## Student project: Gene networks via PascalX

## Daniel Krefl

Computational Biology Group

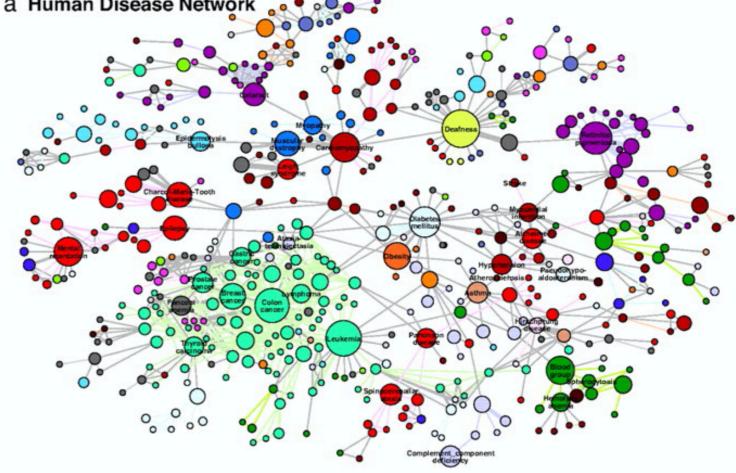
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D. Krefl @ UNIL March '21



(Goh et al '07: The human disease network)

Via harvesting known Gene-Disease relations networks can be constructed and clustered: a Human Disease Network



(from Goh et al PNAS '07: The human disease network)

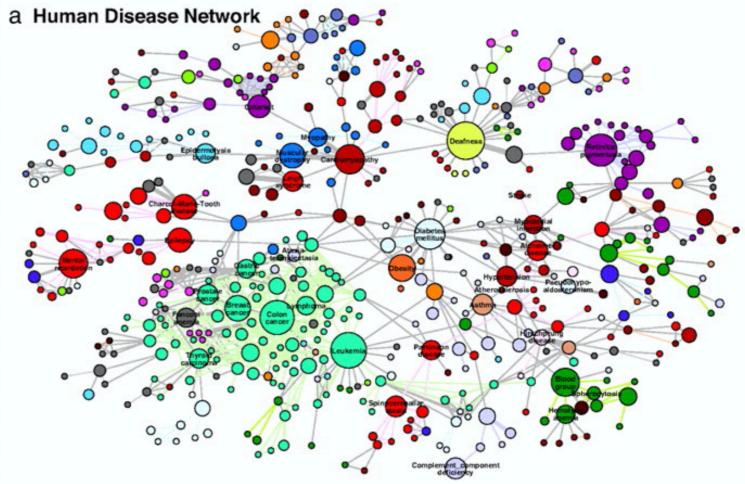


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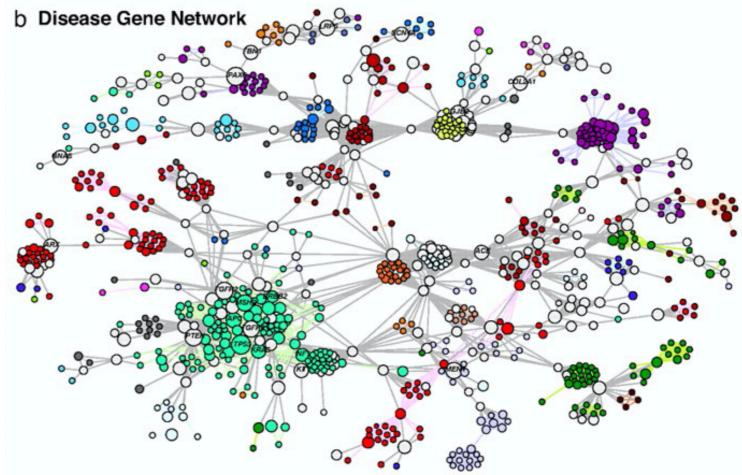


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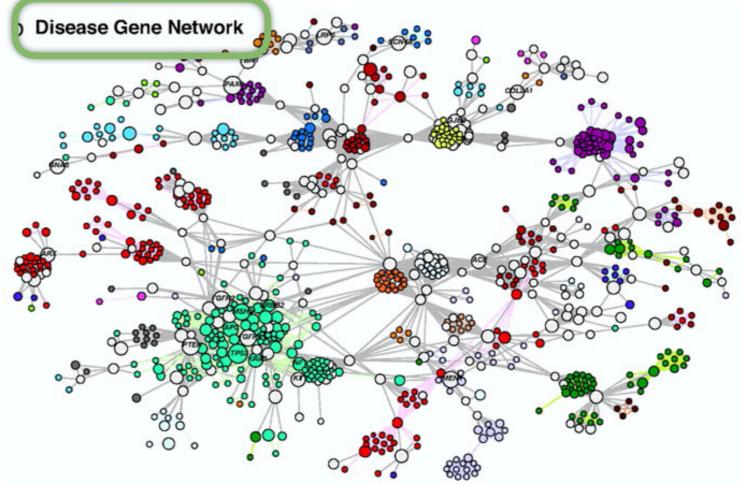


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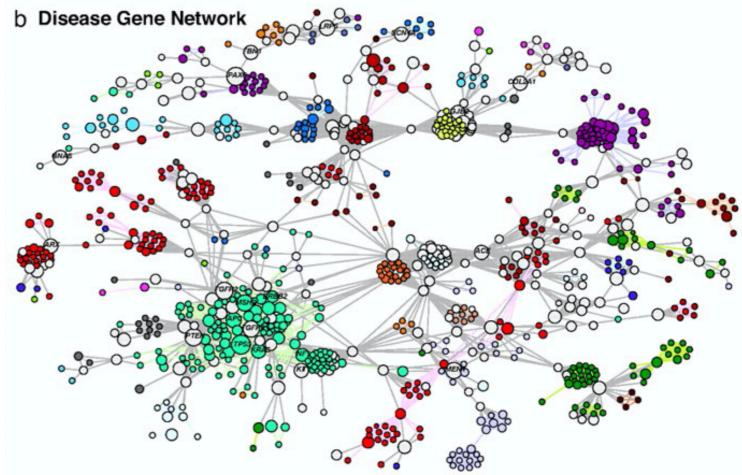


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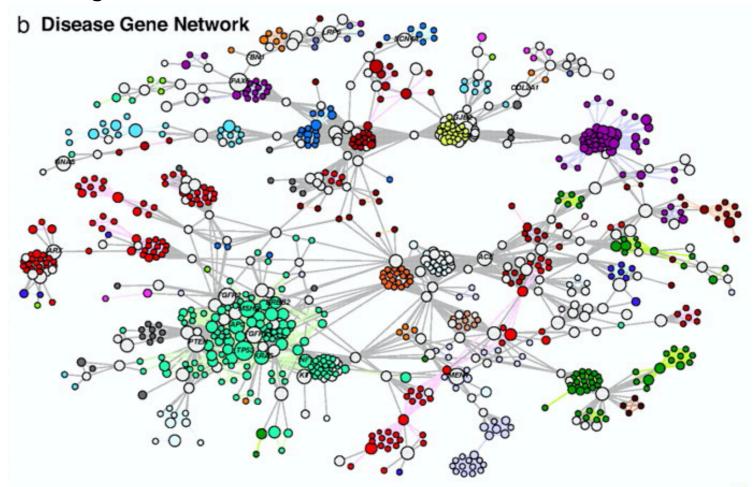




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#### Disease-gene networks yield novel insights:

- Shared genetic origins of diseases
- Multi-pathway association of diseases
- Disfunction of shared functional modules





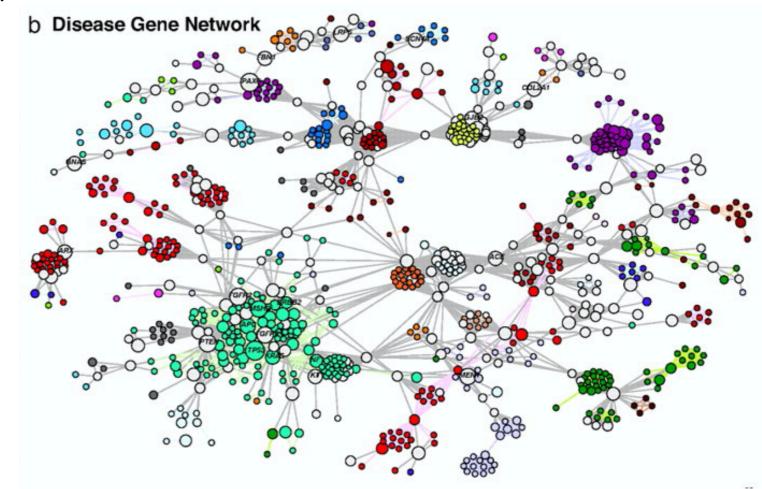


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#### Disease-gene networks have applications:

- Predict adverse drug reactions
- Predict new disease related genes
- Drug repurposing
- Identify shared mechanisms

<u>Good first read:</u> Bauer-Mehren et al., Gene-disease network analysis reveals functional modules in mendelian, complex and environmental diseases



## Project



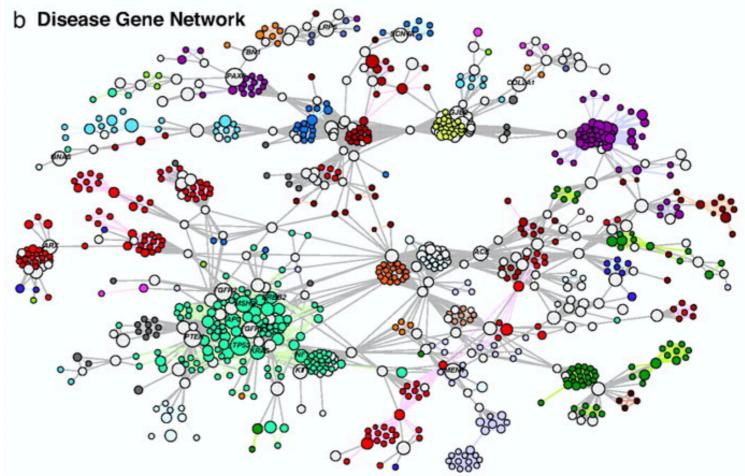
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Construction via text mining:

- High effort
- Not precise
- Not constant



## Project

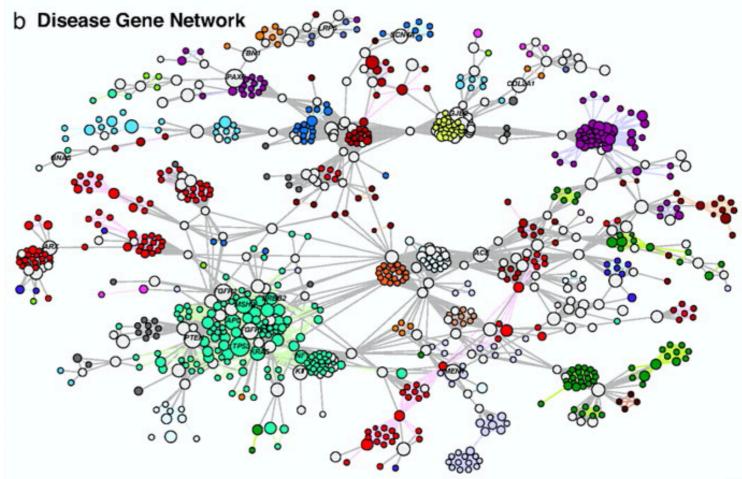


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### THIS PROJECT (base):

Extract such a disease-gene network directly from a set of GWAS



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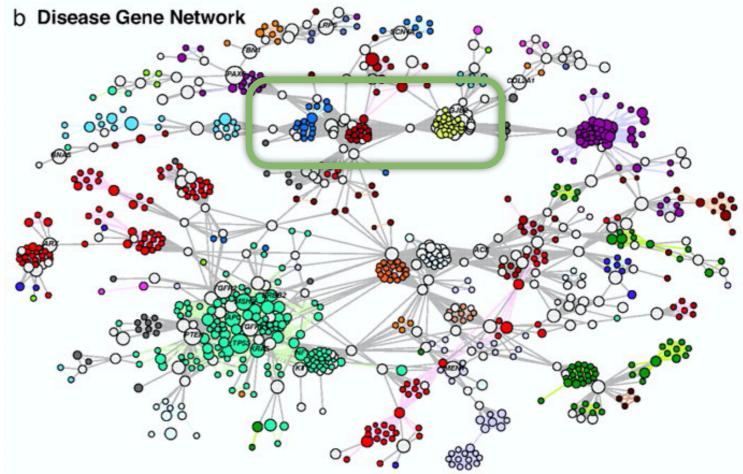


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Collect suitable GWAS summary statistics from public resources

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## Technicalities



Publicly available GWAS summary statistics. (GWAS catalog: https://www.ebi.ac.uk/gwas/downloads/summary-statistics)



**Python** ecosystem: PascalX, jupyter, numpy, scipy, scikit-learn, pandas, matplotlib, ... ( Prior knowledge of Python recommended )

## Outcome

#### You will acquire:

- General knowledge about GWAS studies
- Experience working with large scale GWAS summary statistics
- Data pre-processing skills in python and linux shell
- Big data skills in python
- General knowledge about the spectrum of human diseases and their interplay

# Feel free to contact me by email if you have any questions !

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