**Figure lengends**

Figure 1 EPIG-Seq workflow

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 [1-5]; 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 [1-5].

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.

Yet to be filled in

Figure 6 (needed for MOA in SEQC data) EPIG-Seq results running from the research dataset. 6A. The thumbnails of the extracted patterns extract by EPIG-Seq … 6B. The hierarchical clustering (heatmap) that reveals prominent patterns in the research data

Figure 7 (needed for MOA in TCGA data) EPIG-Seq results running from the research dataset, the thumbnails of the extracted patterns extract by EPIG-Seq

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | 1 | 1 | 1 | 1 | 2 | 2 | 2 | 2 | 3 | 3 | 3 | 3 | 4 | 4 | 4 | 4 |
| TranscriptA | 0 | 16 | 1 | 0 | 1228 | 746 | 166 | 574 | 5207 | 25693 | 1018 | 2622 | 364608 | 58221 | 210304 | 239869 |
| TranscriptB | 36 | 328 | 190 | 178 | 36 | 4 | 0 | 0 | 2581 | 7068 | 298 | 17049 | 23 | 2542 | 799 | 931 |

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

|  |  |  |  |
| --- | --- | --- | --- |
|  | EPIG | EPIG-seq | ORIGEN |
| Data type | Continuous | Count level | Count level |
| Distribution assumption | Gaussian | Poisson | NonParametric |
| Correlation measurement | Person's | CYs | Order statistics |
| Measurement or spreading | Variance | Dispersion | Residue |
| Magnitude measurement | LogRatio | Wilcoxon test | Difference Between means |
| Significant test | SignalToNoise | Variance-to-mean ratio (VMR) | mdFDR means |
| Deliverable results | Co-expression pattern | Co-expression pattern | Co-expression pattern |

Table 2. Comparison of methods

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | 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 2 (addition??). Comparison of methods

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| 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 3. Simulated RNA-seq data with 5 meaningful patterns

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.