rptDB: a prototype Affymetrix .rpt QC tool





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Affymetrix analysis results in the generation of large and complex data sets which need extensive downstream analysis to determine results of biological significance. Users can benefit from a careful QC of their data before beginning analysis to remove individual chips that may adversely affect the final interpretation.

rptDB is a prototype database for the analysis of Affymetrix expression report (.rpt) files. Report files are widely used to QC raw data after hyb, scan and .cel file generation. Only %Present calls, Scale Factors and 3':5' ratios of housekeeping genes are generally used, but there are many other metrics that may also be of importance for QC analysis.

This is a prototype and we would welcome community response and suggestions for

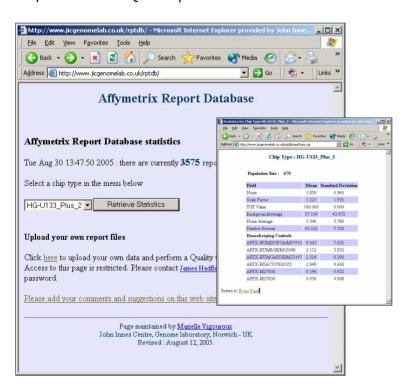
development.

Why use rptDB?

- Currently all data QC is done internally, comparison to external data increases robustness
- Current methods are subjective
- Final goal is a Phred type score for Affymetrix arrays
- Analyse trends across techs/labs/countries

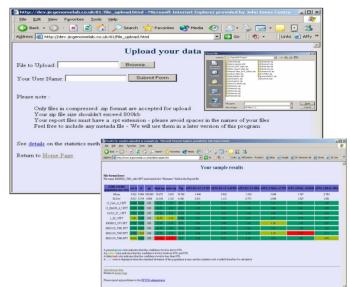
rptDB functions:

- Generate average .rpt file statistics for any chip type
- Upload data for QC analysis

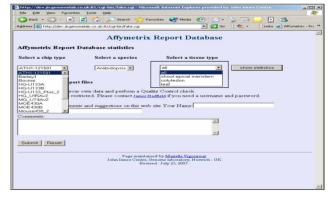


Development:

- Comparison of uploaded data to database and itself
- Non-expression reports
- What does the community want?



Generate average .rpt file statistics for any tissue type (demo)



To Do List:

- Weighting .rpt metrics
- Removal of outliers (1.5*IQR or Median Absolute Deviation)
- Generate average .rpt file statistics for tissue type
- Variance of .rpts (how many .rpt do we need to have a 'good' population estimate?)
- MAIME input
- Arrayexpress/GEO data absorption



The Genome Laboratory offers a complete Affymetrix Authorized Expression Array Processing service. This service includes RNA sample QC, cDNA and cRNA synthesis and QC, frag, hyb, scan and data QC. Prices from £580 per sample/chip including GeneChip array!



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