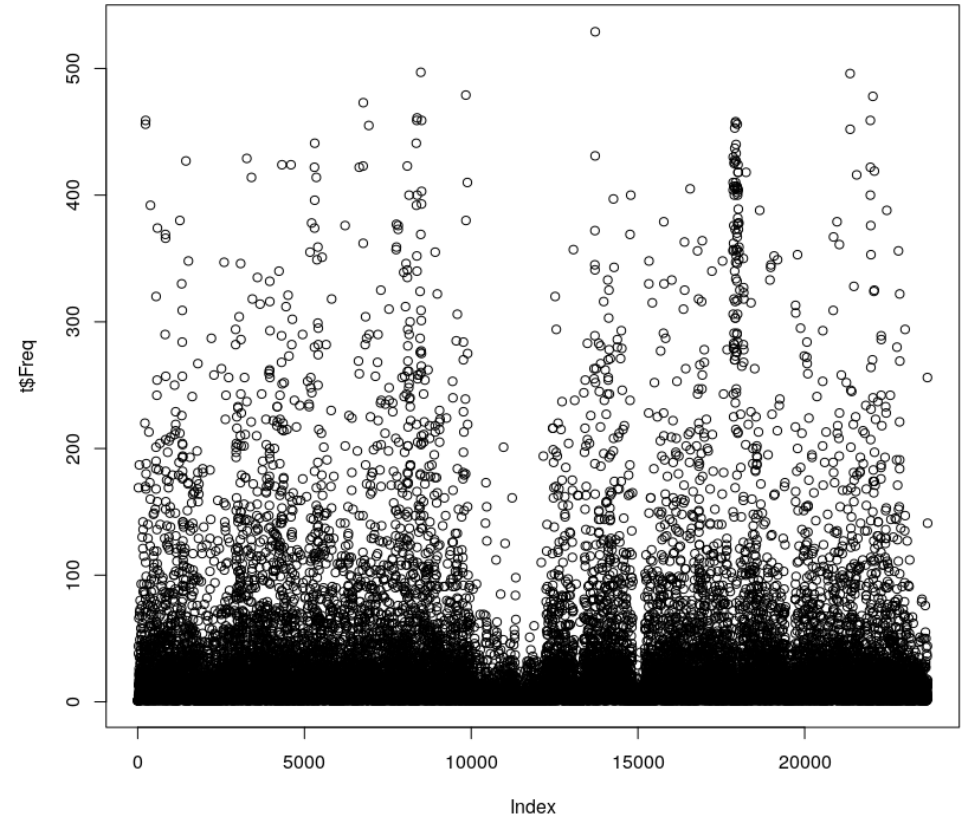


Resilient and sensitive human
genes —
Inner Demons and Inner Angels?

Gene behave differently - and this is good!



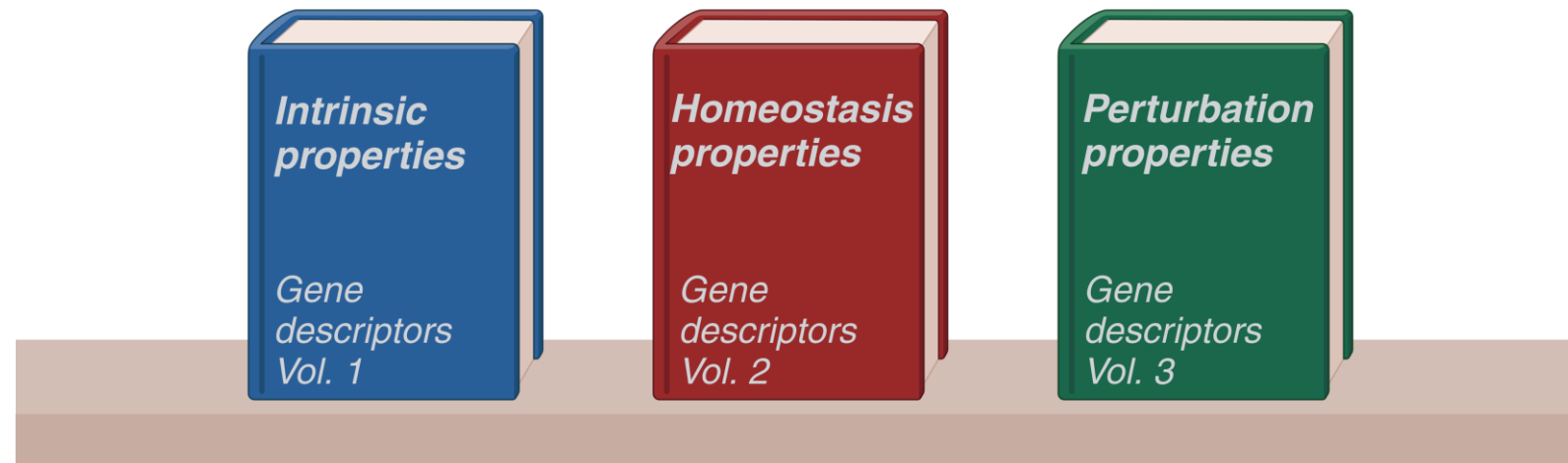
Basic molecular biology meets bioinformatics

Questions:

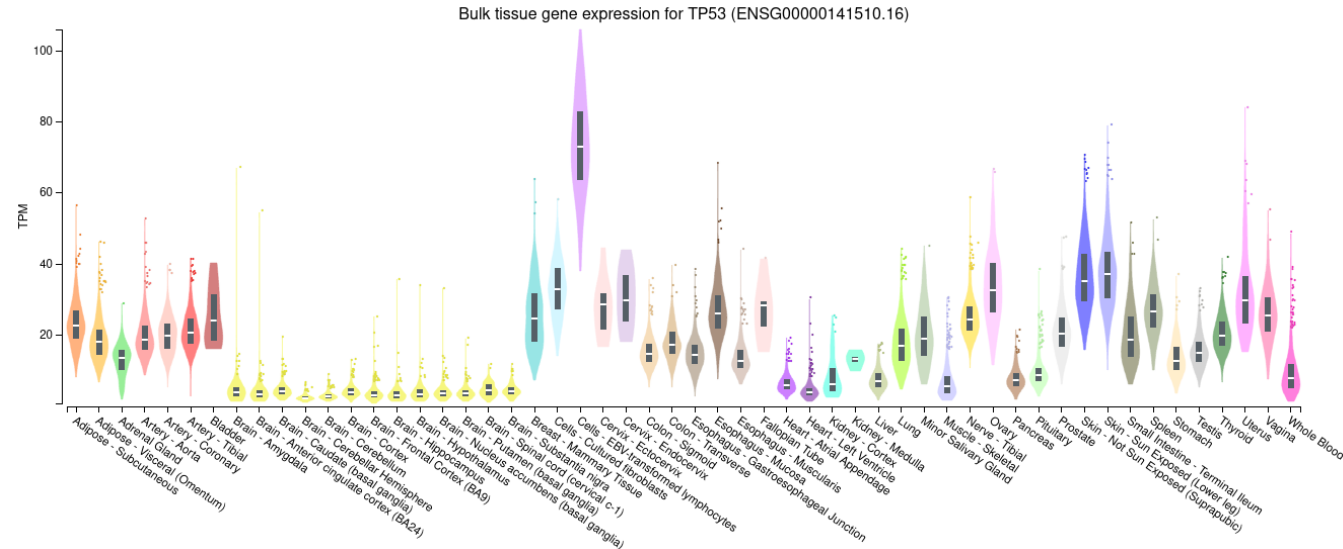
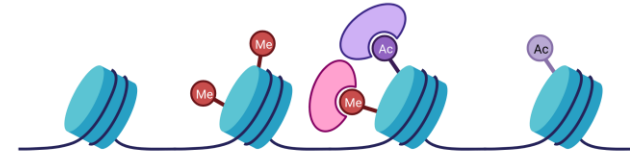
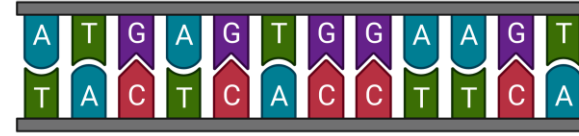
- Can we predict the behaviour of genes?
- What are the underlying rules?

Tasks:

- Create a library of gene characteristics
- Statistics about relationships










Characteristics such as ...



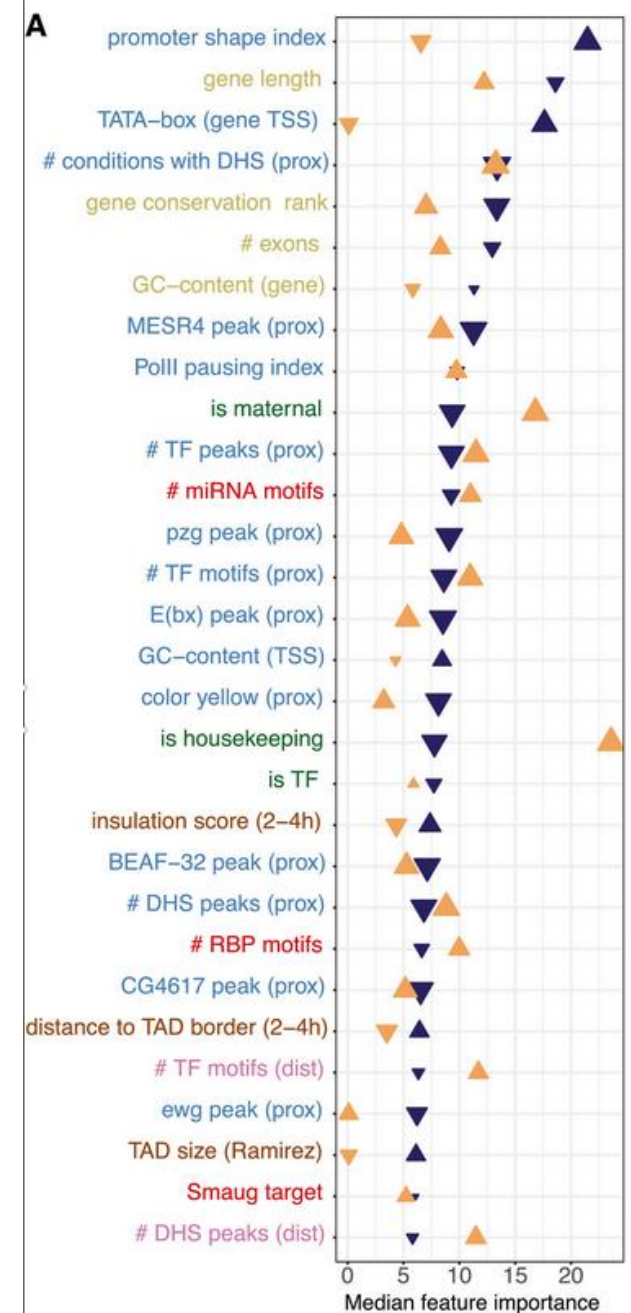
Starting point

Predictive features of gene expression variation reveal mechanistic link with differential expression

Olga M Sigalova , Amirreza Shaeiri , Mattia Forneris , Eileen EM Furlong  , Judith B Zaugg  

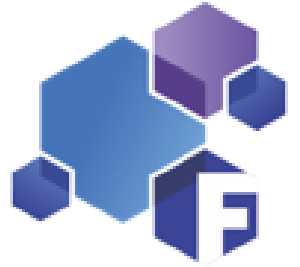
[Author Information](#)

Molecular Systems Biology (2020) 16: e9539 | <https://doi.org/10.15252/msb.20209539>



In case of interest

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Disease diagnosis support system

Angela Serra

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Background

- Data related to frequency of associations of disease-symptoms are needed to enhance the accuracy and efficiency of disease diagnosis, providing valuable support to healthcare professionals in decision-making processes.
- So far, few studies have performed manual curation of disease-symptoms from literature. An example is the paper of Zhou et al. <https://www.nature.com/articles/ncomms5212>

Aims of this work

- Update the curation by Zhou et al., 2014 and obtain a new version 10 years later.
- Implement and benchmark machine learning models for disease prediction from symptoms.
- **Optional:** investigate methodologies of model prediction explanations based on knowledge graphs. (**based on time and preference**)

Example of curation from Zhou et al., 2014

MeSH Disease Term	MeSH Disease Term	symptom similarity score
Histiocytoma, Benign Fibrous	Aneurysm	0.5919371561421504
Histiocytoma, Benign Fibrous	Carcinoma, Basal Cell	0.31047856901085596
Arthropathy, Neurogenic	Corneal Dystrophies, Hereditary	0.13312334531698433
Arthropathy, Neurogenic	Foot Deformities, Congenital	0.1569000128545492
Hemangioendothelioma, Epithelioid	Thyroid Neoplasms	0.15707652855363136
Hemangioendothelioma, Epithelioid	Migraine without Aura	0.10677480081395119
Hemangioendothelioma, Epithelioid	Facies	0.19822637546404606
Alzheimer Disease	Bipolar Disorder	0.4059620244303505
Alzheimer Disease	Ocular Motility Disorders	0.1492454708103799
Alzheimer Disease	Gerstmann-Straussler-Scheinker Disease	0.1833436345531103
Alzheimer Disease	Dyskinesia, Drug-Induced	0.11951603219730665
Alzheimer Disease	Subacute Sclerosing Panencephalitis	0.14061199579752906

Tasks in practice

- Update the curation performed by Zhou et al. and obtain a new version 10 years later.
 - Retrieve data from public databases (python programming skills required)
 - Curate the retrieved associations (data analysis skills required)
- Implement and benchmark machine learning models for disease prediction from symptoms.
 - Design machine learning pipelines (python programming skills required)
 - Testing and model evaluation (data analysis skills required)

Required skills

Project development:

- Python
- Jupyter notebooks
- git

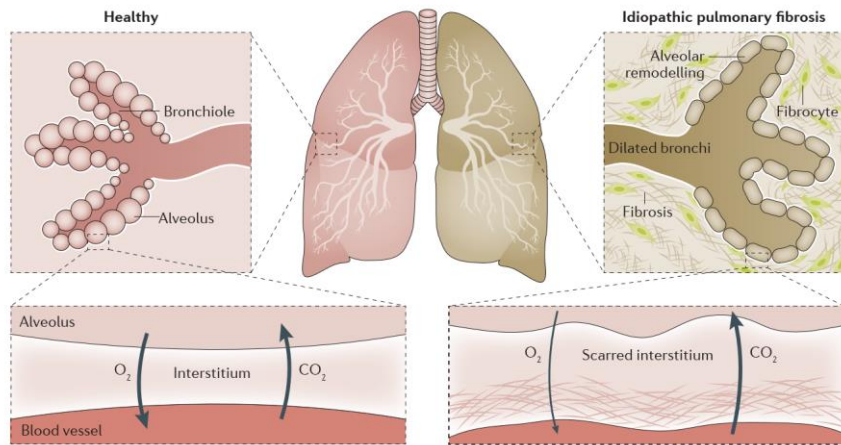
Data collection/curation:

- API calls with requests package
- Json/xml parsing
- regular expressions
- Data manipulation with pandas

Data modeling:

- Numpy
- matplotlib
- Scipy
- scikit-learn

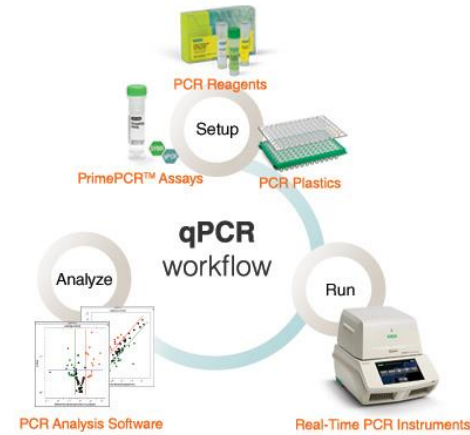
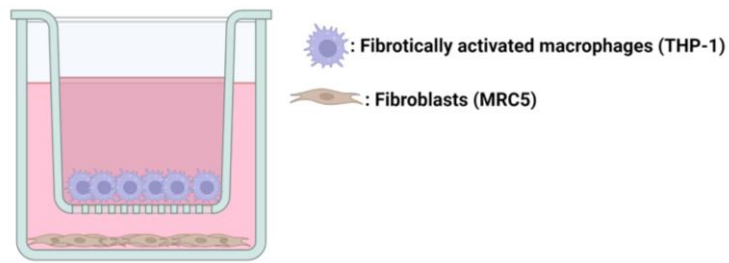
Exploring the Immune Component of Lung Fibrosis



(Martinez et al. 2017)

CO-CULTURE SYSTEMS

Transwell system



You will co-culture macrophages that have been exposed to profibrotic chemicals (bleomycin and TGF β to start) with lung fibroblast cells and look at the effect on the fibroblasts through qRT-PCR. Exploring gene expression of Collagen, alphaSMA and other important indicators of fibrosis.

Skills you will learn:

- Cell culture
- Cell co-culture
- RNA isolation
- qPCR
- qPCR analysis

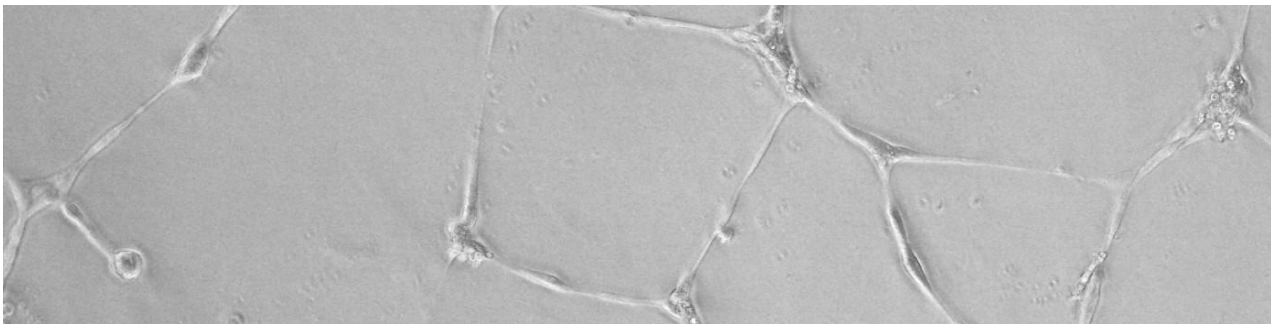
Optional but nice skills that you might already have:

- Cell culture familiarity
- R and Rstudio familiarity

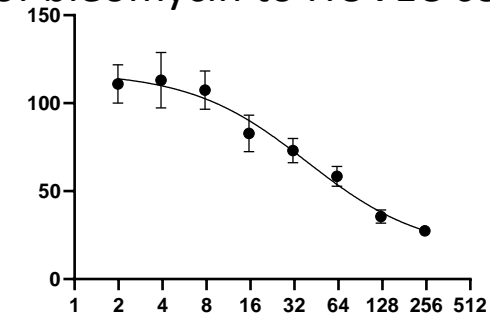
Please get in touch: jack.morikka@tuni.fi

In vitro models towards mechanistic toxicity

- Mechanistic toxicity
- 2D cell culture models
- endothelial and immune cells
- -omics data generation
- → towards mechanistic understanding of underlying mechanisms of toxicity



Toxicity of bleomycin to HUVEC cells



- Skills you need:
 - Curiosity
 - Open minded
 - Willingness to learn new and patience to apply those skills
 - Some lab experience is plus but not needed
- Skills you will obtain:
 - Working in laboratory
 - Cell culture
 - Basics on working in GLP
 - High-throughput data generation
 - qPCR and other molecular biological skills
 - Data analysis and reporting
 - Thesis process

• More info: laura.yla-outinen@tuni.fi

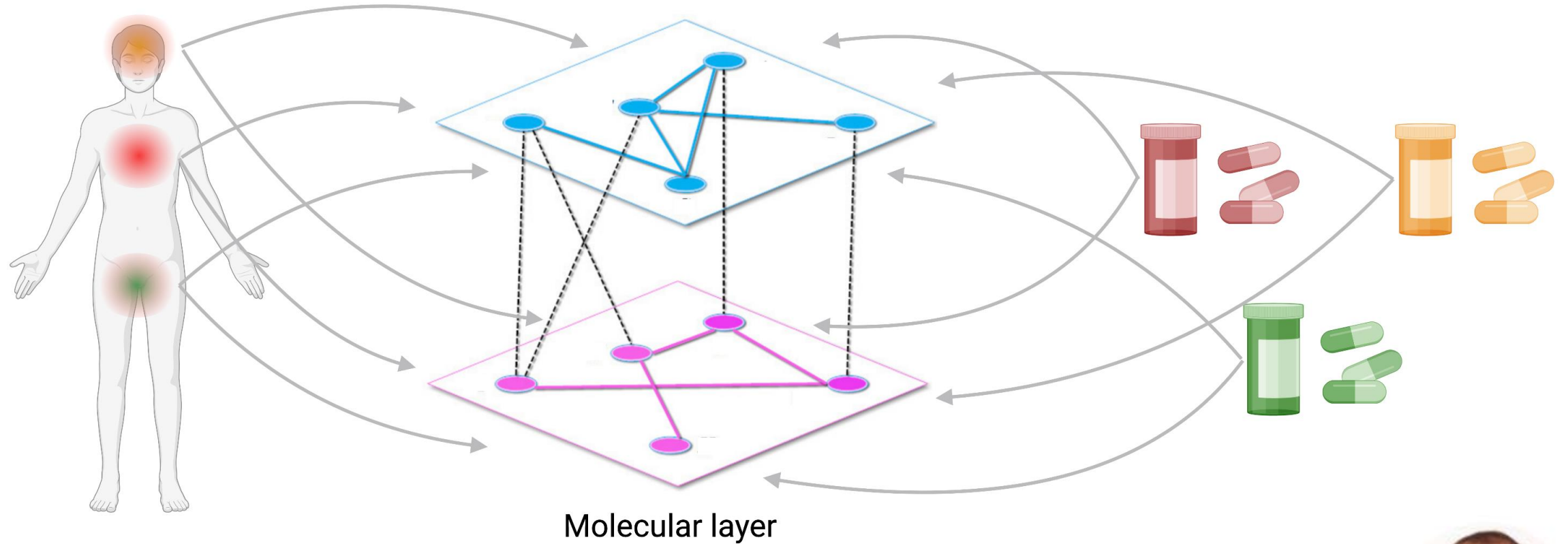


Network models of diseases to design novel therapeutic strategies

Human complex disease

Symptoms layer

Drug treatment



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