**Figure lengends**

Figure 1a EPIG-Seq workflow

Figure 1b CY example

Figure 2 Simulated RNA-Seq data with five patterns (pattern 1-5) carrying biological meaning and pattern 6 as background noise

Figure 3 Unsupervised analyses on gene profiles from simulated data with five patterns and background noise. 3A. A conventional PCA analysis was performed on pair-wise CYs as the covariance matrix. 3B. A hierarchical clustering reveals prominent patterns in simulated data

Figure 4 Parameter-space searching for the optimized default choice for end users. 4A. Parameter optimization in step one: there were four panels with labels on the top indicating the choice of location parameter St1 at [5-10]; within each panel, the x-axis shows the CYs as the similarity measure [0.5 – 0.9]; the color code was for the two-tailed dispersion cut off at 1 – 5 %. The y-axis in each panel was the Adjusted Rand Index [0-1]. 4B. Parameter optimization in step two, x-axis shows the CYs as the similarity measure [0.5 – 0.9]; the y-axis was the Adjusted Rand Index [0-1]; the color code was for indicating the choice of location parameter St2 at [2-5].

Figure 5 EPIG-Seq results running from the simulated dataset (aforementioned). 5A. The thumbnails of the 5 extracted simulated patterns extract by EPIG-Seq. Group1 (labeled as “Baseline”) in red, group2 in green; group3 in blue and group4 in purple. 5B. The hierarchical clustering reveals prominent patterns in simulated data. 5C. conventional PCA analysis was performed on pair-wise CYs as the covariance matrix.

Figure 6 The application of EPIG-Seq on the SEQC toxicity data. 6A. Thumbnails of the four significant extracted patterns extract by EPIG-Seq (the MOA was color coded) 6B MOA data extracted patterns PCA 6C. The hierarchical clustering (heatmap) that reveals prominent patterns in the SEQC data

Figure 7. Thumbnails of the four significant extracted patterns extract by EPIG-Seq on TCGA breast cancer data. (four the breast cancer subtypes and one normal group were color coded)

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 |
| TranscriptA | 0 | 16 | 1 | 0 | 1228 | 746 | 166 | 574 | 5207 | 25693 | 1018 | 2622 |
| TranscriptB | 36 | 328 | 190 | 178 | 36 | 4 | 0 | 0 | 2581 | 7068 | 298 | 17049 |

Figure 1B. Count level measurement of two transcripts (genes) in four groups

|  |  |  |
| --- | --- | --- |
|  | EPIG | EPIG-Seq |
| Data type | Continuous | Count level |
| Distribution assumption | Gaussian | Poisson |
| Correlation measurement | Person's | CYs |
| Measurement or spreading | Variance | Dispersion |
| Magnitude measurement | LogRatio | Wilcoxon test |
| Significant test | SignalToNoise | Variance-to-mean ratio (VMR) |
| Deliverable results | Co-expression pattern | Co-expression pattern |

Table 1. Comparison of EPIG-Seq vs. EPIG

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | EPIG | EPIG-seq | SAMseq | Deseq |
| Data type | Continuous | Count level | Count level | Count level |
| Distribution assumption | Gaussian | Poisson | Poisson | Negative Binomial |
| Correlation measurement | Person's | Cys | N/A | N/A |
| Measurement or spreading | Variance | Dispersion | Dispersion | Dispersion |
| Magnitude measurement | LogRatio | Wilcoxon test | Wilcoxon test | FoldChange |
| Significant test | SignalToNoise | Variance-to-mean ratio (VMR) | NonParametrics | NegBinom test |
| Deliverable results | Co-expression pattern | Co-expression pattern | DEG | DEG |

Table 1 b. Comparison of methods (need??)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Pattern number | Number of genes | Group1 | Group2 | Group3 | Group4 |
| 1 | 200 | 1 | 1.5 | 2.5 | 4 |
| 2 | 200 | 1 | -1.5 | -2.5 | -4 |
| 3 | 200 | 1 | -1.5 | 4 | 2.5 |
| 4 | 200 | 1 | 4 | 2.5 | 1.5 |
| 5 | 200 | 1 | 4 | 4 | 4 |
| 6 | 19000 | 1 | 1 | 1 | 1 |

Table 2. Simulated RNA-seq data with mean fold change

Table 3 Sensitivity and specificity for EPIG and EPIG-seq extracted on simulated patterns

Suppl Table 1) Confusion matrix for EPIG

Suppl Table 2) Confusion matrix for EPIG-Seq

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sample #** | **GS** | **MS** | **# of Patterns** | **# of Genes** |
| 1 | 0.31 | 0.54 | 6 | 192 |
| 2 | 0.37 | 0.51 | 4 | 169 |
| 3 | 0.21 | 0.52 | 6 | 344 |
| 4 | 0.41 | 0.59 | 4 | 197 |

Table 4 General Silhouette of breast cancer data set samples: GS: General Silhouette, MS: Maximum Silhouette

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Pattern # | # of Genes | Top GOBP | p-value | FDR |
| 1 | 9 | GO:0006631 - Fatty acid metabolic process | 3.8E-06 | 4.4E-03 |
| 2 | 10 | GO:0055114 - Oxidation reduction process | 2.3E-02 | 2.1E+01 |
| 3 | 10 | GO:0042592 - Homeostatic process | 6.0E-02 | 5.5E+01 |
| 4 | 4 | **-** | **-** | **-** |

Table 5 GO biological processes of MOA categorized genes

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Pattern # | # of Genes | Breast Cancer Related Biology | p-value | FDR |
| 1 | 29 | GO:0042803 - Protein homodimerization activity (S100A16, CENPF, APOE, PLOD1, TOP2A) | 2.20E-03 | 2.50E+00 |
| 2 | 114 | KEGG:04512 - Extra cellular matrix-receptor interaction | 2.8E-04 | 3.0E-01 |
| 3 | 46 | KEGG:03320 - Peroxisome proliferator-activated receptor signaling pathway | 6.0E-02 | 5.5E+01 |
| 4 | 8 | CD59, ITGB1 and 5 ribosomal protein genes | **-** | **-** |

Table 6 KEGG enrichment of breast cancer categorized genes

##==================Not needed ?? ========================

Need to update on table 4?

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  |  | Seeded |  |  |  |
| Extracted | Group\_A | Group\_B | Group\_C | Group\_D | Group\_E | Group\_F |
| Group\_A | 147 | 0 | 81 | 0 | 48 | 40 |
| Group\_B | 0 | 172 | 0 | 0 | 0 | 17 |
| Group\_C | 20 | 0 | 92 | 0 | 11 | 6 |
| Group\_D | 0 | 0 | 0 | 169 | 30 | 8 |
| Group\_E | 11 | 1 | 5 | 12 | 100 | 1 |

Table 4. EPIG-seq results on simulated RNA-seq data with 5 meaningful patterns (Group A – E)

Need sensitivity and specificity (table 5) following table 4 recovery from the simulated data.