

A key to standard microarray spot identity tracking file formats

Overview

Each microarray spot has a unique position and each spot corresponds to a specific probe DNA from a specific well of a microtitre plate. There are typically thousands to tens of thousands of probe DNAs distributed between tens of source plates and thousands to tens of thousands of spots on each microarray. A single microarray experiment can consist of a few or a hundred microarray hybridisations. Tracking where and what each probe DNA is on each microarray is therefore an important issue.

Most robotic spotters are supplied with a data tracking program that uses an input file to describe the positions of each probe DNA within the microtitre plates and another file that defines how the microarray was printed to produce a description of where each probe DNA is within each microarray. These spot identities can then be imported into a spot finding and quantification tool that will 'append' the fluorescence spot signal. These data are then analysed to determine what affect any given experimental condition or treatment has had on the gene expression of the samples being compared.

For a definition of all terminology used below please refer to "Introduction to printing microarrays".

- The microarray layout used in the following examples
- The microarray input file used in the following examples
- Example microarray spot identity file formats
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 - ◆ Layout Map Xyxy
 - ◆ Layout Map XYyx
 - ◆ Layout Map YXxy
 - ◆ Layout Map YXyx

The microarray layout used in the following examples

1. Meta-grid Layout:

A single 2x2 (X and Y axis) meta-grid printed on each slide
Numbers below refer to the pins that printed the sub-grids

01 02
03 04

Array position from bottom left of slide: 9.24 mm (X-axis), 34.19 mm (Y-axis)
Meta-grid has an array area of 6.10 mm (X-axis) by 6.10 mm (Y-axis)

2. Sub-grid Layout:

Each sub-grid has 4x4 (16) spots
Centre-to-centre spot distance is 400 microns
Numbers below refer to 'Source Visits'

13 14 15 16

```
09 10 11 12
05 06 07 08
01 02 03 04
```

Key to Source Visits
Source '1' to '16' = Imaginary clones

3. Comments:

This is a hypothetical microarray
The arrays contains 64 spots per slide

The microarray input file used in the following examples

The following is a small section of a file that describes a fictitious source plate. Well position is defined by source plate barcode (e.g. TST101), row (A to P) and column (1 to 24). CloneID is a cDNA clone accession code and UniqueID is a well-specific identifier. The columns do not need to be in the order shown. The example shown is a 'tab separated value' (TSV) text file.

CloneID	UniqueID	Row	Column
FC1234	TST101	A	1
FC1235	TST101	A	2
FC1236	TST101	A	3
FC1237	TST101	A	4
Empty	Empty	A	5
Empty	Empty	A	6
Empty	Empty	A	7
Empty	Empty	A	8
Empty	Empty	A	9
Empty	Empty	A	10
Empty	Empty	A	11
Empty	Empty	A	12
Empty	Empty	A	13
Empty	Empty	A	14
Empty	Empty	A	15
Empty	Empty	A	16
Empty	Empty	A	17
Empty	Empty	A	18
Empty	Empty	A	19
Empty	Empty	A	20
Empty	Empty	A	21
Empty	Empty	A	22
Empty	Empty	A	23
Empty	Empty	A	24
FC1238	TST101	B	1
FC1239	TST101	B	2
FC1240	TST101	B	3
FC1241	TST101	B	4
Empty	Empty	B	5
Empty	Empty	B	6
Empty	Empty	B	7

This input file was used to create a series of clone tracking files using the MicroGrid II so that the format structures could be explained using worked examples. These are shown in the following sections, an asterisk denotes an explanation rather than a component of the named file format.

Example microarray spot identity file formats

BioRobotics 'TAM' format

```
[FileInformation]
FileFormat=,1.0 *Version number of the file format
```

The microarray layout used in the following examples

FormatName=,TAM *File format extension
 GeneratedBy=,TAS2.1.5.16 *Arrayer software and version
 BlockCount=,4 *Number of meta-grids
 SpotSize=,180 *Estimated mean spot diameter

[Block1] *Sub-grid being examined
 MetaGridX=,1 *Meta-grid X-axis co-ordinate
 MetaGridY=,1 *Meta-grid Y-axis co-ordinate
 OriginX=,9000 *Distance from top left edge of slide to centre of top left spot
 OriginY=,35300 *Distance from top left edge of slide to centre of top left spot
 BlockSizeX=,4 *Number of spots in each row
 BlockSizeY=,4 *Number of spots in each column
 SpacingX=,400 *X-axis centre-to-centre spot spacing
 SpacingY=,400 *X-axis centre-to-centre spot spacing
 *Information is repeated for each sub-grid on the slide

[mapping] *'comma separated value' spreadsheet that maps clones to wells
 1,1,1,1,,1,9,4,"FC1269","1036",1, {},FC1269,1036,TST101,I,4
 1,1,1,2,,1,1,4,"FC1237","1004",1, {},FC1237,1004,TST101,A,4
 1,1,1,3,,1,9,2,"FC1267","1034",1, {},FC1267,1034,TST101,I,2
 1,1,1,4,,1,1,2,"FC1235","1002",1, {},FC1235,1002,TST101,A,2
 1,1,2,1,,1,11,4,"FC1277","1044",1, {},FC1277,1044,TST101,K,4

*Spreadsheet abbreviated for brevity.
 *Each row of data relates to each spot on the microarray.
 *Origin is top left of slide for all measurements.

*Column 01: Meta-grid X-axis co-ordinate
 *Column 02: Meta-grid Y-axis co-ordinate
 *Column 03: Sub-grid Y-axis co-ordinate
 *Column 04: Sub-grid X-axis co-ordinate
 *Column 05: Plate Barcode
 *Column 06: Plate Number
 *Column 07: Row Number
 *Column 08: Column Number
 *Column 09: Sample Name
 *Column 10: Sample ID
 *Column 11: Block number
 *Column 12: Termination of additional fields
 *Column 13 to End: Source data from the operator (See [Example Array Input File](#))

Axon 'GAL' format

ATF 1.0
 10 5 *first term is the number of headers, not including this, the previous or
 the column header row. The second term is the number of columns
 "Type=GenePix ArrayList V1.0" *Version number of the file format
 "BlockCount=4" *Number of sub-grids
 "BlockType=0"
 "Block1=9000, 35300, 180, 4, 400, 4, 400" *Mapping information for sub-grid 1
 "Block2=13500, 35300, 180, 4, 400, 4, 400" *Mapping information for sub-grid 2
 "Block3=9000, 39800, 180, 4, 400, 4, 400" *Mapping information for sub-grid 3
 "Block4=13500, 39800, 180, 4, 400, 4, 400" *Mapping information for sub-grid 4
 "Supplier=BioRobotics" *Arrayer manufacturer
 "ArrayerSoftwareName=TAS Application Suite (MicroGrid II)" *Arrayer software name
 "ArrayerSoftwareVersion=2.1.5.16" *Arrayer software version
 "Block" "Column" "Row" "ID" "Name"
 *Header for clone mapping 'tab separated value' (TSV) spreadsheet
 1 1 1 1036 FC1269
 1 1 2 1004 FC1237
 1 1 3 1034 FC1267
 1 1 4 1002 FC1235
 1 2 1 1044 FC1277
 1 2 2 1012 FC1245
 1 2 3 1042 FC1275

1	2	4	1010	FC1243
1	3	1	1052	FC1285
1	3	2	1020	FC1253
1	3	3	1050	FC1283
1	3	4	1018	FC1251
1	4	1	1060	FC1293
1	4	2	1028	FC1261
1	4	3	1058	FC1291
1	4	4	1026	FC1259
2	1	1	1040	FC1273
2	1	2	1008	FC1241
2	1	3	1038	FC1271
2	1	4	1006	FC1239
2	2	1	1048	FC1281
2	2	2	1016	FC1249
2	2	3	1046	FC1279
2	2	4	1014	FC1247
2	3	1	1056	FC1289
2	3	2	1024	FC1257

*Spreadsheet abbreviated for brevity.
 *Each row of data relates to each spot on the microarray.
 *Origin is top left of slide for all measurements.

*Block: Sub-grid identification
 *Column: Sub-grid Y-axis co-ordinate
 *Row: Sub-grid X-axis co-ordinate
 *ID: Sample ID (See [Example Array Input File](#))
 *Name: Sample Name (See [Example Array Input File](#))

Molecularware 'MWBR' format

[FileInformation]

FileFormat=,1.0.2 *Version number of the file format
 FormatName=,MwBr *File format extension
 GeneratedBy=,TAS2.1.5.16 *Arrayer software and version
 BlockCount=,4 *Number of sub-grids
 SpotSize=,180 *Estimated mean spot diameter

[Source]

Comment=,Genetix384 *Source plate type
 XWells=,16 *Number of wells in X-axis
 YWells=,24 *Number of wells in Y-axis
 XPitch=,4.5 *Well spacing in X-axis
 YPitch=,4.5 *Well spacing in Y-axis
 PlateCount=,1 *Number of source plates

[Tool]

Description=,2x2 (384 well) split pin *MicroSpot II pin number and type
 PinsX=,2 *Number of MicroSpot pins in X-axis
 PinsY=,2 *Number of MicroSpot pins in Y-axis
 PinPitch=,4500 *Pin-to-pin spacing in the pin-tool

[Target]

TargetWidth=,25000 *Width of the glass microscope slide
 TargetHeight=,75000 *Height of the glass microscope slide
 LeftMargin=,9239 *Meta-grid distance from left of slide
 RightMargin=,9239 *Meta-grid distance from right of slide
 TopMargin=,34189 *Meta-grid distance from top of slide
 BottomMargin=,34189 *Meta-grid distance from bottom of slide
 XSpacing=,0 *Spacing between meta-grids in X-axis
 YSpacing=,0 *Spacing between meta-grids in Y-axis
 NumberOfCopies=,27 *Number of slides being printed

[slides] *Mapping of the slide the microarray was printed on
 Slide1=,1,20000,243000, *List abbreviated to save space

Axon 'GAL' format

```
[Block1] *Sub-grid being examined
MetaGridX=,1 *Meta-grid X-axis co-ordinate
MetaGridY=,1 *Meta-grid Y-axis co-ordinate
OriginX=,9000 *Distance from top left edge of slide to centre of top left spot
OriginY=,35300 *Distance from top left edge of slide to centre of top left spot
BlockSizeX=,4 *Number of spots in each row
BlockSizeY=,4 *Number of spots in each column
SpacingX=,400 *X-axis centre-to-centre spot spacing
SpacingY=,400 *X-axis centre-to-centre spot spacing
*Information is repeated for each sub-grid on the slide
```

```
[mapping]*As for TAM format expect column 3 and 4 are in the reverse order
1,1,1,1,,1,9,4,"FC1269","1036",1, {},FC1269,1036,TST101,I,4
1,1,1,2,,1,1,4,"FC1237","1004",1, {},FC1237,1004,TST101,A,4
```

```
*Spreadsheet abbreviated for brevity.
*Each row of data relates to each spot on the microarray.
*Origin is top left of slide for all measurements.
```

Applied Precision Instruments arrayWoRx 'REF' format

```
#ArrayWoRx Reference File *File Format
#Tag 0x00FF040C
#Version: 2.10 *File format version
#GridOrigin: 34190 9660
#GridRotation: 0
#GridType: Irregular
#GridColumnsRows: 64 1
#GridWidthHeight: 6100 6100 *Array size: X-axis, Y-axis
#NomSpotSpacingColumnRow: 400 400 *X-axis Y-axis centre-to-centre spot distance
#OddRowOffset: 0
#Number_UniqueID_Types: 2
#UniqueID_Type 1: 0
#UniqueID_Type 2: 0
#Column 1: Spot number *Key to the clone spreadsheet
#Column 2: Spot name 1 [gene name] *Key to the clone spreadsheet
#Column 3: Spot name 2 [chromosome] *Key to the clone spreadsheet
#Column 4: Spot type [1=experiment; 2=ratio control] *Key to the clone spreadsheet
#Column 5: Unique ID 1 *Key to the clone spreadsheet
#Column 6: Unique ID 2 *Key to the clone spreadsheet
#Column 7: X coordinate *Key to the clone spreadsheet
#Column 8: Y coordinate *Key to the clone spreadsheet
#Column 9: Spot size 1 [width in um] *Key to the clone spreadsheet
#Column 10: Spot size 2 [height in um] *Key to the clone spreadsheet
#Column 11: Bounding box width [ROI about the spot] *Key to the clone spreadsheet
#Column 12: Bounding box height [ROI about the spot] *Key to the clone spreadsheet
#Column 13: Reserved column 1 *Key to the clone spreadsheet
#Column 14: Reserved column 2 *Key to the clone spreadsheet
#Column 15: Reserved column 3 *Key to the clone spreadsheet
#Column 16: Reserved column 4 *Key to the clone spreadsheet
#Column 17: Reserved column 5 *Key to the clone spreadsheet
#Column 18: Reserved column 6 *Key to the clone spreadsheet
#Column 19: Reserved column 7 *Key to the clone spreadsheet
#Column 20: Reserved column 8 *Key to the clone spreadsheet
#Column 21: Include flag [0=exclude; 1=include] *Key to the clone spreadsheet
#Column 22: Description [optional] *Key to the clone spreadsheet
```

```
*Tab separated value (TSV) clone spreadsheet
```

```
1 FC1262 unknown 1 1029 Unknown 34190 9660 180 180 200 200 * * * * * * * * 1 Plate 1, Well H1
2 FC1294 unknown 1 1061 Unknown 34590 9660 180 180 200 200 * * * * * * * * 1 Plate 1, Well P1
3 FC1264 unknown 1 1031 Unknown 34990 9660 180 180 200 200 * * * * * * * * 1 Plate 1, Well H3
4 FC1296 unknown 1 1063 Unknown 35390 9660 180 180 200 200 * * * * * * * * 1 Plate 1, Well P3
```

```
*Spreadsheet abbreviated for brevity.
```

*Each row of data relates to each spot on the microarray.
*Origin is bottom left of slide for all measurements.

Quantarray file format

*'Tab separated value' (TSV) text file

1	1	1	1	1036
1	1	2	1	1004
1	1	3	1	1034
1	1	4	1	1002
1	1	1	2	1044
1	1	2	2	1012
1	1	3	2	1042
1	1	4	2	1010
1	1	1	3	1052
1	1	2	3	1020
1	1	3	3	1050
1	1	4	3	1018

*Spreadsheet abbreviated for brevity.

*Each row of data relates to each spot on the microarray.

*Origin is top left of slide for all measurements.

*Column 01: Meta-grid X-axis co-ordinate

*Column 02: Meta-grid Y-axis co-ordinate

*Column 03: Sub-grid Y-axis co-ordinate

*Column 04: Sub-grid X-axis co-ordinate

*Column 05: 'UniqueID' (See [Example Array Input File](#))

Imagene file format

*'Tab separated value' (TSV) text file

1	1	1	1	1036
1	1	1	2	1004
1	1	1	3	1034
1	1	1	4	1002
1	1	2	1	1044
1	1	2	2	1012
1	1	2	3	1042
1	1	2	4	1010
1	1	3	1	1052
1	1	3	2	1020
1	1	3	3	1050
1	1	3	4	1018

*Spreadsheet abbreviated for brevity.

*Each row of data relates to each spot on the microarray.

*Origin is top left of slide for all measurements.

*Column 01: Meta-grid X-axis co-ordinate

*Column 02: Meta-grid Y-axis co-ordinate

*Column 03: Sub-grid X-axis co-ordinate

*Column 04: Sub-grid Y-axis co-ordinate

*Column 05: 'UniqueID' (See [Example Array Input File](#))

Layout Map XYxy

*'Tab separated value' (TSV) text file

1	1	1	1	1036
1	1	1	2	1004
1	1	1	3	1034
1	1	1	4	1002

1	1	2	1	1044
1	1	2	2	1012
1	1	2	3	1042
1	1	2	4	1010
1	1	3	1	1052
1	1	3	2	1020
1	1	3	3	1050
1	1	3	4	1018

*Spreadsheet abbreviated for brevity.
 *Each row of data relates to each spot on the microarray.
 *Origin is top left of slide for all measurements.

*Column 01: Meta-grid X-axis co-ordinate
 *Column 02: Meta-grid Y-axis co-ordinate
 *Column 03: Sub-grid X-axis co-ordinate
 *Column 04: Sub-grid Y-axis co-ordinate
 *Column 05: 'UniqueID' (See [Example Array Input File](#))

Layout Map XYyx

*'Tab separated value' (TSV) text file

1	1	1	1	1036
1	1	2	1	1004
1	1	3	1	1034
1	1	4	1	1002
1	1	1	2	1044
1	1	2	2	1012
1	1	3	2	1042
1	1	4	2	1010
1	1	1	3	1052
1	1	2	3	1020
1	1	3	3	1050
1	1	4	3	1018

*Spreadsheet abbreviated for brevity.
 *Each row of data relates to each spot on the microarray.
 *Origin is top left of slide for all measurements.

*Column 01: Meta-grid X-axis co-ordinate
 *Column 02: Meta-grid Y-axis co-ordinate
 *Column 03: Sub-grid Y-axis co-ordinate
 *Column 04: Sub-grid X-axis co-ordinate
 *Column 05: 'UniqueID' (See [Example Array Input File](#))

Layout Map YXxy

*'Tab separated value' (TSV) text file

1	1	1	1	1036
1	1	1	2	1004
1	1	1	3	1034
1	1	1	4	1002
1	1	2	1	1044
1	1	2	2	1012
1	1	2	3	1042
1	1	2	4	1010
1	1	3	1	1052
1	1	3	2	1020
1	1	3	3	1050
1	1	3	4	1018

*Spreadsheet abbreviated for brevity.
 *Each row of data relates to each spot on the microarray.
 *Origin is top left of slide for all measurements.

Layout Map XYxy

*Column 01: Meta-grid Y-axis co-ordinate
*Column 02: Meta-grid X-axis co-ordinate
*Column 03: Sub-grid X-axis co-ordinate
*Column 04: Sub-grid Y-axis co-ordinate
*Column 05: 'UniqueID' (See [Example Array Input File](#))

Layout Map YXyx

*'Tab separated value' (TSV) text file

1	1	1	1	1036
1	1	2	1	1004
1	1	3	1	1034
1	1	4	1	1002
1	1	1	2	1044
1	1	2	2	1012
1	1	3	2	1042
1	1	4	2	1010
1	1	1	3	1052
1	1	2	3	1020
1	1	3	3	1050
1	1	4	3	1018

*Spreadsheet abbreviated for brevity.
*Each row of data relates to each spot on the microarray.
*Origin is top left of slide for all measurements.

*Column 01: Meta-grid Y-axis co-ordinate
*Column 02: Meta-grid X-axis co-ordinate
*Column 03: Sub-grid Y-axis co-ordinate
*Column 04: Sub-grid X-axis co-ordinate
*Column 05: 'UniqueID' (See [Example Array Input File](#))

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