Pathways and Genes under positive selection in metabolic diseases

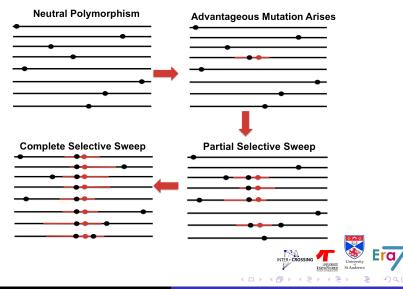
Alexandra Vatsiou

3rd International Conference on Epidemiology and Public Health

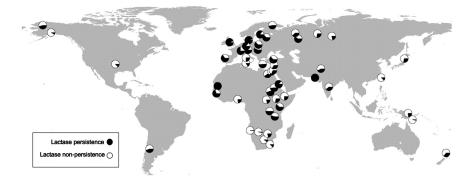
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Positive Selection



Why do we study positive selection?



Ingram et al. 2009



Gene Set Enrichment Analysis (GSEA)



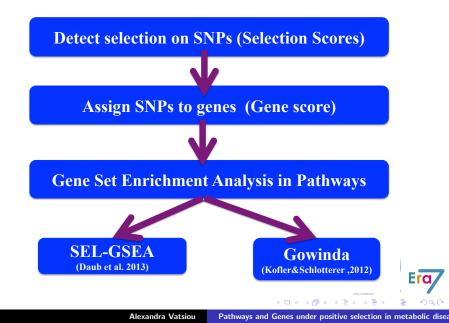
Gene Set Enrichment Analysis (GSEA)

Data

- SNP data: Hapmap phase II (3 populations (CEU, YRI, CHB+JTP)
- Gene data: Entrez NCBI database on the 5/2014 (Number of genes: 27081)
- Gene Sets: Biosystems database on the 5/2014. (Number of pathways: 2362)



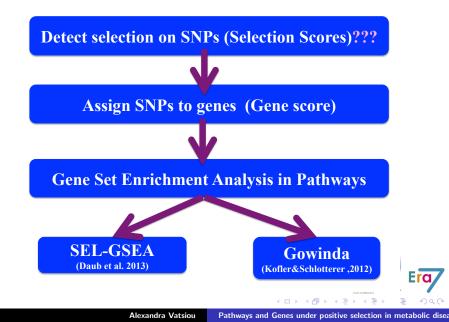
How to detect positive selection on pathways?



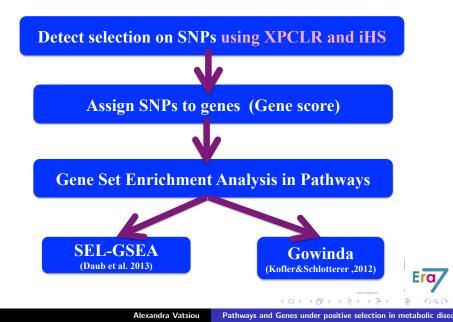
- Python tool for Gene and Gene Set Enrichment Analysis following Daub et al. (2013) methodology
- Osing SNP data and a gene-set list
- **3** User-friendly and flexible
- Freely available: https://github.com/INTERCROSSING/SEL_GSEA



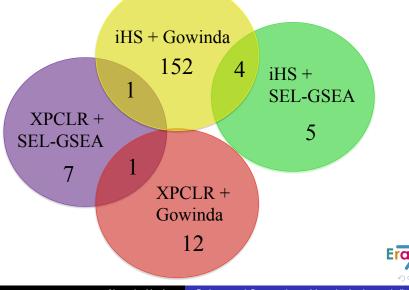
Which method to use to detect selection on SNPs?



Which method to use to detect selection?



Results of GSEA



What about metabolic diseases?



"Diabetes has increased dramatically over the past 20 years. That proves that diabetes is caused by global warming!"



From hunting ... to ... burgers







From hunting ... to ... burgers



- Glycolysis and gluconeogenesis (4.2e-05)
- Signal attenuation (0.0003)
- **3** Glucose transport (0.003)



683 genes directly or indirectly associated with:

- obesity or
- 2 metabolic syndrome or
- diabetes



- 25 candidate genes for positive selection
- 2 12 of them play a risk role
- **③** 7 of them play a protective role
- It of them were detected to be under positive selection before
- Is new candidates for metabolic diseases



- multifactorial diseases
- 2 study the whole system



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Thank you for your attention.



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Any Questions?

