Jetset: selecting an optimal Affymetrix probe set to represent a gene

Qiyuan Li, Aron C Eklund

August 22, 2011

Contents

1 Introduction

On Affymetrix gene expression microarrays, a given gene may be detected by multiple probe sets which may deliver inconsistent or even contradictory measurements. Therefore, obtaining an unambiguous expression estimate of a pre-specified gene can be nontrivial. We developed scoring methods to assess each probe set for specificity, coverage, and degradation resistance. We used these scores to select the optimal probe set for each gene, and thus create a simple one-to-one mapping between gene and probe set.

`jetset` is a package enabling the selection of optimal probe sets from the HG-U95Av2, HG-U133A, HG-U133 Plus 2.0, or U133 X3P microarray platforms.

```
> library(jetset)
```

2 Contents of the package

The jetset package contains the following objects:

```
> ls("package:jetset")
```

```
 [1] "eg2ps.hgu133a"      "eg2ps.hgu133plus2"  "eg2ps.hgu95av2"
 [4] "eg2ps.u133x3p"      "jmap"               "jscores"
 [7] "scores.hgu133a"     "scores.hgu133plus2" "scores.hgu95av2"
[10] "scores.u133x3p"
```

The functions jmap and jscores are the intended user-level interface, and scores.* and eg2ps.* are data sets that support these functions.

In this document, we describe only one (*.hgu95av2) of each family of data sets.

2.1 jmap

jmap is a function that returns the best probe sets matching a list of Entrez GeneIDs, gene symbols, or gene aliases.

2.2 jscores

jscores is a function that returns the jetset scores for all probe sets matching a list of Entrez GeneIDs, gene symbols, aliases, or ensembl IDs.

2.3 scores.hgu95av2

scores.hgu95av2 is a data frame with Entrez IDs and pre-calculated quality control scores for each probe set ID. All scores range from 0 to 1, and a higher score indicates better (predicted) performance.

```
> head(scores.hgu95av2)
```

```
          nProbes EntrezID process specificity coverage
1000_at        16     5595   222.0      0.6250        1
1001_at        16     7075   816.0      0.8750        1
1002_f_at      16     <NA>      NA          NA       NA
1003_s_at      16      643  1963.5      0.6875        1
1004_at        16      643   329.0      0.5625        1
1005_at        16     1843   941.0      0.6875        1
```

- The Entrez GeneID (*EntrezID*) is a unique gene identifier. Note: as in other Bioconductor packages, the GeneID is stored as type *character*.
- The processivity requirement (*process*) is the number of consecutive bases that must be synthesized to generate a target that can be detected by the probe set.
- The *specificity* score is the fraction of the probes in a probe set that are likely to detect the targeted gene and unlikely to detect other genes.
- The *coverage* score is the fraction of the splice isoforms belonging to the targeted gene that are detected by the probe set.

Note that the robustness score and overall score are not stored in this data; instead these scores are calculated on-the-fly when the score data is retrieved using jscores.

- The robustness score (*robust*) is intended to quantify robustness against transcript degradation. The robustness score uses the processivity requirement to estimate the signal intensity of a probe set, relative to the ideal case of perfect processivity.
- The *overall* score is the product of the specificity score, coverage score, and robustness score.

2.4 eg2ps.hgu95av2

eg2ps.hgu95av2 is an character vector, of which the values are probe set IDs and the names are Entrez GeneIDs.

```
> head(eg2ps.hgu95av2)
```

```
                      10                      100                     1000
               "38912_at"              "41654_at"              "2053_at"
                100008588                100008589                   10001
"AFFX-HUMRGE/M10098_3_at"      "AFFX-M27830_5_at"             "35432_at"
```

3 Simple probe set selection

A typical application of the jetset packages is to identify probe sets corresponding to a published list of genes.

3.1 Selecting probe sets by Entrez Gene ID

The Entrez GeneID is an unambiguous way to specify a gene; however the numeric ID is not particularly descriptive, which may explain why this is not commonly provided in publications.

```
> jmap("hgu95av2", eg = "2099")

     2099
"1681_at"

> jmap("hgu133a", eg = "2099")

       2099
"205225_at"

> jmap("hgu133plus2", eg = "2099")

       2099
"205225_at"

> jmap("u133x3p", eg = "2099")

            2099
"g4503602_3p_at"
```

Entrez GeneID 2099 corresponds to the estrogen receptor (ESR1) gene, which is an important indicator of breast cancer phenotype.

3.2 Selecting probe sets by ensembl ID

The ensembl ID is another unambiguous way to specify a gene.

```
> jmap("hgu95av2", ensembl = "ENSG00000091831")

ENSG00000091831
      "1681_at"

> jmap("hgu133a", ensembl = "ENSG00000091831")

ENSG00000091831
    "205225_at"
```

3.3 Selecting by gene symbol

Often, we know the official HUGO gene symbols, and want the corresponding probe sets.

```
> jmap("hgu133a", symbol = c("ESR1", "ERBB2", "AURKA"))

         ESR1          ERBB2          AURKA
  "205225_at" "216836_s_at" "208079_s_at"
```

Unfortunately, the gene symbol for a given gene can change. Furthermore, in rare cases a HUGO gene symbol can correspond to two distinct genes.

3.4 Selecting by gene alias

If we have gene symbols, but they are not the *official* symbols, the gene aliases might be useful.

```
> jmap("u133x3p", alias = c("P53", "HER-2", "K-RAS"))
```

```
                  P53                    HER-2                   K-RAS
"g8400737_3p_at" "Hs.323910.2.A1_3p_a_at"  "Hs.37003.0.S1_3p_x_at"
```

4 Probe set quality scores

We might want to compare quality scores for all probe sets corresponding to a gene of interest. For this example, the STAT1 gene is used because it is detected by several probe sets.

```
> jscores("hgu95av2", symbol = "STAT1")
```

```
                           nProbes EntrezID process specificity coverage
32859_at                        16     6772    74.5      0.4375      0.5
32860_g_at                      16     6772   405.5      0.7500      0.5
33338_at                        16     6772   168.5      0.7500      0.5
33339_g_at                      16     6772  1203.0      0.7500      1.0
AFFX-HUMISGF3A/M97935_3_at      20     6772   451.0      0.7500      0.5
AFFX-HUMISGF3A/M97935_5_at      20     6772  2863.5      0.7500      1.0
AFFX-HUMISGF3A/M97935_MA_at     20     6772  1773.5      0.8500      1.0
AFFX-HUMISGF3A/M97935_MB_at     20     6772  1536.0      0.6500      0.5
                                robust     overall symbol
32859_at                   0.883141136 0.193187124  STAT1
32860_g_at                 0.508445547 0.190667080  STAT1
33338_at                   0.754977281 0.283116480  STAT1
33339_g_at                 0.134435239 0.100826429  STAT1
AFFX-HUMISGF3A/M97935_3_at 0.471284303 0.176731613  STAT1
AFFX-HUMISGF3A/M97935_5_at 0.008425592 0.006319194  STAT1
AFFX-HUMISGF3A/M97935_MA_at 0.051907122 0.044121054  STAT1
AFFX-HUMISGF3A/M97935_MB_at 0.077139816 0.025070440  STAT1
```

We can confirm that `jmap` returns the probe set with the highest overall score:

```
> jmap("hgu95av2", symbol = "STAT1")
```

```
     STAT1
"33338_at"
```

5 Jetset algorithm details

We downloaded probe sequences corresponding to four human gene expression microarrays from Affymetrix: U95Av2, U133A, U133 Plus 2.0, and X3P. We used NCBI BLASTN to search the 25-base probe sequences for matches to the Refseq human RNA database (Pruitt, et al., 2005). The BLASTN search was run with the default parameters, except that filtering was turned off, the word size was set to 8 to increase sensitivity, and the expectation value was set to 1 to reduce output size.

```
blastall -p blastn -d refseq.human.rna -i probe.hgu133a.fa -o hgu133a.refseq.20110817.bls
-F F -m 8 -e 1 -W 8 -a 8
```

We used the alignment score (bit score) between each probe and cDNA as an indication of probe sensitivity. We defined three levels of alignment: a strong alignment has a score between 48 and 51, indicating that at least 24 bases are identical and that the probe is very likely to detect the target. A moderate alignment has a score between 32 and 47, corresponding to an uninterrupted alignment of length 16 to 23 bases; the probe may or may not respond to the target. A weak alignment has a score less than 32 and is unlikely to respond to the target.

Specificity. A probe was considered to specifically detect a given gene if it aligned strongly to at least one transcript of the gene, but did not have a strong or moderate alignment to a transcript from another gene. The gene specifically detected by the largest number of probes in a probe set was considered the targeted gene of the probe set. We defined the specificity score S_s of a probe set as the fraction of its probes that specifically detect the targeted gene.

Coverage. A transcript of the targeted gene was considered detected by a probe set if the transcript has a strong alignment to the majority of the probes in the probe set. The coverage score S_c of a probe set is defined as the fraction of all transcripts belonging to the targeted gene that are detected by the probe set.

Robustness. The processivity requirement for a probe-transcript alignment is the number of bases between the 5' end of the alignment and the 3' end of the transcript sequence; this corresponds to the length of labeled target that must be synthesized by in vitro transcription to reach the query region. The overall processivity requirement N of a probe set is the median processivity requirement for all strong alignments between probes in the probe set and transcripts in the targeted gene. We define the robustness score S_r of a probe set as the probability that synthesis of the target up to the processivity requirement is achieved without interruption: $S_r = (1-p)^n$

Here, p is the probability of the IVT synthesis being interrupted at each base, due to either transcript degradation or lack of enzyme processivity. The value of p is likely to be variable in clinical specimens, but for simplicity we use a value corresponding to the manufacturer's design criteria: 1/300 for the X3P array, or 1/600 for the other arrays.

Overall score. We define the overall score S_o as the product of the three scores described above: $S_o = S_s * S_c * S_r$

For a given gene, the probe set targeting this gene with the highest overall score is selected to represent the gene.

6 Reference

Qiyuan Li, Nicolai J. Birkbak, Balazs Gyorffy, Zoltan Szallasi and Aron C. Eklund (2010). Jetset: selecting an optimal microarray probe set to represent a gene. Manuscript in preparation.

7 R sessionInfo

The results in this file were generated using the following packages:

```
> sessionInfo()

R version 2.13.1 (2011-07-08)
Platform: x86_64-apple-darwin9.8.0/x86_64 (64-bit)

locale:
[1] C/en_US.UTF-8/C/C/en_US.UTF-8/en_US.UTF-8

attached base packages:
[1] stats     graphics  grDevices utils     datasets  methods   base

other attached packages:
[1] jetset_0.99.1 RSQLite_0.9-4 DBI_0.2-5

loaded via a namespace (and not attached):
[1] AnnotationDbi_1.14.1 Biobase_2.12.1       org.Hs.eg.db_2.5.0
[4] tools_2.13.1
```