Introduction COVID19 Disease Map & WikiPathways

Martina Summer-Kutmon, PhD

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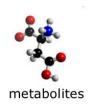


Outline

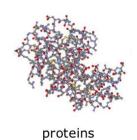
- Introduction
- COVID19 Disease Map
- WikiPathways

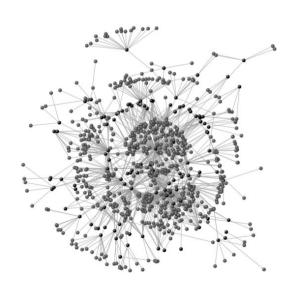
Molecular systems biology

Molecules of life do not function in isolation







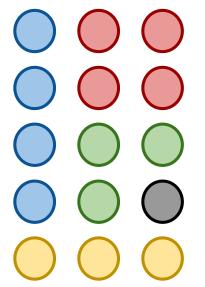


but form complex networks that define a cell

Introduction

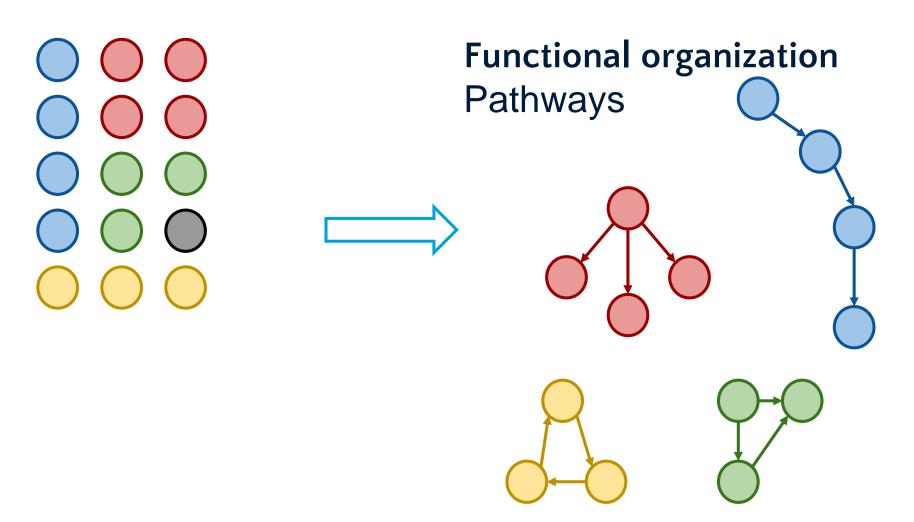
| | | Quantitative |
|--|--------------|----------------------|
| | measurements | Icolated data paints |
| | | Isolated data points |
| | | |
| | | |

Introduction



Comparative statistics
Isolated lists
Clustering
Isolated groups
Gene sets
Functional groups

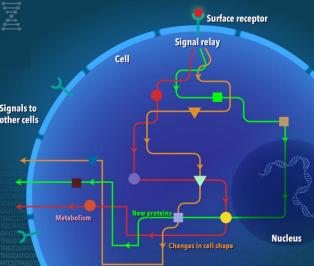
Introduction



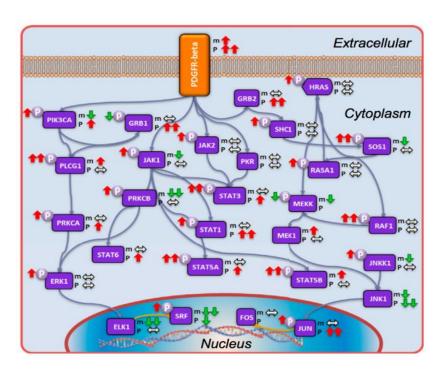
Pathway models

- Detailed curation of biological processes
- More than images > machine-readable pathway models

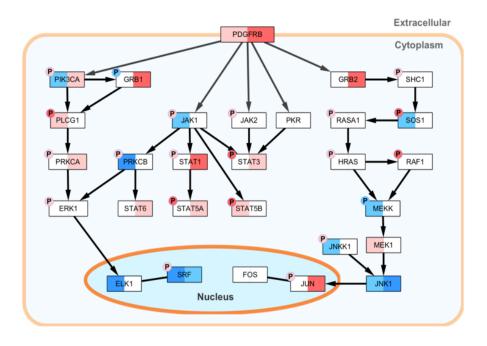
Essential to better understand, validate and simulate molecular mechanisms



Biological pathways



Static image Zhang et al, Cell 2016



PDGFR-beta pathway with transcriptomic/phosphoproteomic data

www.wikipathways.org/instance/WP3972

Outline

Introduction



- COVID19 Disease Map
- WikiPathways

COVID19

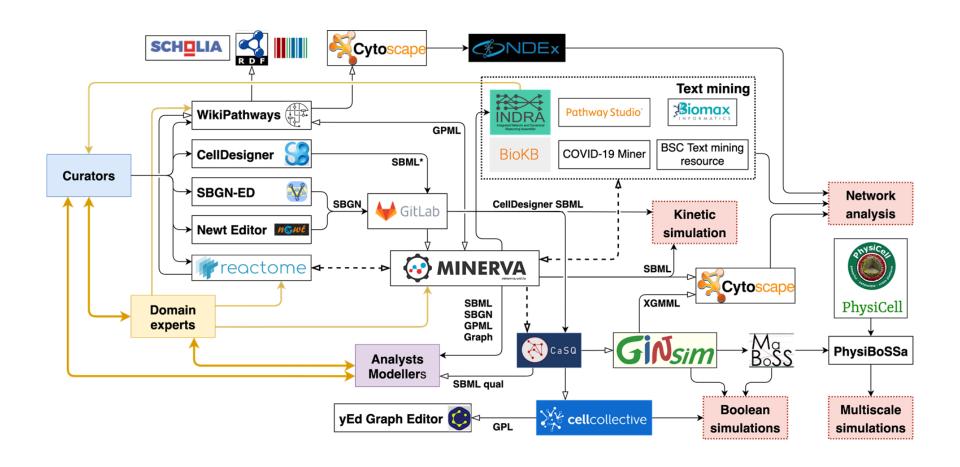
- Over 146,000 publications about COVID19 / SARS-CoV2 since 2020*
- Molecular pathophysiology is complex
 - biological pathways
 - cell types
 - organs

^{*} PubMed query "covid-19[Title/Abstract] or sars-cov-2[Title/Abstract]"

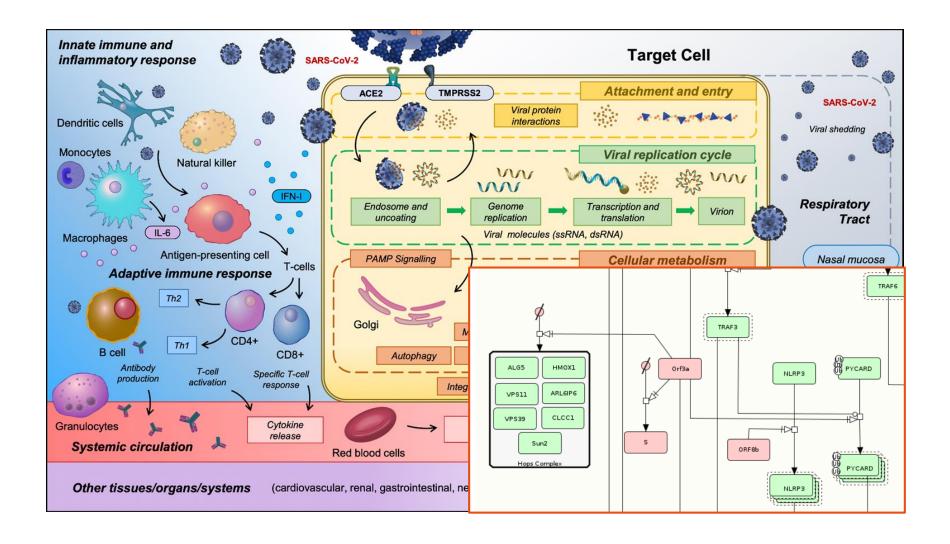
COVID-19 Disease Map

- Collaborative effort
 - 230 biocurators, domain experts, modellers and data analysts from 120 institutions in 30 countries
 - Participation of established resources and communities (Disease Maps, Reactome, WikiPathways)
- Aim: an open-access collection of curated computational diagrams and models of molecular mechanisms implicated in the disease

COVID-19 Disease Map Integration



COVID-19 Disease Map



COVID19 Disease Map

- 41 diagrams
- 1,836 interactions between 5,499 elements
- supported by 617 publications and preprints
- Models are available in SBML, SBGNML and GPML
- Conversions and integration supported by MINERVA

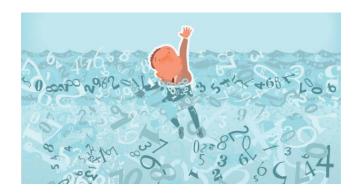
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WikiPathways

 Launched in 2008 as an experiment in communitybased curation of biological pathways



Too much data!

Difficult to keep knowledge up-to-date, accessible and integrated



Taking advantage of direct participation by a greater portion of the community (crowdsourcing)

WikiPathways



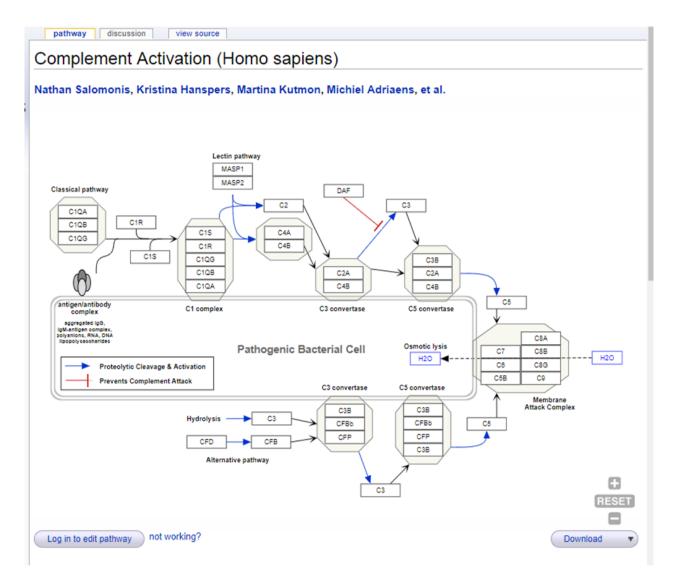
- A wikipedia for pathways
 - Build on MediaWiki (same software wiki package as used by wikipedia.org)
 - Collection and curation of knowledge
 - Community curated
 - Everybody can contribute pathways
 - Everybody can edit and curate pathways
 - Everybody can use the pathway collections

WikiPathways

Advantages

- Fast
 - New findings can be added immediately
- Collaborative
 - Researchers can exchange ideas and discuss pathways
 - Collaborations with other manually curated pathway databases (Reactome, NetPath)
- Flexible
 - Pathways under development or hypothetical pathways
 - Disease specific pathways
 - Cell-type specific pathways

Pathway pages

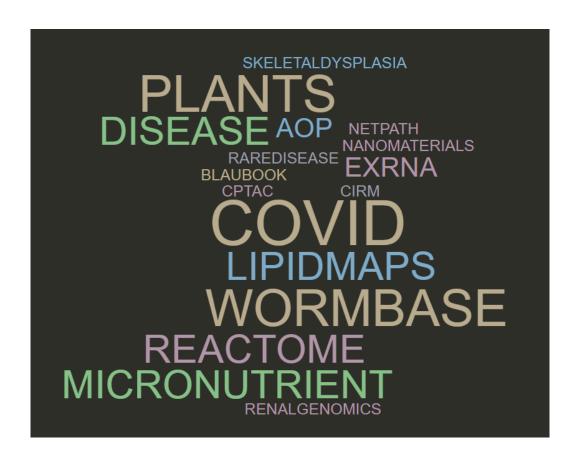


Title
Authors
Clickable diagram
Quality tags
Ontology tags
Bibliography
History
External
references

Discussion page Download

Community portals

- Special interest groups
- Portal pages to highlight communities



WikiPathways content

Statistics

- 2,995 pathways
- 777 contributors



July 2021 release

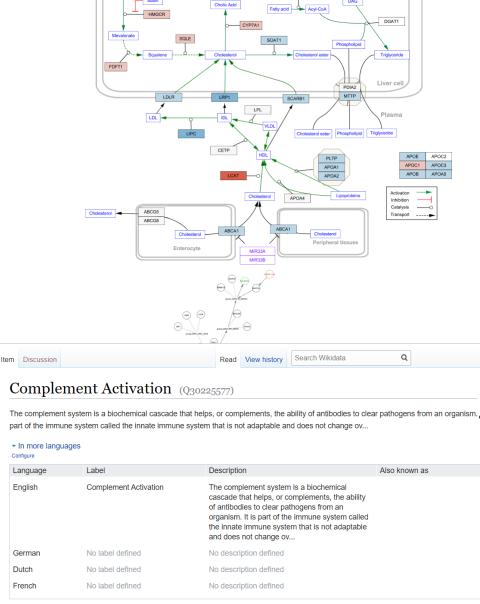
- Curated collection
- 2,078 pathways in 25 species
- Focus still mainly on human pathways
- In the last month: 368 edits from 26 contributors and 10 new pathways

Data accessibility

- Download
 - For each pathway
 - Collections in monthly releases
- Data formats
 - GPML (graphical pathway markup language)
 - PNG, SVG, PDF (images)
 - BioPAX (biological pathway exchange language)
 - Gene lists / GMT files

Data accessibility

- Programmatic access
 - REST API
 - RDF, semantic web
 - rWikiPathways
 - Cytoscape app
 - **NDEx**
 - wikidata

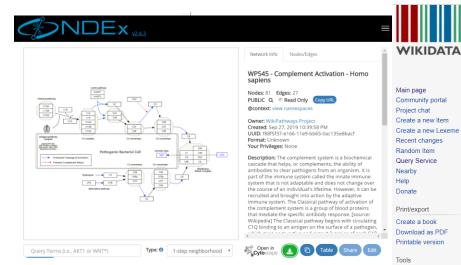


Configure

Dutch

French

Acyl-CoA synthetase



Summary

Summary

- COVID19 molecular mechanisms
- Curation efforts in COVID19 Disease Map projects
- How can you use these models when analysing your omics data?
 - Reproducible data analysis workflows
 - Integration of different resources

Questions?

Martina Summer-Kutmon, PhD

martina.kutmon@maastrichtuniversity.nl

Twitter: mkutmon











