matrix Series format

We refer to the official documentation on GEO for a description of this format:

<http://www.ncbi.nlm.nih.gov/geo/info/overview.html>

<https://www.ncbi.nlm.nih.gov/geo/info/soft.html>

## References

- [1] S. Microsystems. Java float.toString(float f), 2008. <http://www.j2ee.me/javase/6/docs/api/java/lang/Float.html>.
- [2] Y. Shafranovich. Common format and mime type for comma-separated values (csv) files, 2005. <http://www.rfc-editor.org/rfc/rfc4180.txt>.