

Healthy ageing and growth in early life: the interaction between genes, the environment and development

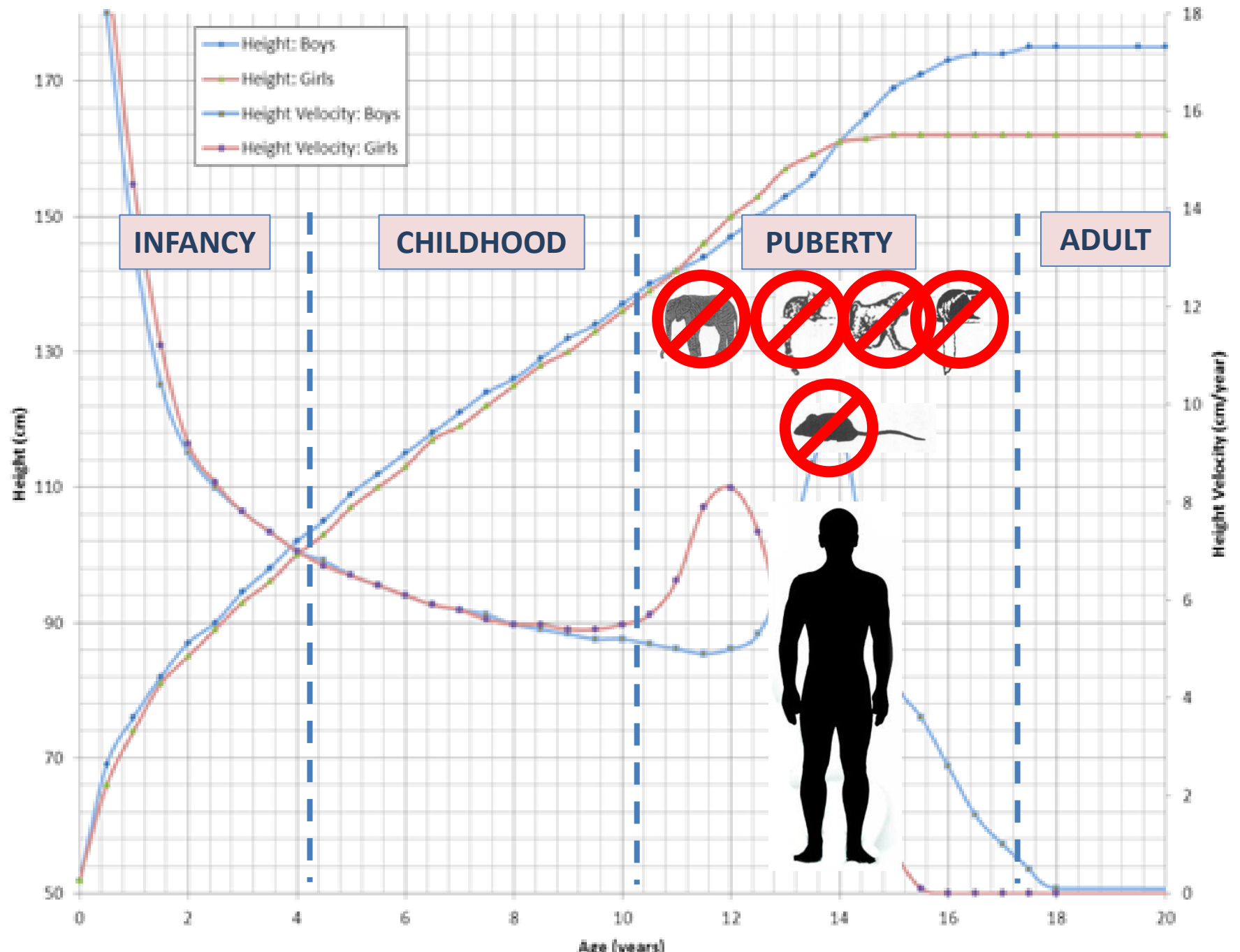
Adam Stevens

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University of Manchester

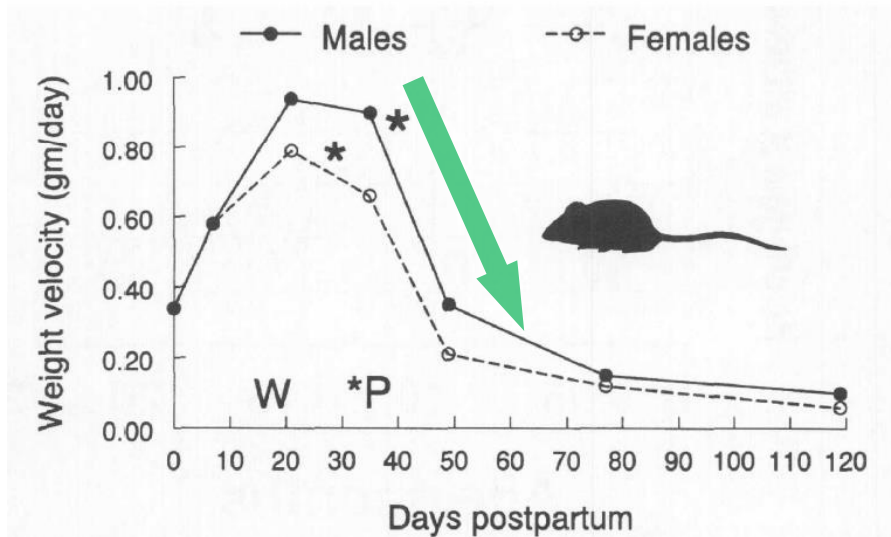
Outline

- **Background**
 - Human growth is unique
 - The interaction between growth, the environment and development
 - What is 'omic data
 - Network models
- **Age-dependent gene expression & the effect of the environment on child growth**
 - Age-related changes in gene expression – defining networks of gene interactions
 - The effect of latitude & summer daylight exposure on growth
 - Evolutionary age of a gene is related to growth and metabolism
- **Growth trajectories and links to health in later life**
 - Network models of rate of growth
 - Age of puberty and health
 - Leukaemia as an example
- **Conclusions**

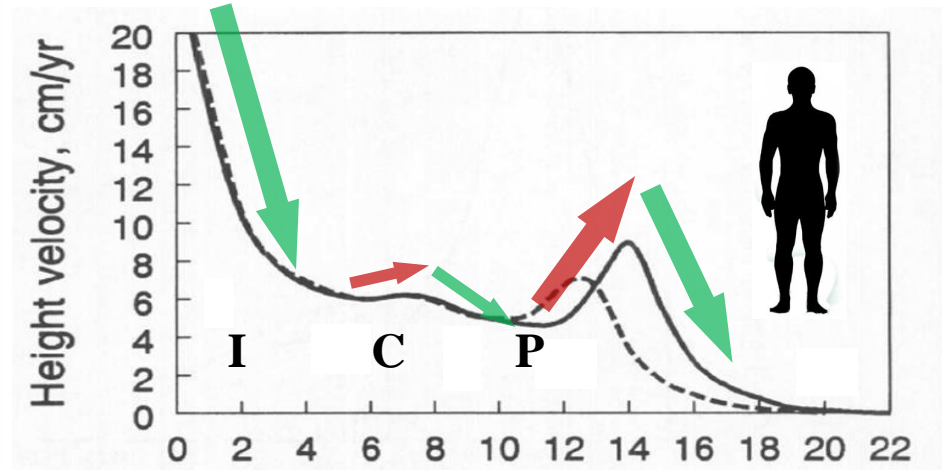
Human Growth



Human growth pattern is unique



W = weaning, *P = puberty (Tanner 1962 redrawn by Bogin 1999)



I = Infancy, C = Childhood, P = puberty (from Bogin 1999)

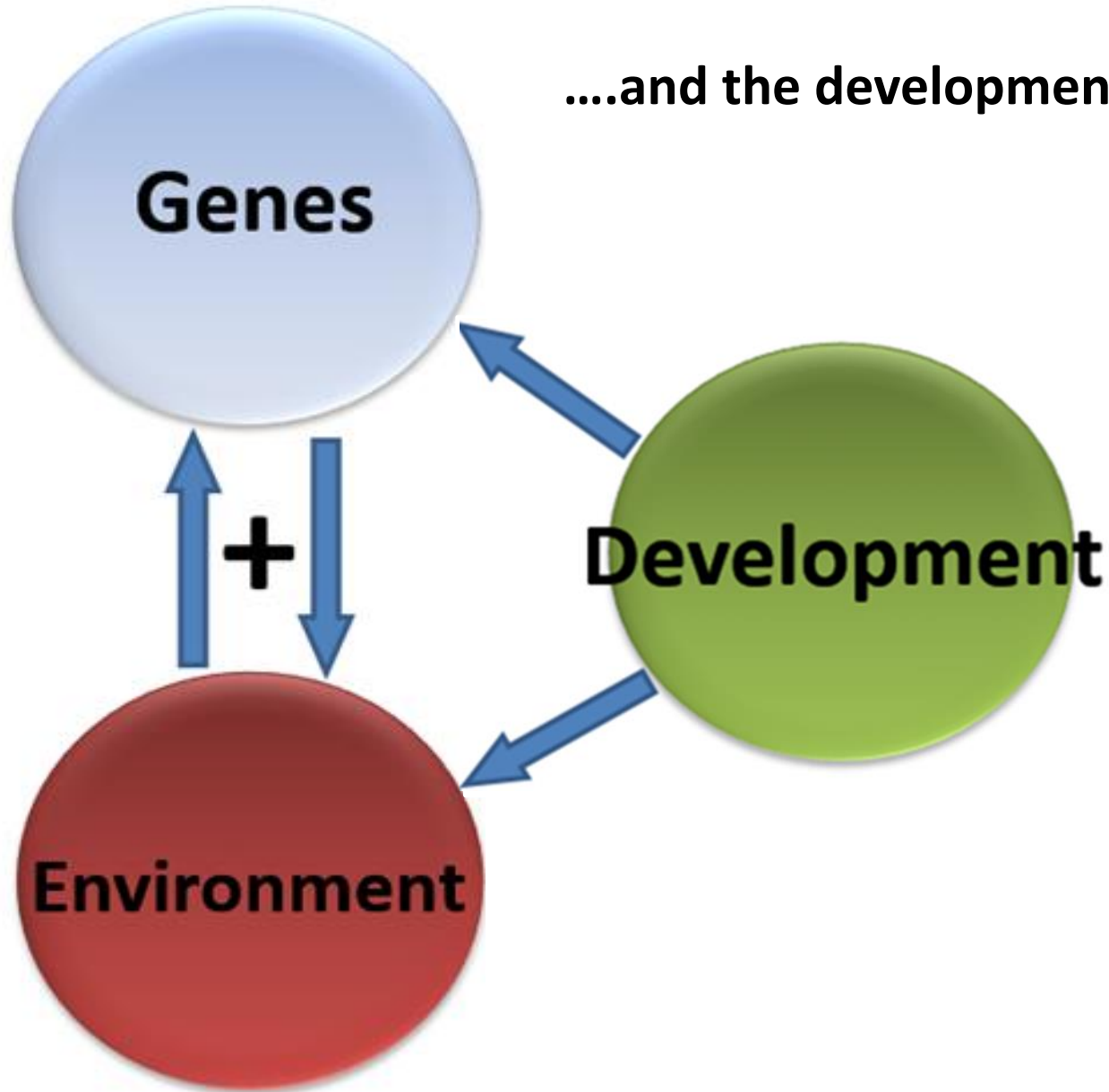
- Age-related, tissue-independent gene expression shown in mice

Finkelstain GP *et al.* Endocrinology 2009;150(4):1791-800

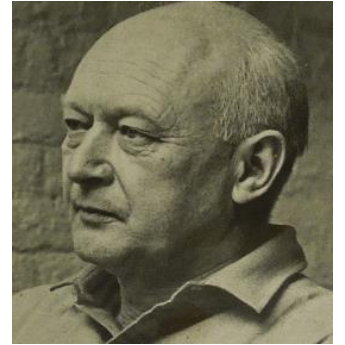
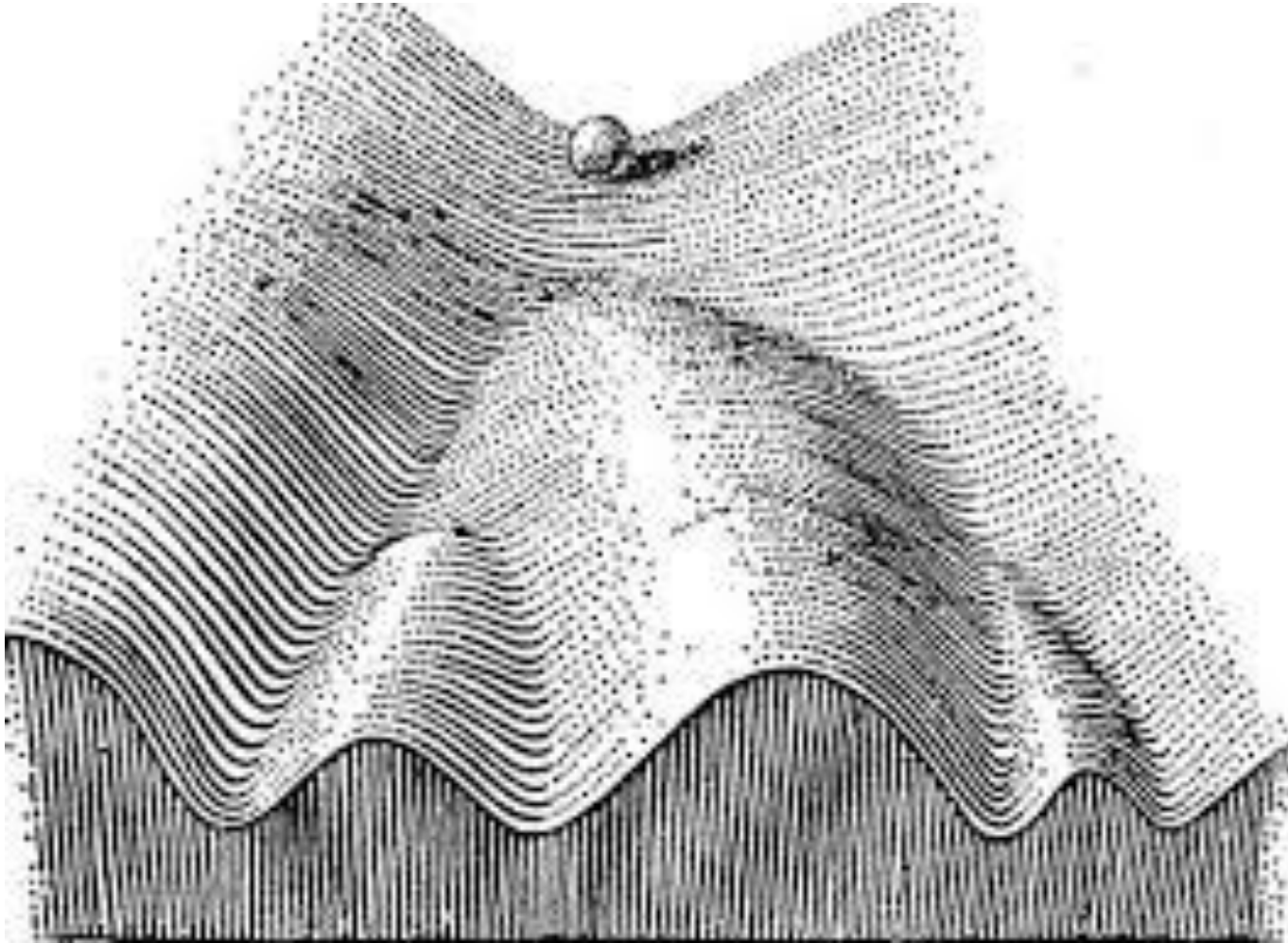
• ?

Genes interact with the environment

....and the developmental process



How do genes effect development?



C.H. Waddington 1905-1975

Waddington's Landscape

....is a metaphor for how gene regulation modulates development

What is 'Omic Data

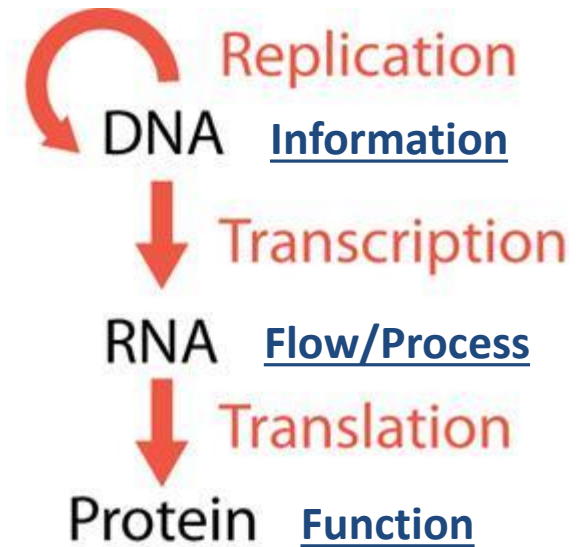
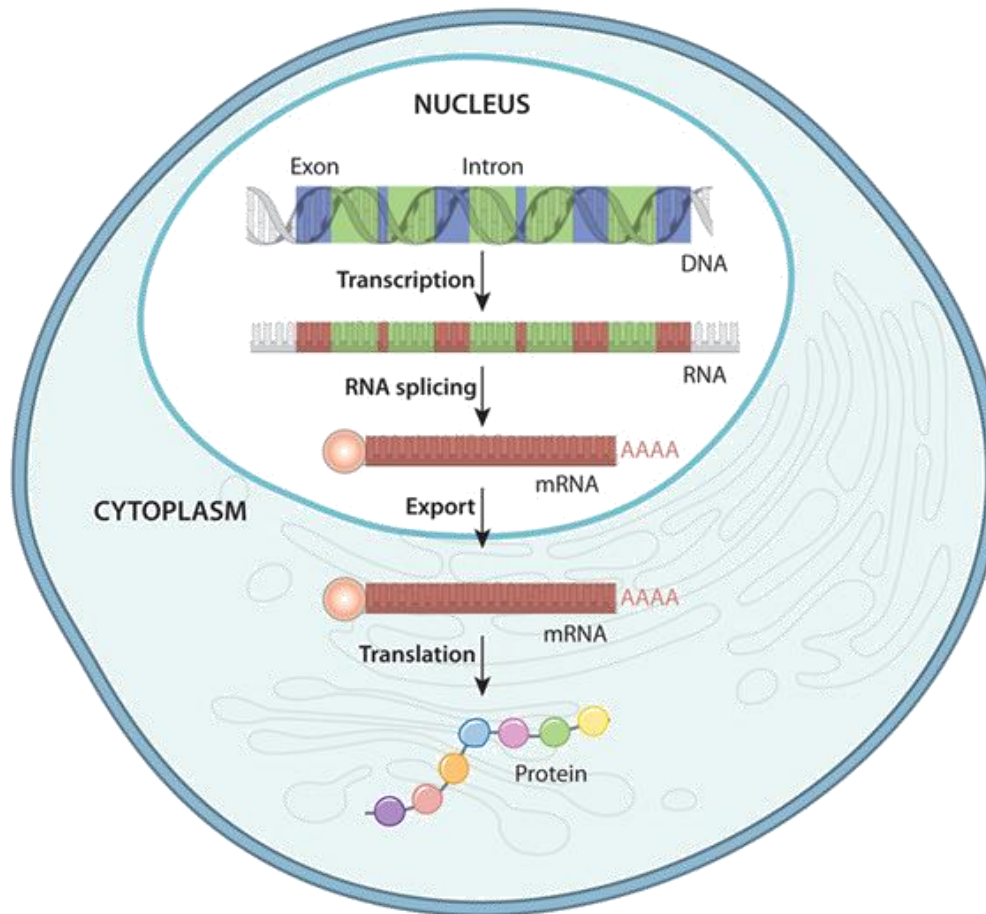
"big data" - a complete set of information about a feature of cell

Genes to messenger to proteins

DNA \rightarrow mRNA \rightarrow Protein

Biological information flow

Central Concept of Molecular Biology



What is 'Omic Data

'Omic data sets include:

- Genetic
- Transcriptomics – Gene Expression
- Proteomics
- Metabolome



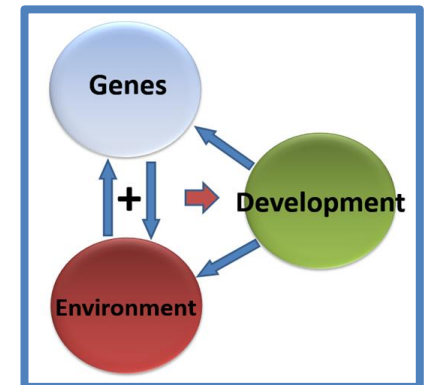
Fixed



Gene:Environment:
Development

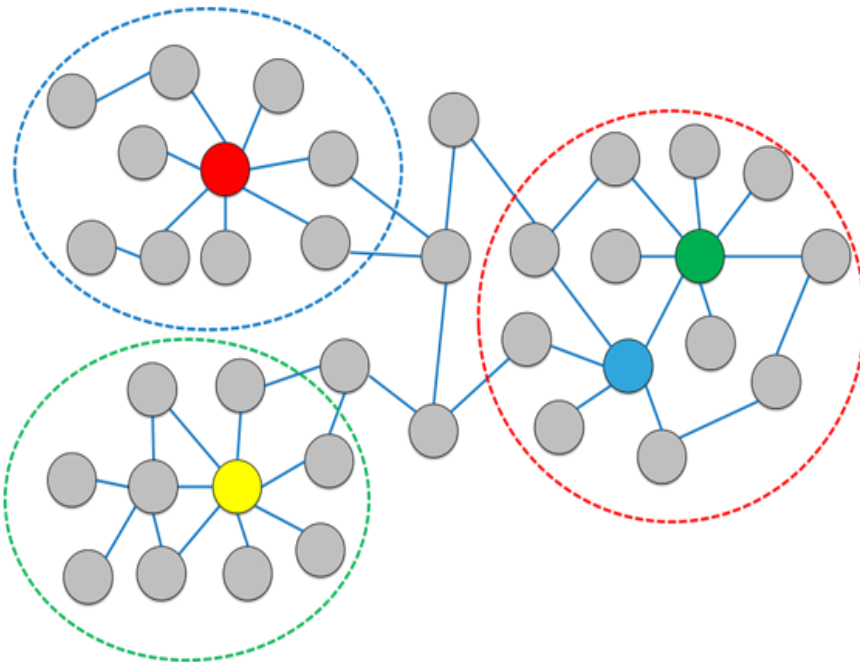
~ 22 000 genes in humans

How is 'omic data analysed?

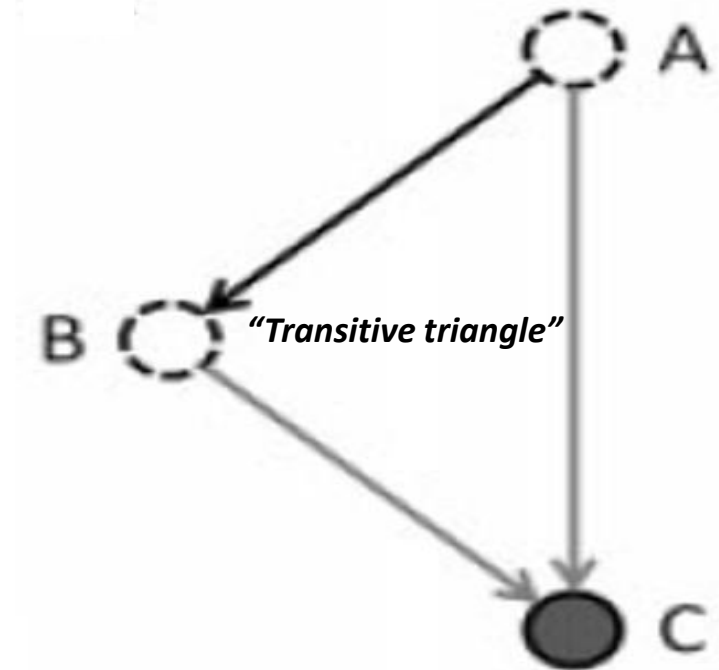


Network Analysis

Clusters of genes

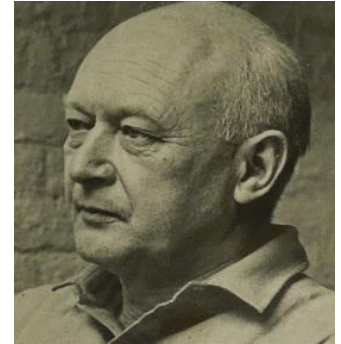
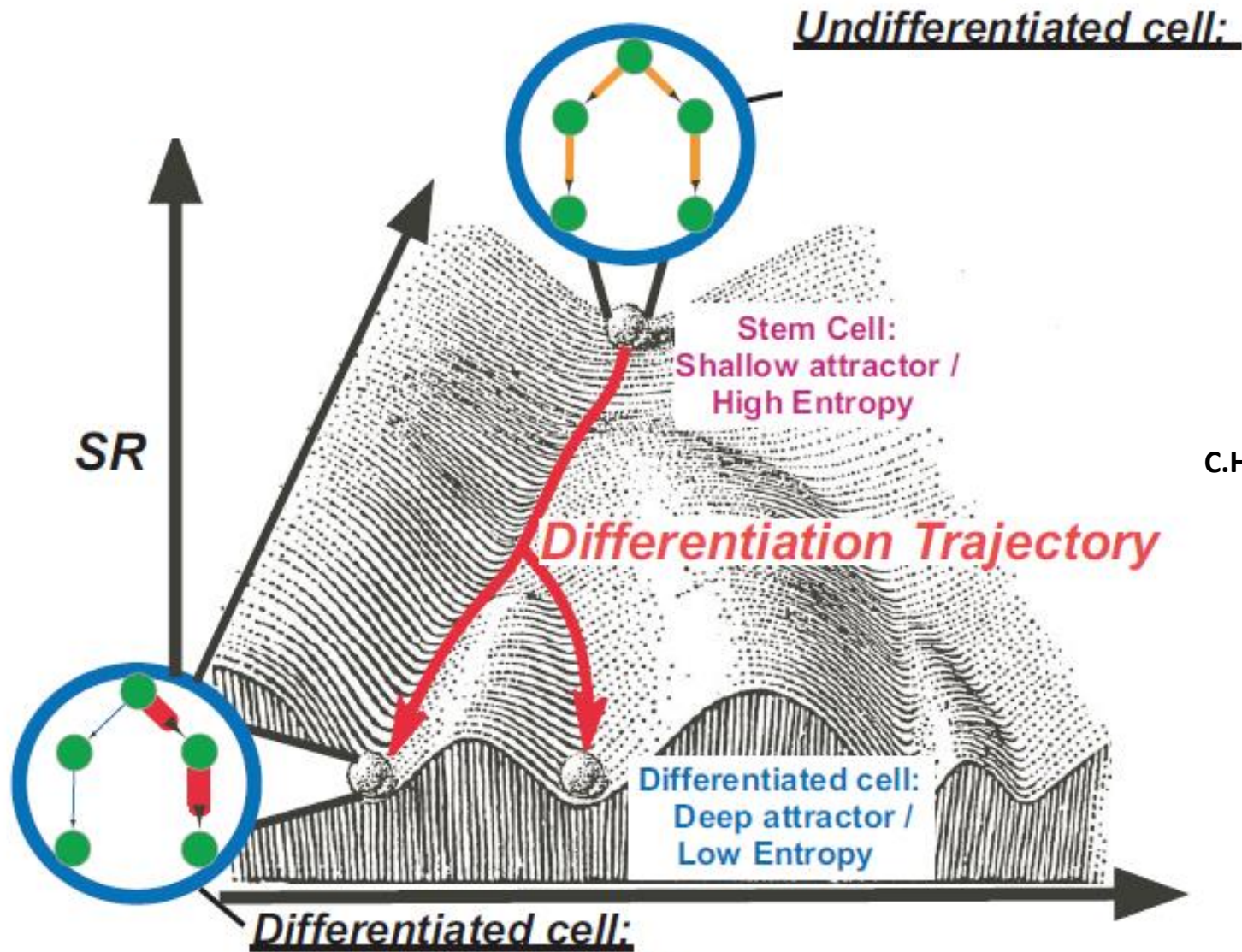


Causal Pathways



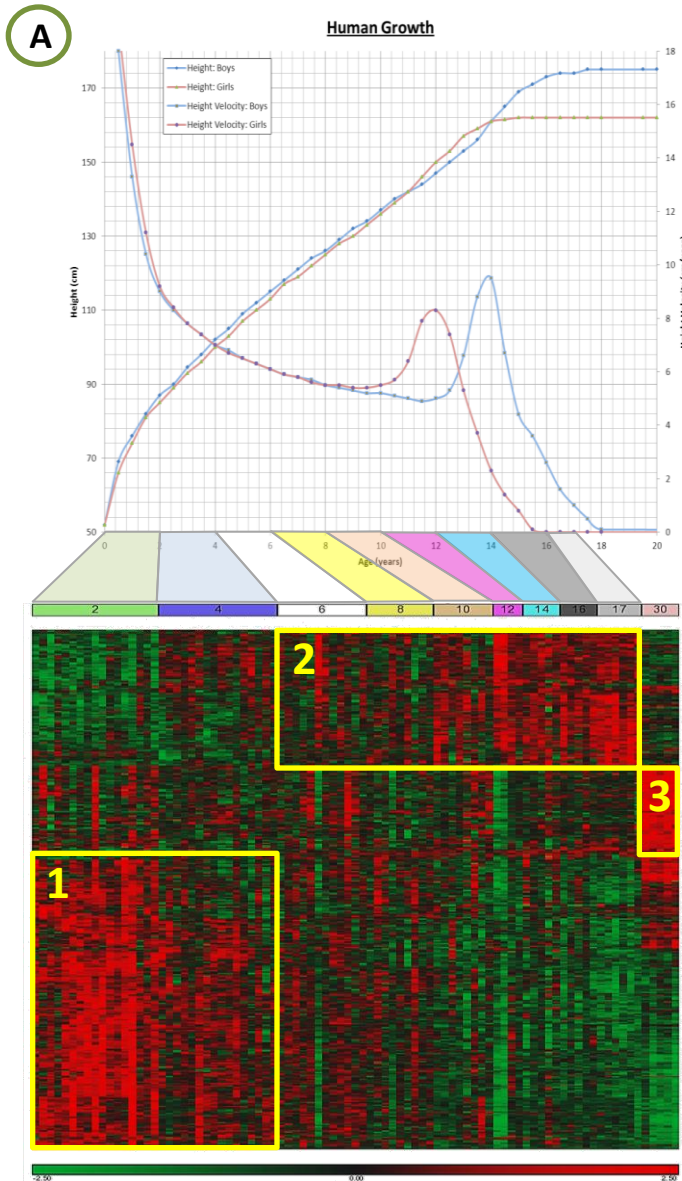
- Function
- Prediction

Waddington's Differentiation Landscape

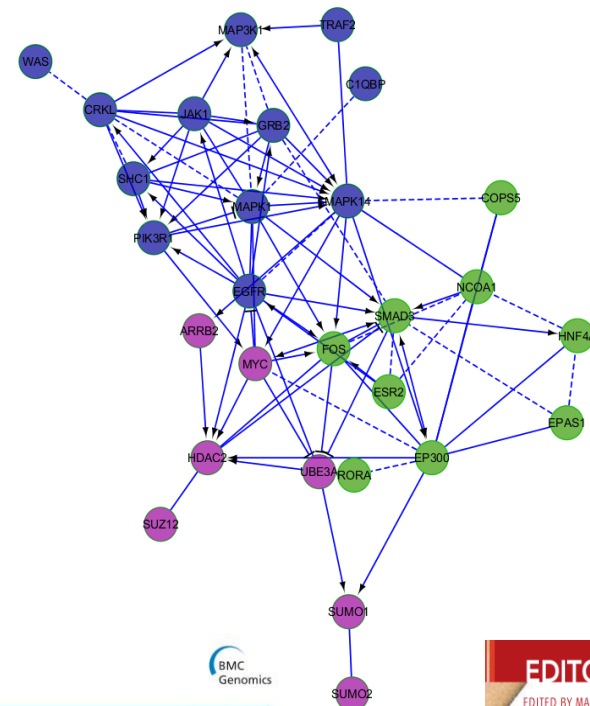
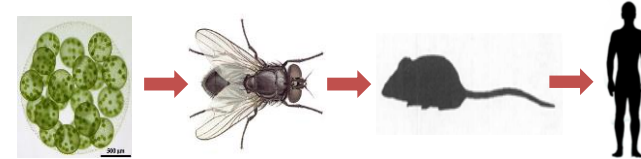


C.H. Waddington 1905-1975

Evolutionary conserved growth pathways are associated with the phases of childhood growth



Evolutionarily Conserved Growth Pathways



Stevens et al. BMC Genomics 2013, 14:547
http://www.biomedcentral.com/1471-2164/14/547

RESEARCH ARTICLE

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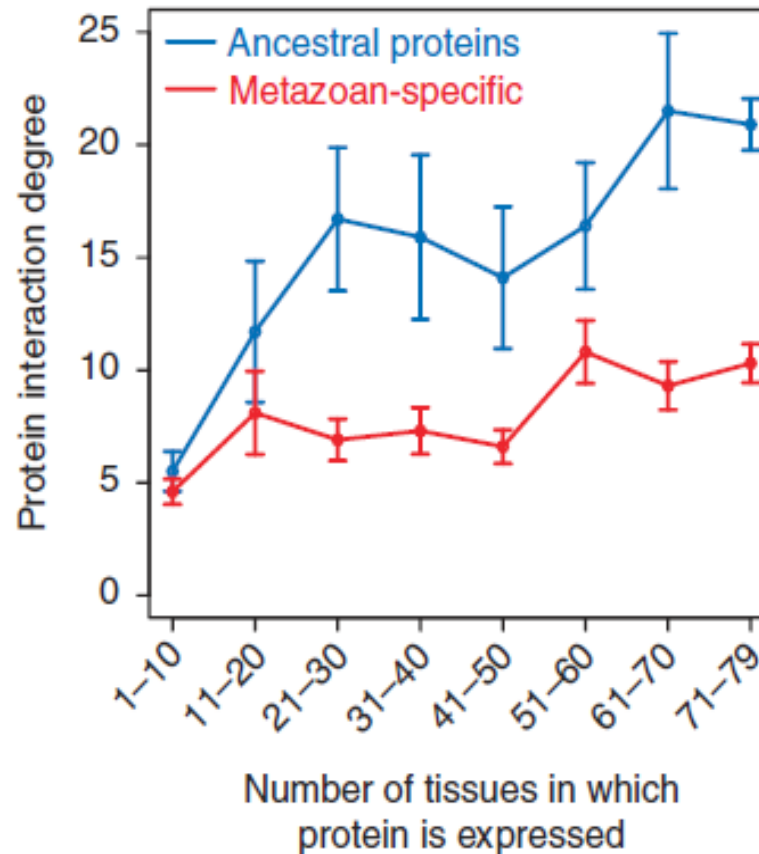
Human growth is associated with distinct patterns of gene expression in evolutionarily conserved networks

Adam Stevens^{1*}, Daniel Hanson¹, Andrew Whatmore¹, Benoit Destenaves², Pierre Chatelain³ and Peter Clayton¹



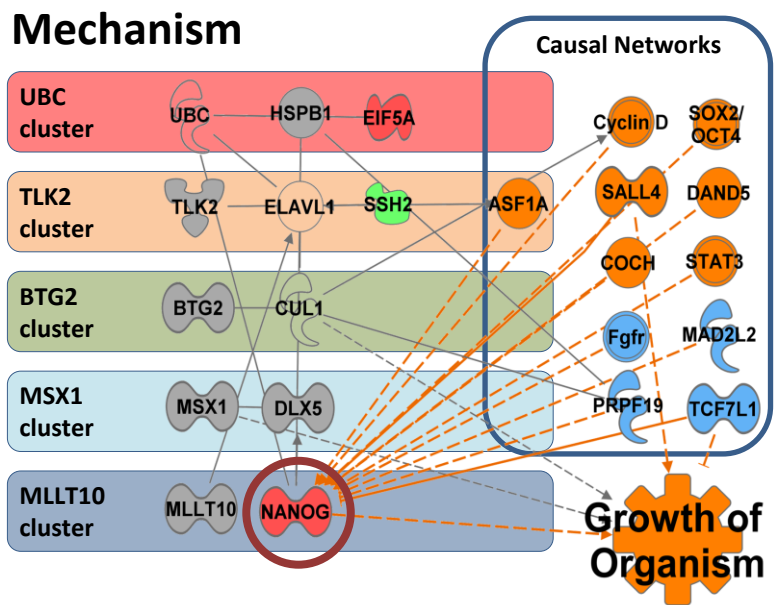
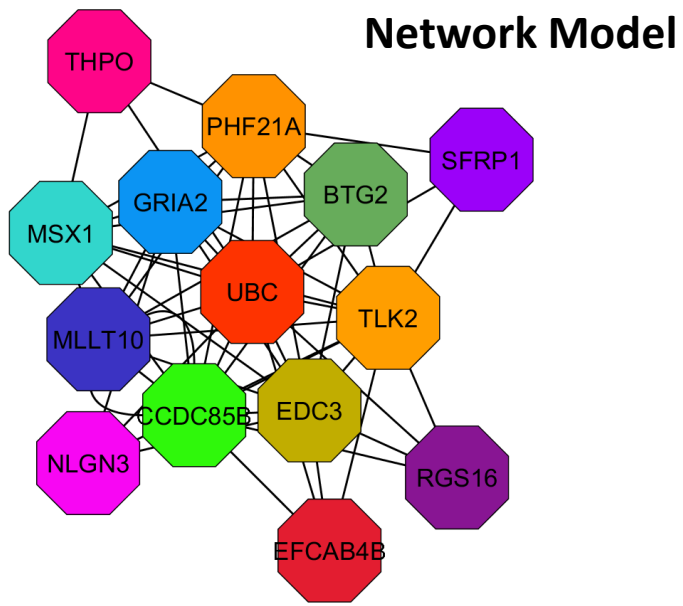
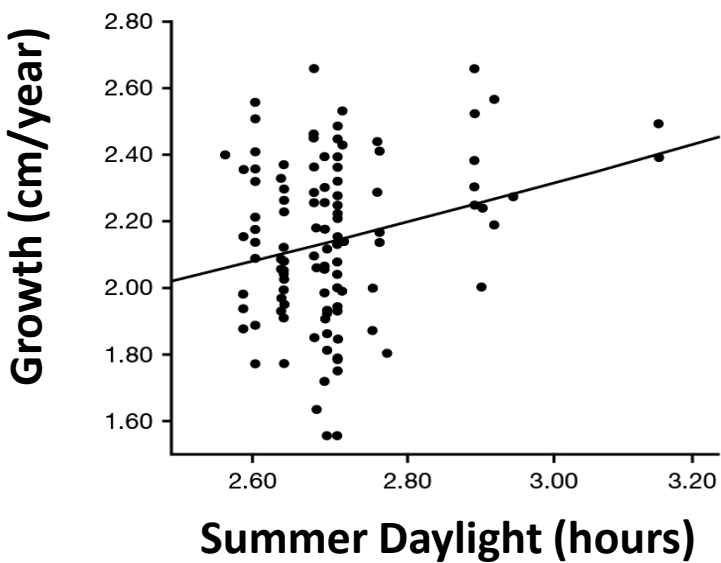
SCIENCE VOL 341 20 SEPTEMBER 2013

The evolutionary age of genes is associated with network properties



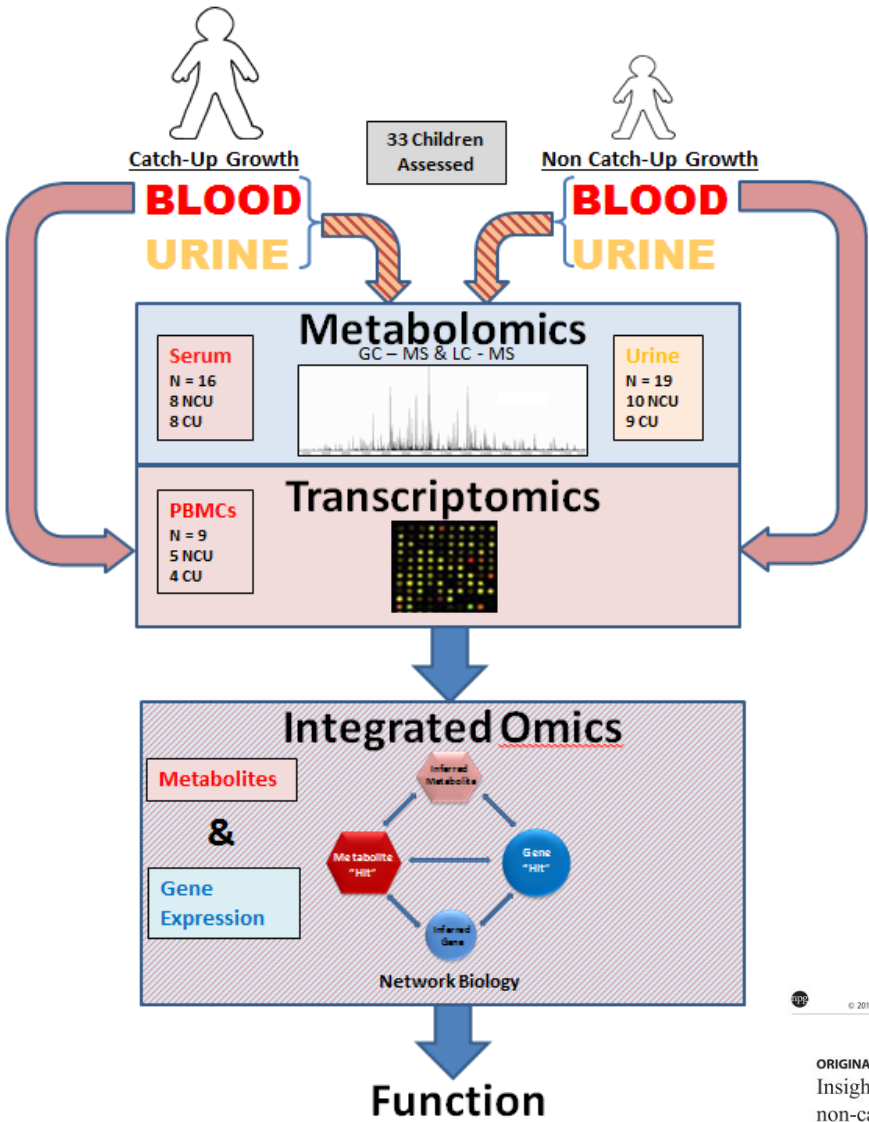
Recently evolved proteins make few protein interactions.

The Effect of Latitude and Summer Daylight Exposure on Growth



Catch-Up Growth in SGA children

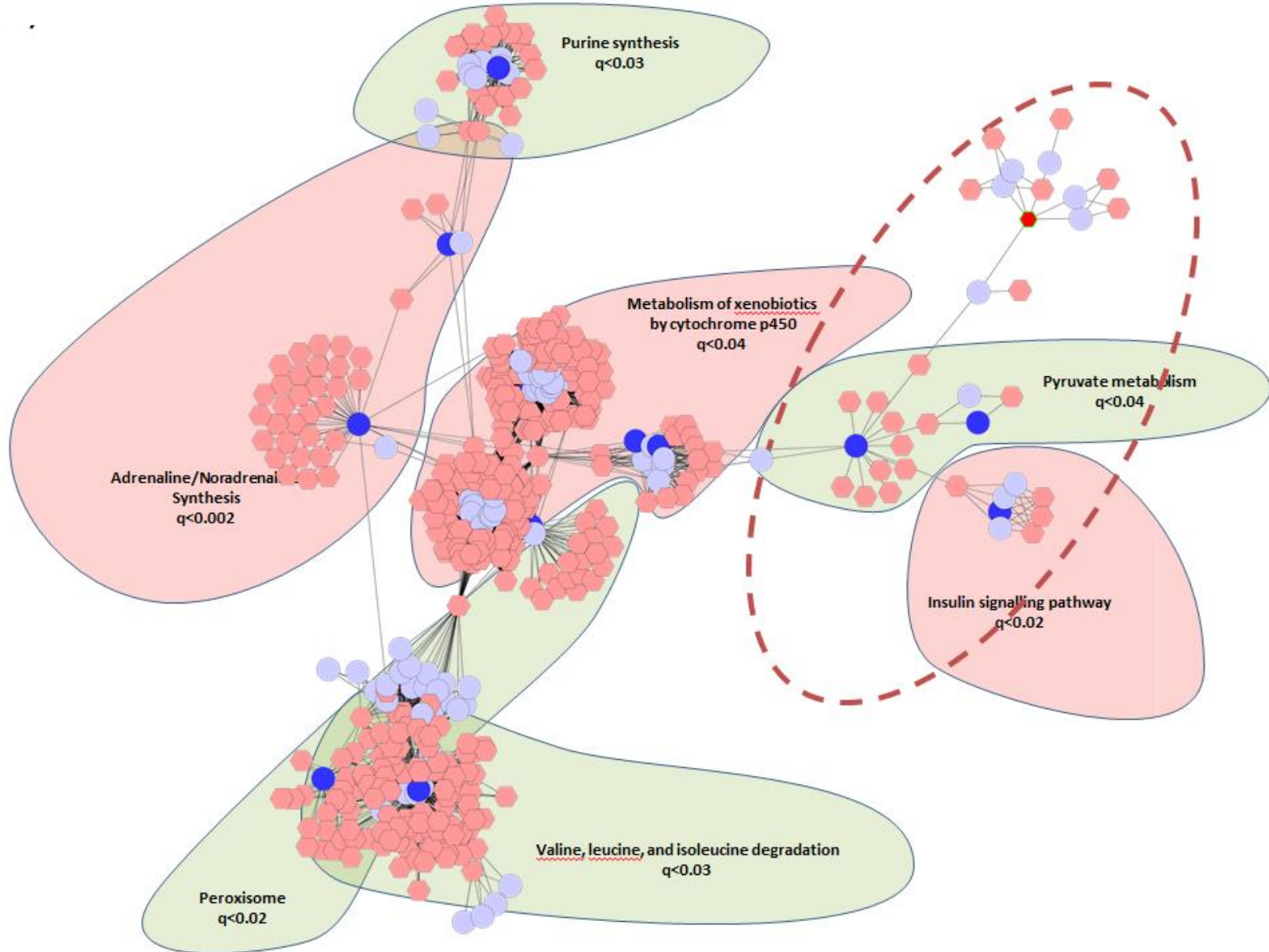
Small for Gestational Age Children



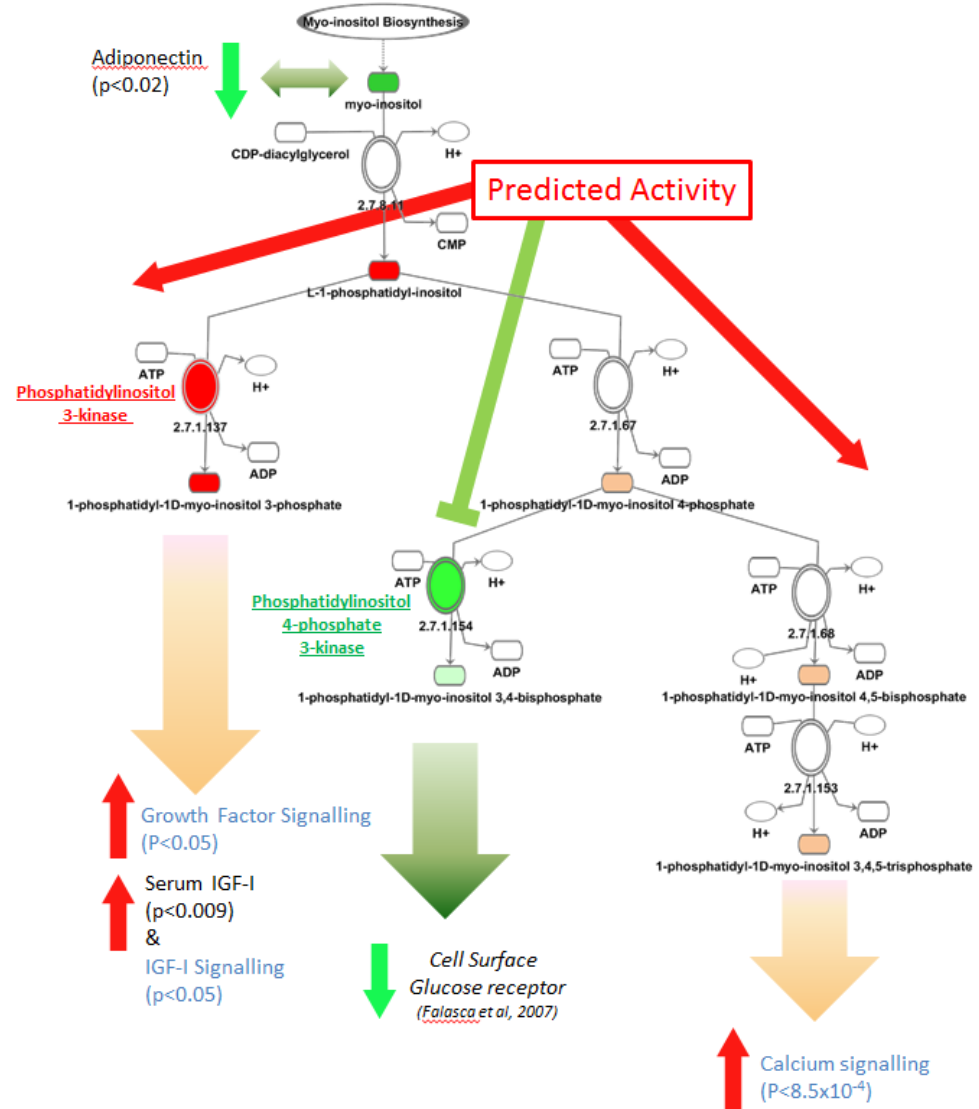
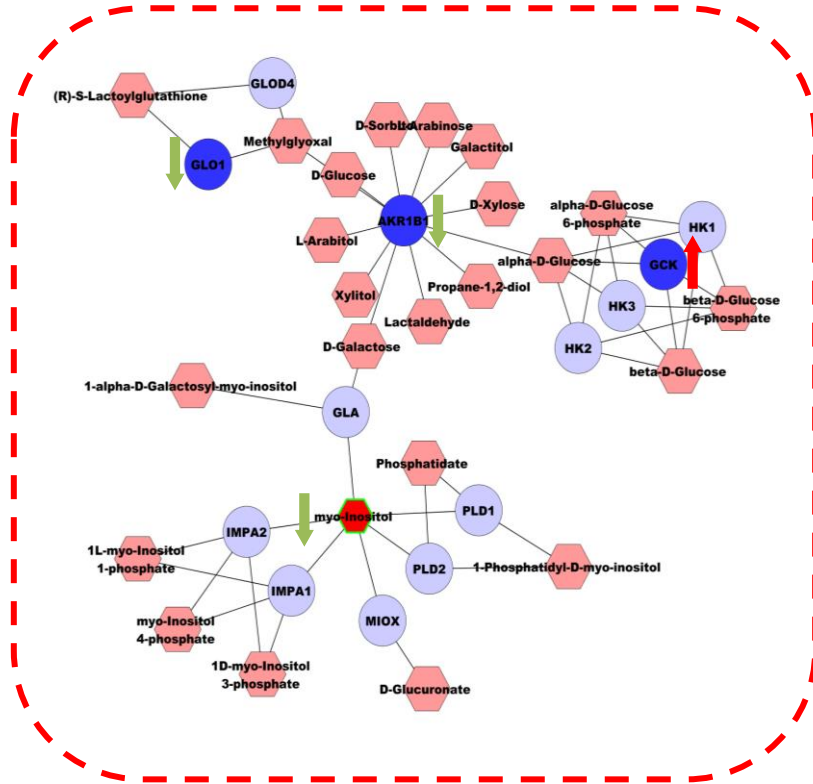
ORIGINAL ARTICLE
Insights into the pathophysiology of catch-up compared with non-catch-up growth in children born small for gestational age: an integrated analysis of metabolic and transcriptomic data

A Stevens^{1,2,14}, C Bonshek^{1,2,14}, A Whatmore^{1,2}, I Butcher^{1,2}, D Hanson^{1,2}, C De Leonibus^{1,2}, G Shaikh¹, M Brown^{1,5}, E O'Shea^{1,2}, S Victor⁶, P Powell⁷, P Settle⁸, B Padmakumar⁹, A Tan¹, E Odeka¹, C Cooper^{1,2}, J Birch¹, A Shenoy^{1,2}, M Westwood¹, L Patel^{1,2}, BW Dunn^{1,2} and P Clayton^{1,2}

Catch-Up Growth in SGA children



Catch-Up Growth in SGA children



Red= metabolomic change

Blue = gene expression change - protein "seed"

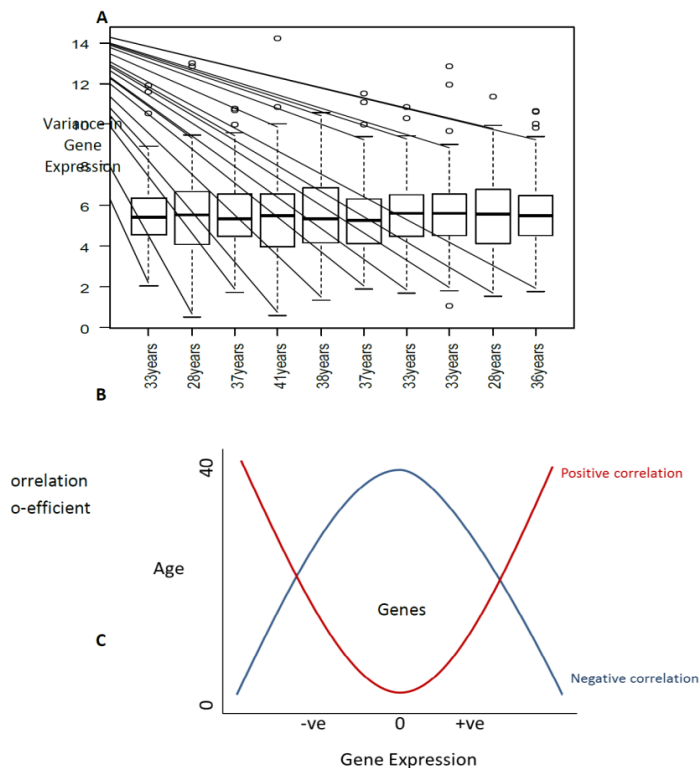


Figure 1. A) Boxplots displaying the variance of gene expression within individual blastocyst embryos with different maternal ages. **B)** Spearman's rank correlation co-efficient calculated for every gene, in relation to maternal age. Red dotted line represents correlation threshold cut-off of 0.75 **C)** Figure depicting positive and negative correlation analysis patterns.

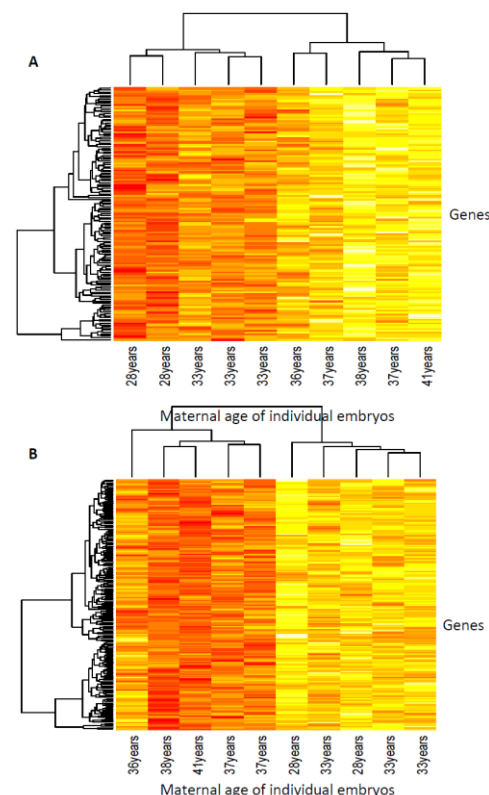


Figure 2. Genes highly correlated with maternal age within the blastocyst embryo. A) Genes positively correlated ($R > 0.76$) with maternal age. **B)** Genes negatively correlated ($R > 0.74$) with maternal age. Yellow represents higher levels of expression and red represents lower levels of expression.

Human blastocysts (n=10)

329 genes correlated with maternal age: 139 positively, 190 negatively

Tipping point at female age = 35, maps onto decline in female fertility

Epigenetic regulators overrepresented (11 ZFPs, HIST1H2AE, METTL2B, L6)

Conclusions

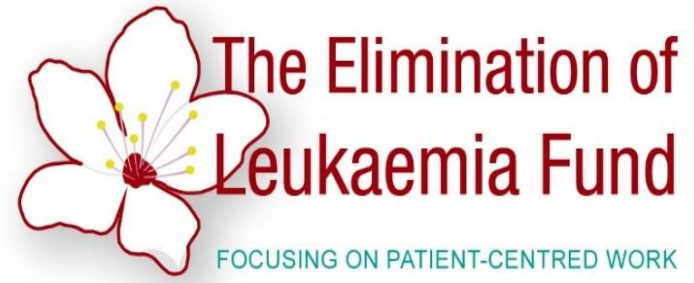
- Human growth has features that are unique in the animal kingdom
- 'omic data and network modelling gives us the tools to relate gene:environment:development
- The evolutionary age of a gene can act as a marker to relate growth and metabolic function
- Changes of growth rate in early life are related to health in later life

Chiara De Leonibus
Philip Murray
Dan Hanson
Andrew Whatmore
Peter Clayton

Stefan Meyer

Chris Knight
Neil Swainston

Pierre Chatelain



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