

# From gene expression to pathway fingerprints and correlation networks

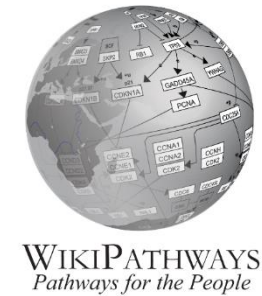
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@s\_kariotis #EuroBioC2017

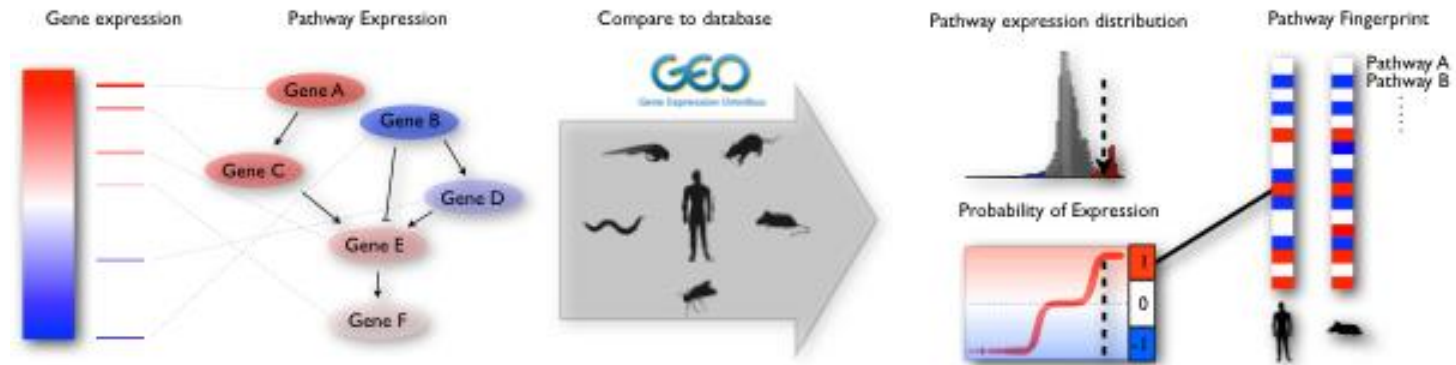
# Why and how we use pathways?

- Uncover higher level functional molecular activities and relationships
- We attempt to represent, in a standardized way:
  - pathway activity, using **pathprint**
  - networked pathway activity correlation, using **pcxn**



# Pathprint: from gene expression to fingerprints

- A functional approach that:
  - compares gene expression as a tertiary summary statistic for a set of pathways
  - generates a set of pathway activities



\*Altschuler GM et al. Pathprinting: An integrative approach to understand the functional basis of disease. *Genome Med.* 2013;5: 68.

# Packages: pathprint & pathprintGEOData

- Pathway fingerprinting
  - use existing data (188,390 samples in *pathprintGEOData*)
  - get new (GEO) dataset and utilize `exprs2fingerprint.R`
- Fingerprint analysis
  - Intra-sample comparisons
    - heatmap
  - Investigate the functional distance between pluripotent fingerprints
    - `consensusFingerprint.R`
    - `consensusDistance.R`
  - Identify similar arrays
    - Fingerprint & metadata matrices

# Pathway Co-expression Network [<http://pcxn.org>]



- MsigDB and Pathprint for scientifically interesting pathways
- **Explore** a network by focusing on single pathways and their most correlated neighbours, e.g. use GSEA results!
- **Analyse** relationships between groups of pathways shown to be enriched in a collection by gene set enrichment

# Packages: pcxn & pcxnData

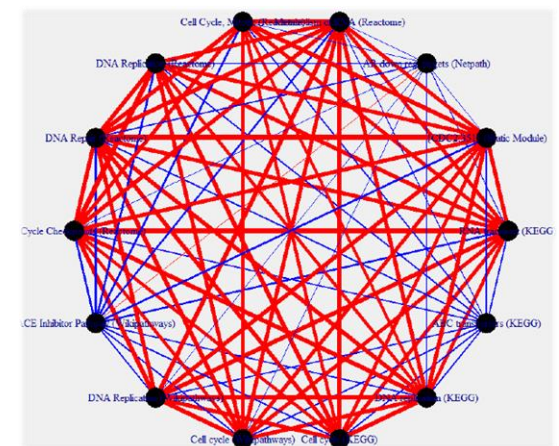
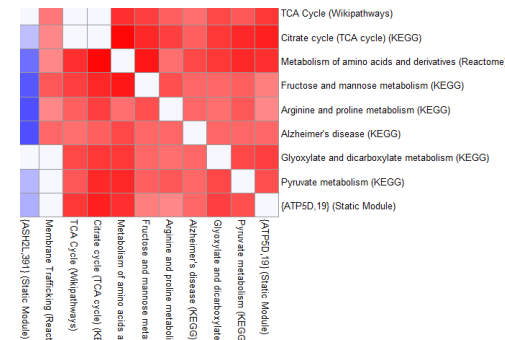
- Pre-calculated matrices of correlation coefficients and p-values (*pcxnData*)

- Create pcxn object
  - Explore correlated pathways using an interesting pathway
  - Analyse correlation relationships among multiple pathways

```
pcxn_object  Formal class 'pcxn'
  ..@ type : chr "pcxn_explore"
  ..@ data : chr [1:49, 1:6] "Fructose and mannose..."
  .. ..- attr(*, "dimnames")=List of 2
  .. .. ..$ : chr [1:49] "8" "302" "305" "1598" ...
  .. .. ..$ : chr [1:6] "Pathway.A" "Pathway.B" "P..."
  ..@ geneset_groups:List of 1
  .. ..$ query_geneset: chr "Alzheimer's disease (..."
```

- Utilize pcxn object
  - Draw a heatmap (clustering gene sets)
  - Create a network

- Acquire the gene members of a pathway

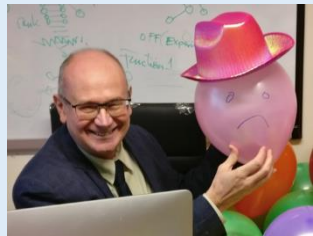




# Hide Lab

Center for **G**enome **T**ranslation

Winston Hide



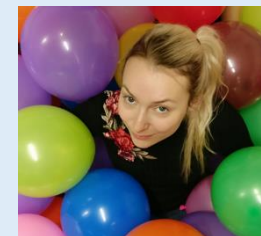
Wenbin Wei



David Jones



Sarah Morgan



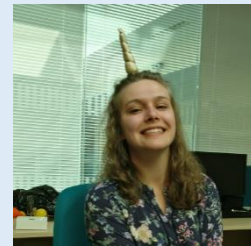
Yered Pita-Juarez



Gabriel Altschuler



Sandeep Amberkar



Claire Green



Katjusa Koler



Viv Junker