

# Introduction to the gsplom Package

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## Contents

1	Background	1
2	How to produce SCAN estimates for Agilent two-color microarrays	3
3	Conclusion	4

## 1 Background

This vignette describes how to normalize samples with the *Single-Channel Array Normalization* (SCAN) and *Universal exPression Codes* (UPC) methods.

```
> library(GEOquery)
> tmpDir = tempdir()
> library(GEOquery)
> getGEOSuppFiles("GSM555237", makeDirectory=FALSE, baseDir=tmpDir)
> celFilePath = file.path(tmpDir, "GSM555237.CEL.gz")
```

To normalize the sample, we invoke the `SCAN` function. This function requires one mandatory parameter: a path specifying the location of the file to be normalized.

```
> library(SCAN.UPC)
> normalized = SCAN(celFilePath)
```

For convenience, it is also possible to download microarray samples from GEO and normalize them in a single step. To do this, substitute the file path with a GEO identifier.

```
> normalized = SCAN("GSM555237")
```

The `SCAN` function returns an *ExpressionSet* object containing a row for each probe-set value. Detailed status information, including the number of iterations required for mathematical convergence of the mixture model, is printed to the console.

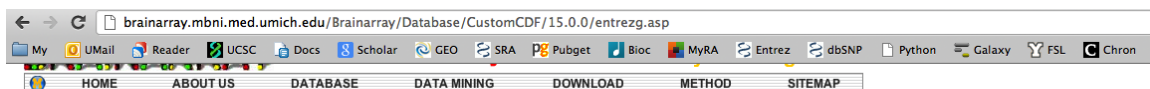
Multiple input files can be processed in one command via specifying wildcard characters (e.g., "\*.CEL") or GEO experiment identifiers (e.g., "GSE22309"). In this case, the `SCAN` function returns an *ExpressionSet* object with a row for each probeset and a column for each input file.

Using the optional `outFilePath` parameter, the normalized values can be saved to a text file. The example below demonstrates this option.

```
> normalized = SCAN(CELFilePath, outFilePath="output_file.txt")
```

By default, `SCAN` maps Affymetrix probes to "probeset" identifiers provided by the manufacturer. However, these mappings may be outdated and include problematic probes (for example, those that may cross hybridize). In addition, multiple probesets may be assigned to a single gene. As an alternative, the BrainArray resource (see [http://brainarray.mbni.med.umich.edu/Brainarray/Database/CustomCDF/genomic\\_curated\\_CDF.asp](http://brainarray.mbni.med.umich.edu/Brainarray/Database/CustomCDF/genomic_curated_CDF.asp)) provides regularly updated mappings that exclude problematic probes and map to genes rather than probesets. When invoking `SCAN`, users can specify such alternative mappings via the `probeSummaryPackage` parameter. (Packages other than those provided by BrainArray can be used if they conform to the standards of the `AnnotationDbi` package.)

BrainArray packages can be downloaded manually from [http://brainarray.mbni.med.umich.edu/Brainarray/Database/CustomCDF/CDF\\_download.asp](http://brainarray.mbni.med.umich.edu/Brainarray/Database/CustomCDF/CDF_download.asp). When downloading, be sure to download the R source package for probe-level mappings (example below).



Species	Chip	Original Probe Count	Custom CDF Name	Statistics of Current Version		Statistics of Previous Version		% of Common Probes in Version		% of Common Probesets in Version		% of Identical Probesets in Version		R Packages		CDF Seq Map Desc
				Probe %	Probeset #	Probe %	Probeset #	Current	Previous	Current	Previous	Current	Previous	Source	Win32	
Anopheles gambiae	PlasmodiumAnopheles	250758	PlasmodiumAnopheles_Ag_ENTREZG	1.7	408	1.7	408	100.00	100.00	100.00	100.00	100.00	100.00	CP	CP	O
Arabidopsis thaliana	AG	131822	AG_At_ENTREZG	83.2	7359	83.1	7352	99.78	99.89	99.71	99.81	99.06	99.16	CP	CP	O
Arabidopsis thaliana	AGRONOMICS1	6046951	AGRONOMICS1_At_ENTREZG	20.0	30851	19.7	30749	98.69	99.79	99.45	99.78	92.63	92.93	CP	CP	O
Arabidopsis thaliana	ATH1121501	251078	ATH1121501_At_ENTREZG	84.9	21236	84.9	21225	99.77	99.84	99.69	99.74	99.16	99.21	CP	CP	O
Arabidopsis thaliana	aragene10st	628424	aragene10st_At_ENTREZG	93.3	27602									CP	CP	O
Arabidopsis thaliana	aragene11st	628424	aragene11st_At_ENTREZG	93.3	27602									CP	CP	O
Bos taurus	Bovine	265627	Bovine_Bt_ENTREZG	43.1	9409	43.0	9403	99.83	100.00	99.94	100.00	98.35	98.42	CP	CPA	O
Caenorhabditis elegans	Celegans	249165	Celegans_Ce_ENTREZG	78.8	17165	78.9	17198	99.83	99.68	99.84	99.65	97.08	96.89	CPA	CPA	O
Canis familiaris	Canine2	473162	Canine2_Cf_ENTREZG	53.1	16755	50.1	15664	88.21	93.44	89.33	95.56	70.34	75.24	CPA	CPA	O
Canis familiaris	Canine2PM	486081	Canine2PM_Cf_ENTREZG	51.7	16755	48.8	15664	88.21	93.44	89.33	95.56	70.34	75.24	CPA	CPA	O
Canis familiaris	cangene11st	621953	cangene11st_Cf_ENTREZG	66.6	17768									CPA	CPA	O
Danio rerio	Zebrafish	249752	Zebrafish_Dr_ENTREZG	53.1	8548	47.0	7696	84.62	95.52	84.45	93.80	75.96	84.37	CPA	CPA	O
Danio rerio	zebgene10st	1245559	zebgene10st_Dr_ENTREZG	41.8	23877									CPA	CPA	O
Danio rerio	zebgene11st	1245558	zebgene11st_Dr_ENTREZG	41.8	23877									CPA	CPA	O
Drosophila melanogaster	DrosGenome1	195994	DrosGenome1_Dm_ENTREZG	91.0	11719	91.2	11788	99.78	99.54	99.69	99.11	98.99	98.41	CPA	CPA	O
Drosophila melanogaster	Drosophila2	265400	Drosophila2_Dm_ENTREZG	70.6	12746	71.0	12847	99.55	99.00	99.36	98.58	97.97	97.20	CPA	CPA	O
Equus caballus	equgene10st	537520	equgene10st_EQca_ENTREZG	69.1	17624									CP	CP	O
Gallus gallus	Chicken	424097	Chicken_Gg_ENTREZG	43.3	12492	43.3	12492	100.00	100.00	100.00	100.00	100.00	100.00	CPA	CPA	O
Gallus gallus	chigene10st	464100	chigene10st_Gg_ENTREZG	69.6	13310									CPA	CPA	O
Gallus gallus	chigene11st	464100	chigene11st_Gg_ENTREZG	69.6	13310									CPA	CPA	O
Homo sapiens	HCG110	30313	HCG110_Hs_ENTREZG	72.2	1292	72.3	1295	99.70	99.62	99.85	99.61	98.84	98.61	CPA	CPA	O
Homo sapiens	HGFocus	98149	HGFocus_Hs_ENTREZG	78.9	7820	79.2	7856	99.59	99.17	99.65	99.20	98.82	98.37	CPA	CPA	O
Homo sapiens	HGU133A	247965	HGU133A_Hs_ENTREZG	69.0	12012	69.2	12078	99.28	99.07	99.55	99.01	98.04	97.50	CPA	CPA	O
Homo sapiens	HGU133A2	247899	HGU133A2_Hs_ENTREZG	69.0	12012	69.2	12078	99.28	99.07	99.55	99.01	98.04	97.50	CPA	CPA	O

After such a package has been downloaded, it can be installed using code such as the following.

```
> install.packages("hgu95ahsentrezgprobe_15.0.0.tar.gz", repos=NULL, type="source")
```

Or instead of downloading BrainArray packages manually, it is now possible to download these packages via the `InstallBrainArrayPackage` function.

```
> pkgName = InstallBrainArrayPackage(celFilePath, "15.0.0", "hs", "entrezg")
```

These mappings can be applied during normalization using code such as the following.

```
> normalized = SCAN(celFilePath, probeSummaryPackage=pkgName)
```

## 2 How to produce SCAN estimates for Agilent two-color microarrays

The `SCAN.UPC` package also supports the ability to normalize Agilent two-color microarrays. The general concept is similar to Affymetrix arrays; however, `SCAN` also corrects for biases that can arise due to the dyes used in each channel, as well as inter-channel correlation. (This package does not yet support normalizing Agilent one-color arrays.)

### 3 Conclusion

Please see the `SCAN.UPC` documentation for full descriptions of functions and the various options they support.