

FIRMAGene: Finding Isoforms using Robust Multichip Analysis for (Affymetrix) Gene platforms

Mark Robinson
mrobinson@wehi.edu.au

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1 Introduction

This document gives a brief introduction to the **FIRMAGene** package, which is designed to detect *differential* splicing events using the Affymetrix Gene 1.0 ST platform. On this platform, there are probes for each known exon along the gene, but not necessarily the (generally) 4 probes per probe selection region (PSR) that the Exon 1.0 ST chip gives. After robustly fitting the RMA linear model, a persistence of non-zero residuals (all in the same direction) are often evidence of alternative splice forms. We illustrate a standard processing of the data for

2 An analysis of the Affymetrix public tissue panel dataset

Using the R `aroma.affymetrix` package, we process the data and get access to the residuals. If you are new to using `aroma.affymetrix`, there are installation and setup instructions at:

<http://groups.google.com/group/aroma-affymetrix/>

Here, we use the Affymetrix 33-sample (11-tissue) dataset to illustrate some tissue-specific alternative splicing candidates.

First, we preprocess the data.

```
> library(aroma.affymetrix)
```

```
R.cache v0.1.7 (2008-02-27) successfully loaded. See ?R.cache for help.
```

```
R.rsp v0.3.4 (2008-03-06) successfully loaded. See ?R.rsp for help.
```

```
Type browseRsp() to open the RSP main menu in your browser.
```

```
aroma.apd v0.1.3 (2006-06-14) successfully loaded. See ?aroma.apd for help.
```

```
Patching /Users/mrobinson/.Rpatches/aroma.affymetrix/20090318/AffymetrixCdfFile.computeAffinities.R
```

```
Patching /Users/mrobinson/.Rpatches/aroma.affymetrix/20090318/AffymetrixCelFile.BG.R
```

```
Patching /Users/mrobinson/.Rpatches/aroma.affymetrix/20090318/AffymetrixCelSet.BG.R
```

```
Patching /Users/mrobinson/.Rpatches/aroma.affymetrix/20090318/AffymetrixCelSet.convertToUnique.R
```

```
Patching /Users/mrobinson/.Rpatches/aroma.affymetrix/20090318/AffymetrixCelSet.cpgBoxplots.R
```

```
Patching /Users/mrobinson/.Rpatches/aroma.affymetrix/20090318/AffymetrixCelSet.writeSgr.R
```

```
Patching /Users/mrobinson/.Rpatches/aroma.affymetrix/20090318/AromaCellCpgFile.R
```

```
Patching /Users/mrobinson/.Rpatches/aroma.affymetrix/20090318/MatSmoothing.R
```

```
Patching /Users/mrobinson/.Rpatches/aroma.affymetrix/20090318/bpmapCluster2Cdf.R
```

```
> cdf <- AffymetrixCdfFile$fromChipType("HuGene-1_0-st-v1", verbose = -1)
```