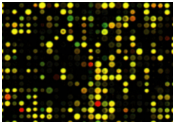


Duncan Gillies - Interests

- **Biomechanical Modelling**
 - Soft tissue modelling; endoscope guidance
- **Probabilistic Inference and Machine Learning**
 - Bayesian Modelling: Hepatitis C and Neurone development
 - Pre-operative prediction of Laryngoscopy
- **Statistical Pattern Recognition**
 - Embolic signal detection in transcranial Doppler ultrasound.
 - Peak height analysis in Sanger sequencing data.
 - Data fusion in Microarrays

Modelling Regulatory Networks

The most widely adopted approach is a hierarchical one:

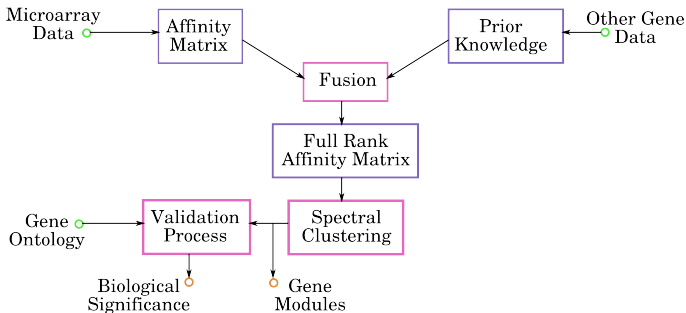


Data → Modules → Mechanisms

However there are many problems

- Experimental Error
- Time Resolution
- Overlapping patterns
- Large numbers of genes, but few experimental runs

Incorporating Prior Knowledge



Prior Knowledge (?????)

- Transcription factor binding motifs
- ChIP on chip
- Protein-Protein Interactions
- Gene Ontology

Extracting more appropriate prior knowledge

Can we make use of the increasingly large number of data sets of RNA Microarrays

- Pooling the data doesn't work.
- Fusing individual microarrays using maximum entropy can sometimes work, but only on a small scale

However an untried idea is:

- Mining the microarray data space itself

The Hunt for Prior Models



- Collect all microarrays for a particular form of cancer
- Calculate all pairwise similarities (affinity matrix)
- (Transform into geodesic distances)
- Feature Selection
 - Multidimensional Scaling
- Search for coherent regions of the lower dimension space
 - Visually by reconstructing the microarray images
 - Using split and merge segmentation