Introduction to the gsplom Package

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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 probeset value. Detailed status information, including the number of iterations required for mathematical convergence of the mixture model, is printed to the console.

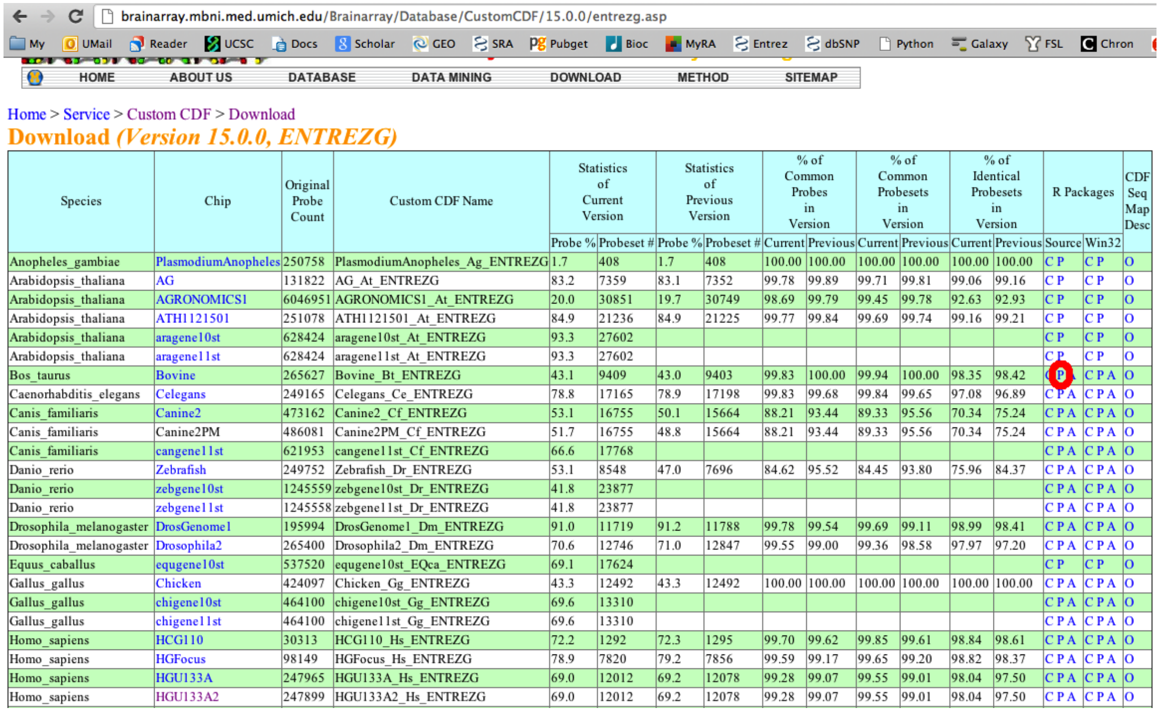
Multiple input files can be processed in one command via specifying wildcard characters (e.g., "*.CEL") or GEO experiment identifiers (e.g., "GSE22309"). In this case, the `SCAN` function returns an *ExpressionSet* object with a row for each probeset and a column for each input file.

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 However, these mappings may be outdated and include problematic probes (for example, those that may cross hybridize).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`) 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`. When downloading, be sure to download the R source package for probe-level mappings (example below).



Home > Service > Custom CDF > Download

Download (Version 15.0.0, ENTREZG)

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	C P	C P	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	C P	C P	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	C P	C P	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	C P	C P	O
Arabidopsis_thaliana	aragene10st	628424	aragene10st_At_ENTREZG	93.3	27602									C P	C P	O
Arabidopsis_thaliana	aragene11st	628424	aragene11st_At_ENTREZG	93.3	27602									C P	C P	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	C P A	C P A	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	C P A	C P A	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	C P A	C P A	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	C P A	C P A	O
Canis_familiaris	cangene11st	621953	cangene11st_Cf_ENTREZG	66.6	17768									C P A	C P A	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	C P A	C P A	O
Danio_rerio	zebgene10st	1245559	zebgene10st_Dr_ENTREZG	41.8	23877									C P A	C P A	O
Danio_rerio	zebgene11st	1245558	zebgene11st_Dr_ENTREZG	41.8	23877									C P A	C P A	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	C P A	C P A	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	C P A	C P A	O
Equus_caballus	equgene10st	537520	equgene10st_EQca_ENTREZG	69.1	17624									C P	C P	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	C P A	C P A	O
Gallus_gallus	chigene10st	464100	chigene10st_Gg_ENTREZG	69.6	13310									C P A	C P A	O
Gallus_gallus	chigene11st	464100	chigene11st_Gg_ENTREZG	69.6	13310									C P A	C P A	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	C P A	C P A	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	C P A	C P A	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	C P A	C P A	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	C P A	C P A	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.