**RNAnet - A Map of Human Genes**

W.B. Langdon, A.P. Harrison, O. Sanchez-Grailet
Department of Mathematical and Biological Science, University of Essex
{wlangdon,harry,osanch}@essex.ac.uk

**RNAnet** is a Firefox based web tool to explore human Affymetrix mRNA data in GEO using Ensembl gene and exon definitions.

RNAnet is able to:
- Get correlation heatmaps and scatter plots for all probes in a probeset, all probes uniquely mapped to an exon, an arbitrary (user defined) list of probes, and all exons.
- Web based detection of spatial flaws and one CEL normalisation.

**Materials**
- So far, RNAnet uses all the HG-U133 2+ Genechips.
- Best probe chosen (no G-spots!). Covers at least one exon from 14,288 Ensembl genes.
- All exon correlations calculated across 2,757 arrays (290 million correlations).

**Methods**
- Static method: eigen analyse (PCA) group exons with similar interactions.
- Interactive method: user selects genes or exons of interest.
- Combined method: PCA map guides user as to what might be interesting.

**Eigen analysis of Human Exon Correlations**
- Correlation of 24,132 exons as square symmetric matrix.
- Most eigen vectors short, <8,000.
- Eigen analysis can approximate 300 million correlations with 400 thousand numbers.

**Conclusions**
- Correlations between human exons are highly non-random. The network formed by pairs of strongly correlated exons is a “small world”.
- RNAnet provides an interactive tool to explore RNA expression (protein gene and non-protein coding) of thousands of published 3’ GeneChips covering virtually all medically interesting human tissues.
- Future: extend to other arrays, other organisms.

**Availability**
http://bioinformatics.essex.ac.uk/users/wlangdon/rnanet/index.html

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