

FAIR in times of Crisis

Virus Outbreak Data Network (VODAN)

FAIR Data Points as a service for data-driven research
(COVID-19 pressure-cooker use case)

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Barend Mons

The VODAN Implementation Network is one of the joint activities carried out by **CODATA**, **RDA**, **WDS**, and **GO FAIR** (Link to the [Data Together Statement](#)).

Read the full statement on [Data Together COVID-19 Appeal and Actions](#).

Active GO FAIR Implementation Network

The spread of the virus causing the COVID-19 outbreak is far from over. During this epidemic and in earlier occasions, we have seen severely suboptimal data management and data reuse. Moreover, access to the immensely valuable data of past and current epidemics is not always equally accessible for different affected populations and countries. For instance, the data from the past Ebola epidemics are very difficult to find, to access, and if accessible, they are not interoperable, *let alone reusable*. Under the urgent need to harness machine-learning and future AI approaches to discover meaningful patterns in epidemic outbreaks, we need to do better and ensure that data are FAIR (in this sense also meaning **F**ederated, **A**I-Ready).

Purpose of the Implementation Network



Editorial



Dear GO FAIR community,

This issue of the Newsletter will have a significantly longer editorial than what you are used to. The reason is that we are at a natural inflection point with GO FAIR, where we need to collectively reflect on our achievement and future ambitions.

GO FAIR was originally conceived as a temporary initiative, with the aim to ‘kick-start’ early developments towards the EOSC, while taking on an additional global perspective. After a little over two years on a roller coaster of amazing community building, we can conclude that GO FAIR achieved a visibility which is much higher than we expected. The main reason is that the instrument we chose, Open Implementation Networks (INs), clearly answered an unmet need.



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The VODAN IN: support of a FAIR-based infrastructure for COVID-19

Barend Mons

European Journal of Human Genetics (2020) | [Cite this article](#)

189 Accesses | 2 Altmetric | [Metrics](#)

The VODAN core consortium

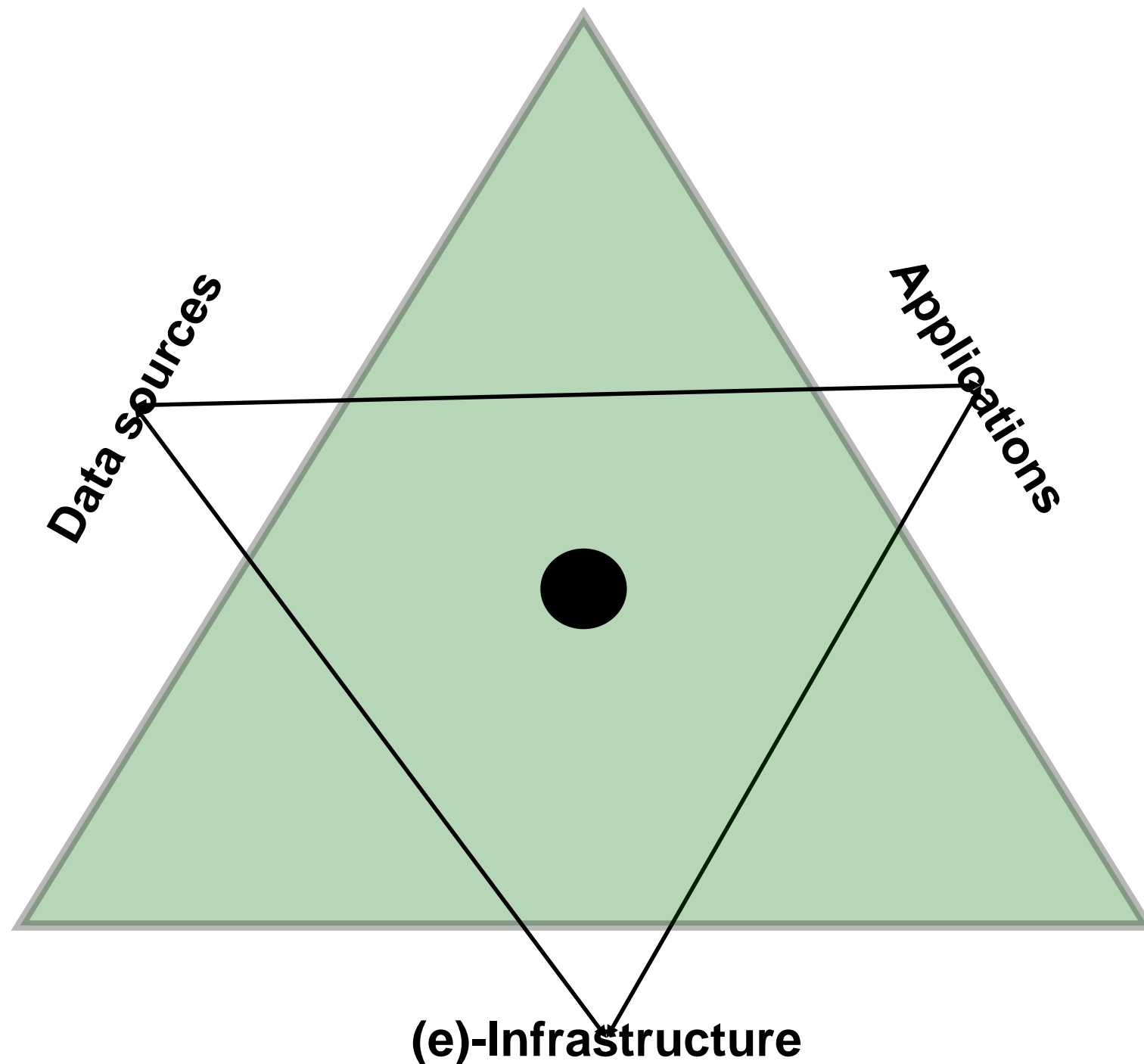
Origin and first weeks

The Virus Outbreak Data Network (VODAN) Implementation Network (IN)¹ was conceived to kick-start a 'community of communities' that could design and rapidly build a truly international and interoperable, distributed data network infrastructure that supports evidence-based responses to the viral outbreak. The IN has a longer-term goal to reuse the resulting data and service infrastructure, also for future outbreaks.

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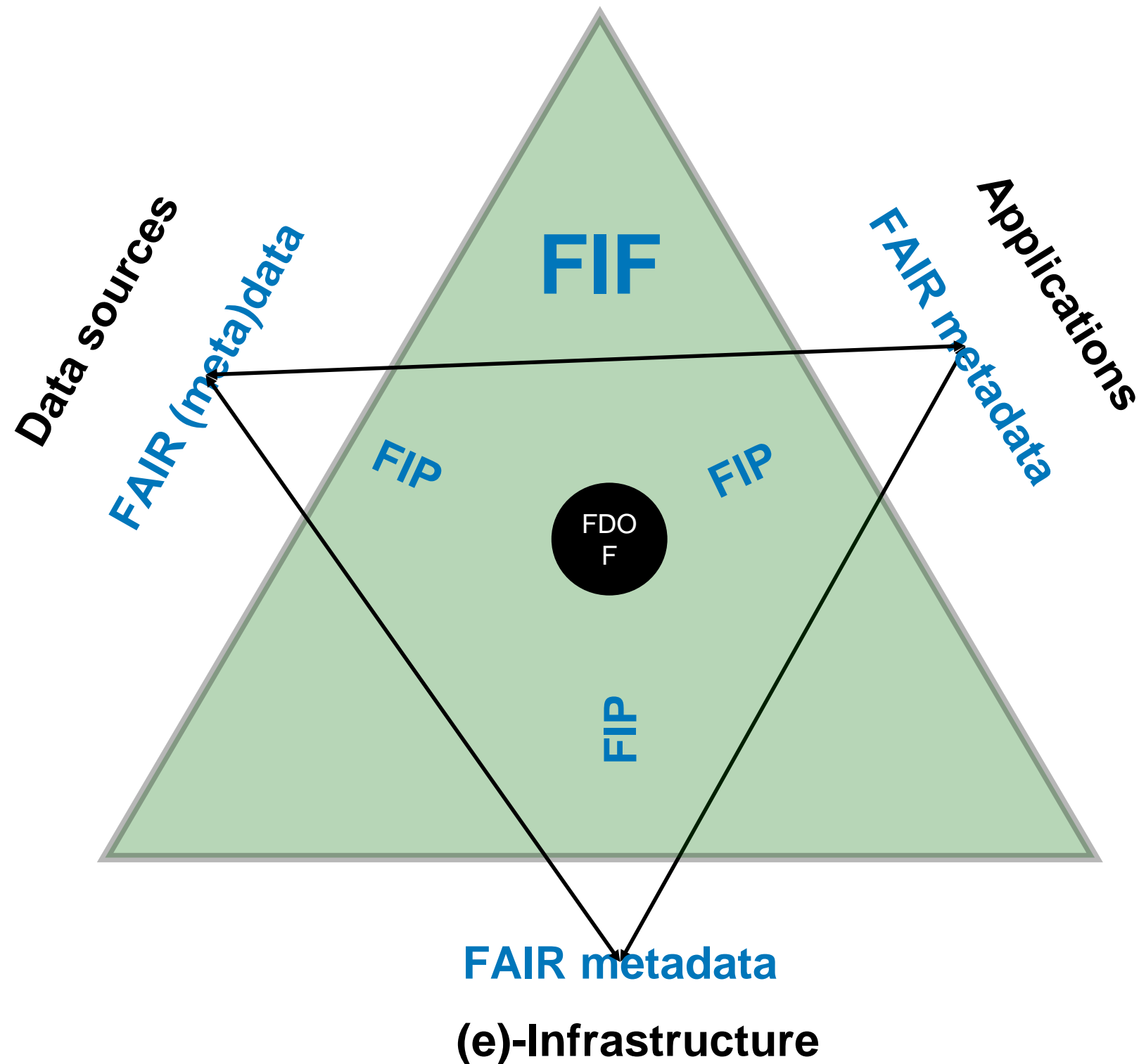
Minimal Valuable “EOSC”: 1: basic principles (generic)

- ✓ For H2M, M2H and M2M
- ✓ Based on FAIR GP
- ✓ Architecture according to FIF
- ✓ All elements machine-actionable where possible
- ✓ As open as possible, as closed as necessary
- ✓ As distributed as possible, as centralised as necessary



Minimal Valuable “EOSC”: 2: Basic Implementation Choices

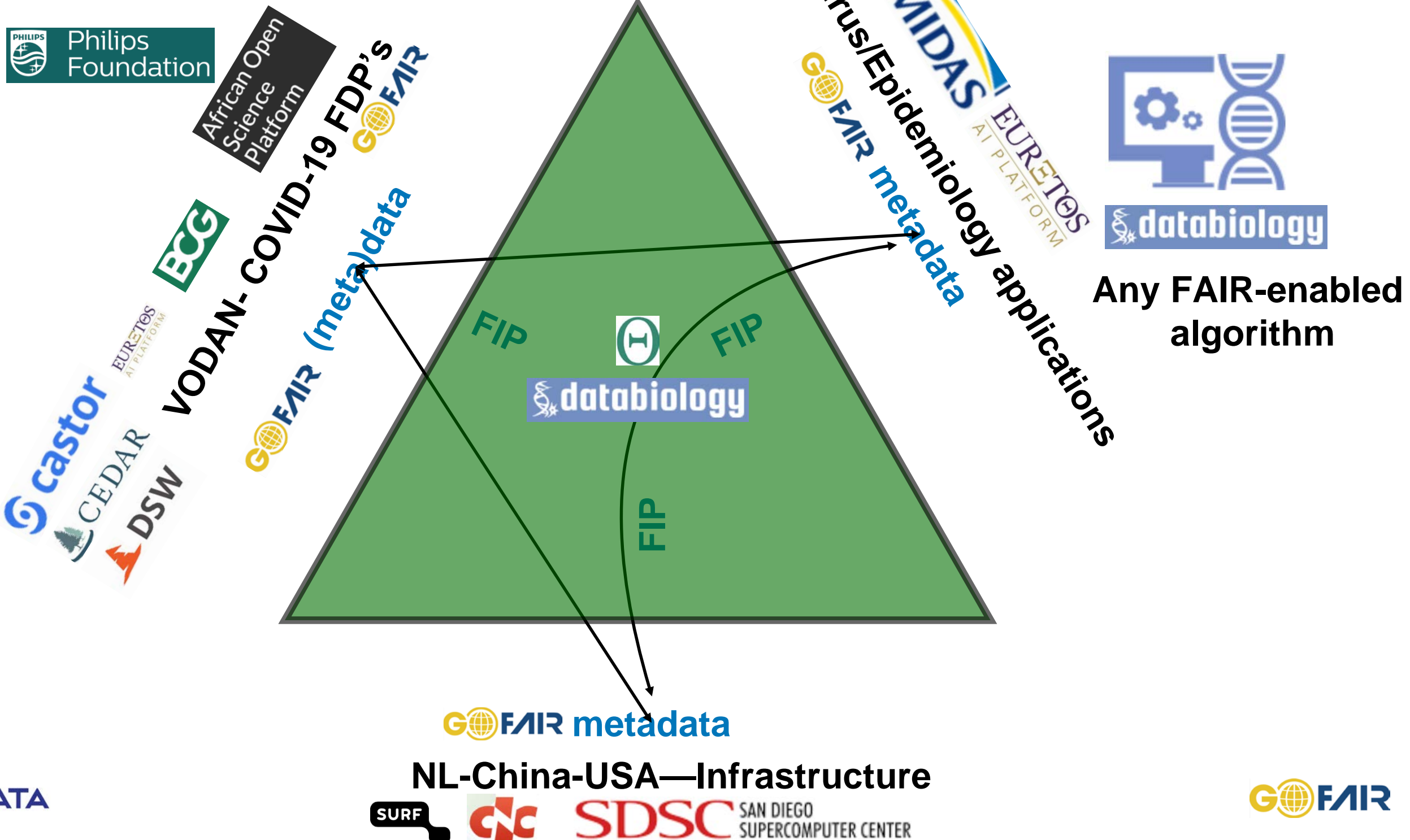
- ✓ Based on FAIR GP
- ✓ Implementation is FAIR implementation Framework (FIF)
- ✓ Architecture FIF based on FD(o)F
- ✓ All elements have FAIR metadata, some data are FAIR
- ✓ All elements become ‘inter’-actionable via FAIR implementation profiles (FIP)



Minimal Valuable “EOSC”: 3: Corona demonstration use case (0.1 alpha)

Q2-3 2020

- ✓ Driving use case: Corona > COVID-19 outbreaks
- ✓ Implementation data sources: FAIR data points with Corona relevant data (RWO and EK)
- ✓ Architecture for FD(o)F routing: Data Biology
- ✓ All elements have FAIR implementation profiles associated
- ✓ Funded, done in a small GO FAIR ad hoc Implementation network: VODAN



Genomic epidemiology of novel coronavirus (hCoV-19)

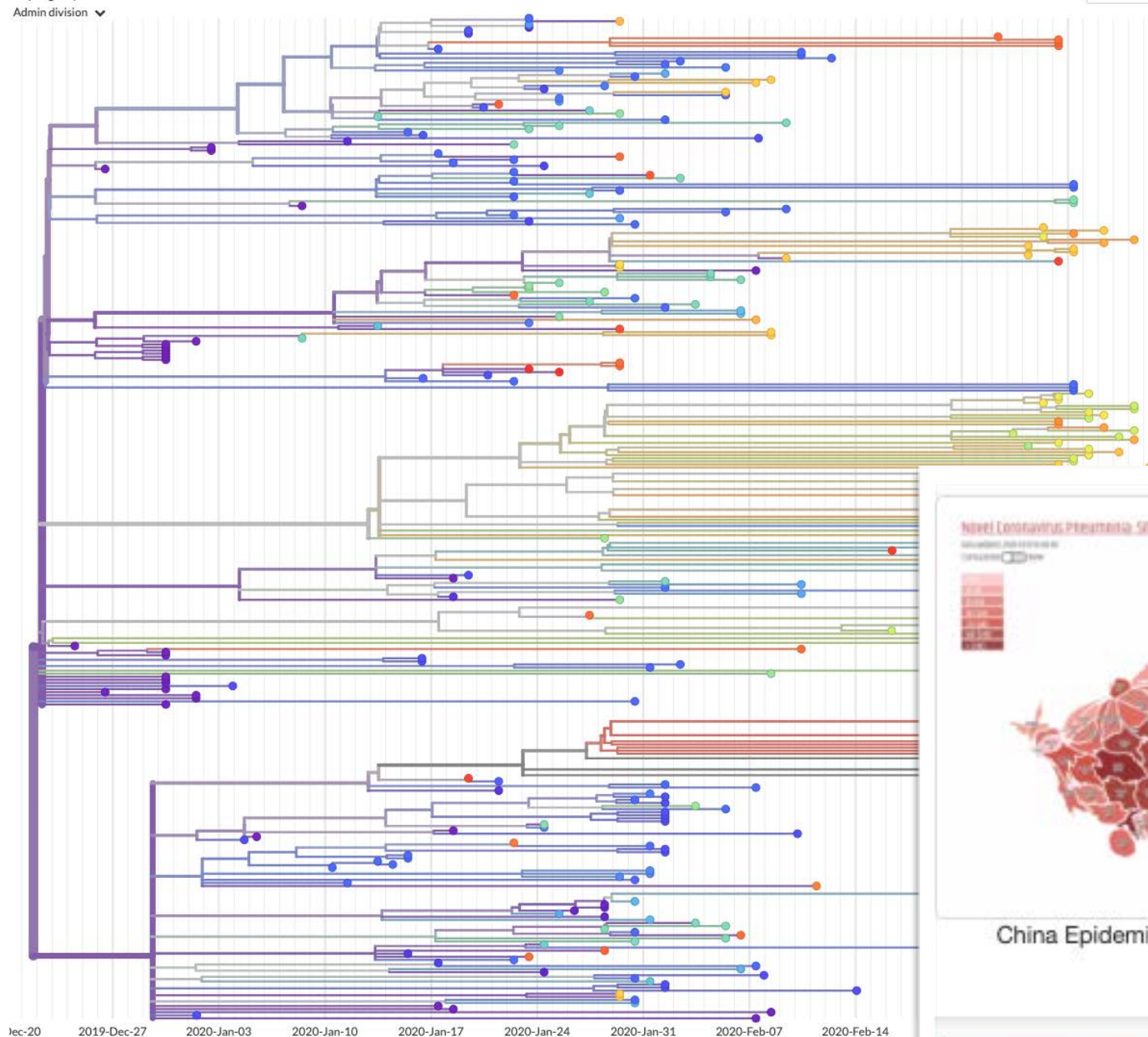
Built with github.com/nextstrain/ncov using data from [GISAIID](https://gisaid.org/).

Showing 326 of 326 genomes sampled between Dec 2019 and Mar 2020.

Phylogeny

Admin division

RESET LAYOUT



Transmissions

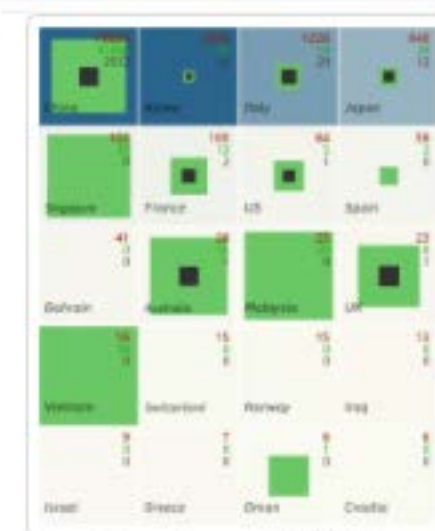
**VODAN adds
visitable FAIR RWO data
Across borders**



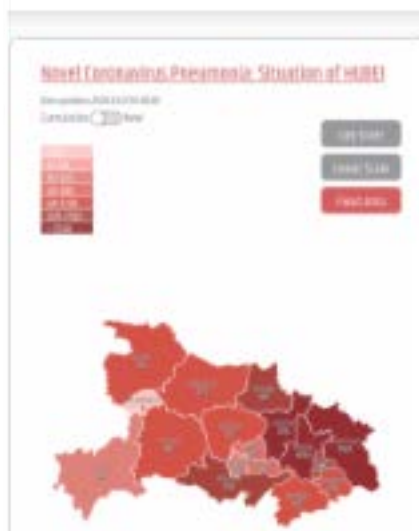
China Epidemic Map



Cure Square (China)



Cure Square (Global)



Hubei Epidemic Map

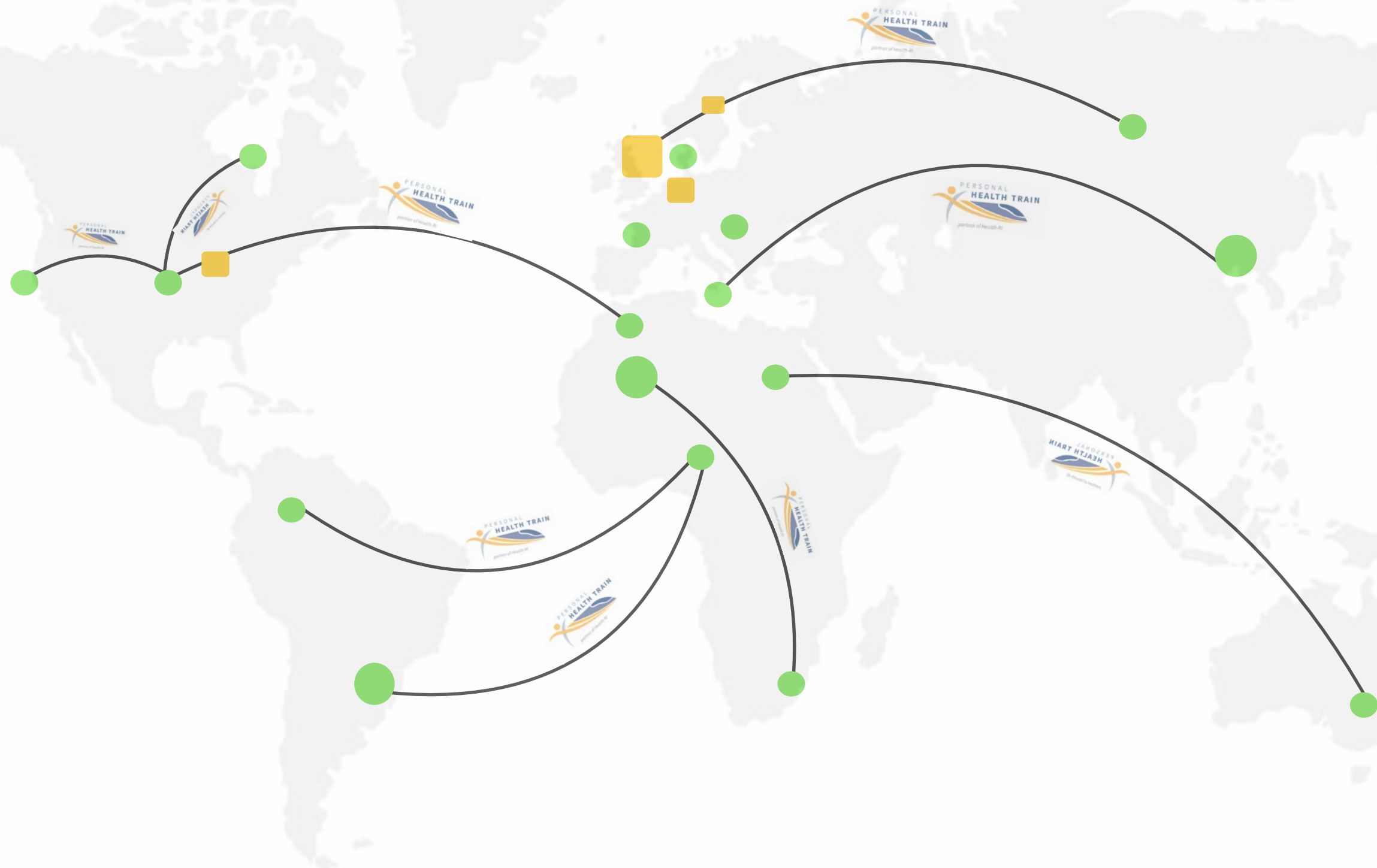


World Epidemic Map



Border Control

The VODAN-IN approach: distributed analytics over FAIR data



 FAIR reference (EK) data stations

 FAIR RWO data stations

 Trains - FAIR algorithms

→ **COVID-19 FAIR data model (extensible)**

→ **FDP-in-a-box**

→ **PHT-infrastructure**



The machine knows what we mean....

The end of data travel.....

Federated AI Ready.....

**‘Why did we not already
have this’ ?**

Is this a dream

(as some advocate, also in COVID-19 crisis)?

Disease Modelling Workflow (COVID-19)

New Publications
Real World Observations
Clinical and Self reporting

AI-ready Established
Knowledge
Plus selected connectors
Subhypotheses

A1

FAIR abstract
Paper1

FAIR abstract
Paper 2

FAIR abstract
Paper 3

A2

Case Report
Forms/ EPD

Clinical
measurements

Self Reporting
(apps)

EURETOS (Other tools if available)
AI PLATFORM

C
Greatest Common
Denominator (GDC)
'Connectome'

Multiple Algorithms

D

Interactive disease Model(s)

B

SARS-Cov-2/human proteome

ACE2/ACE

Cytokine Storm (CRS)

Renin-angiotensin system

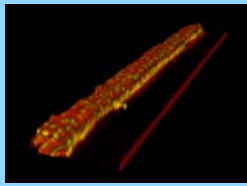
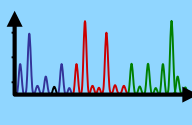
Further sub-hypotheses

E

Expert introduced concept

Drug, mechanism, cell type etc.

F

G

Expert
Curation, annotation and
Hypothesis discussion
Disease phase alignment

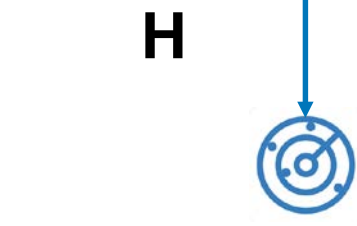
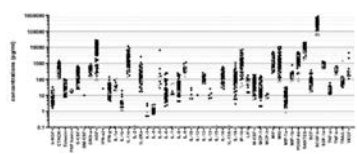
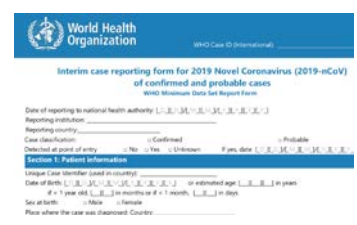
1

2

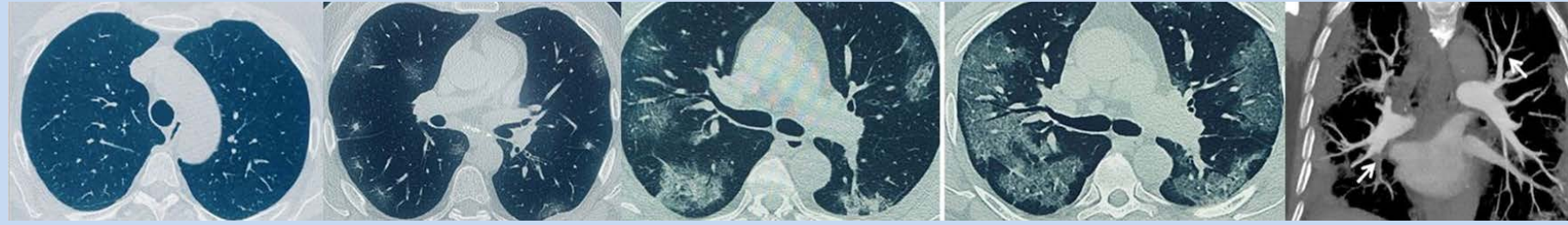
3

...

Systematic *in silico*
Rationalisation



Community annotation options



I

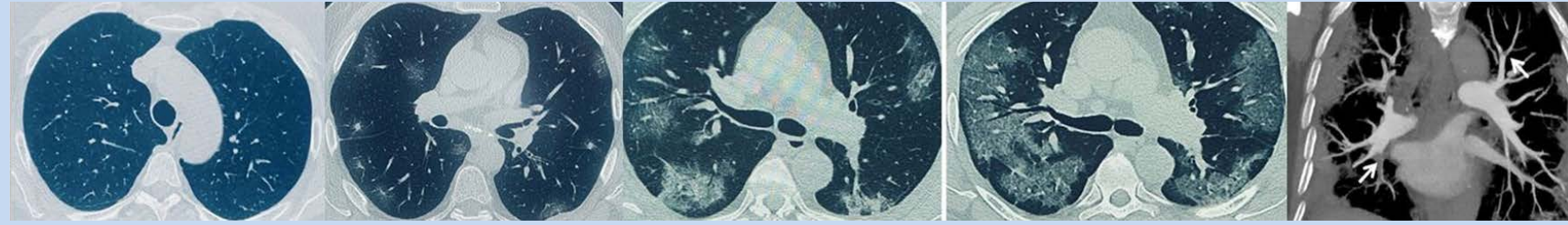
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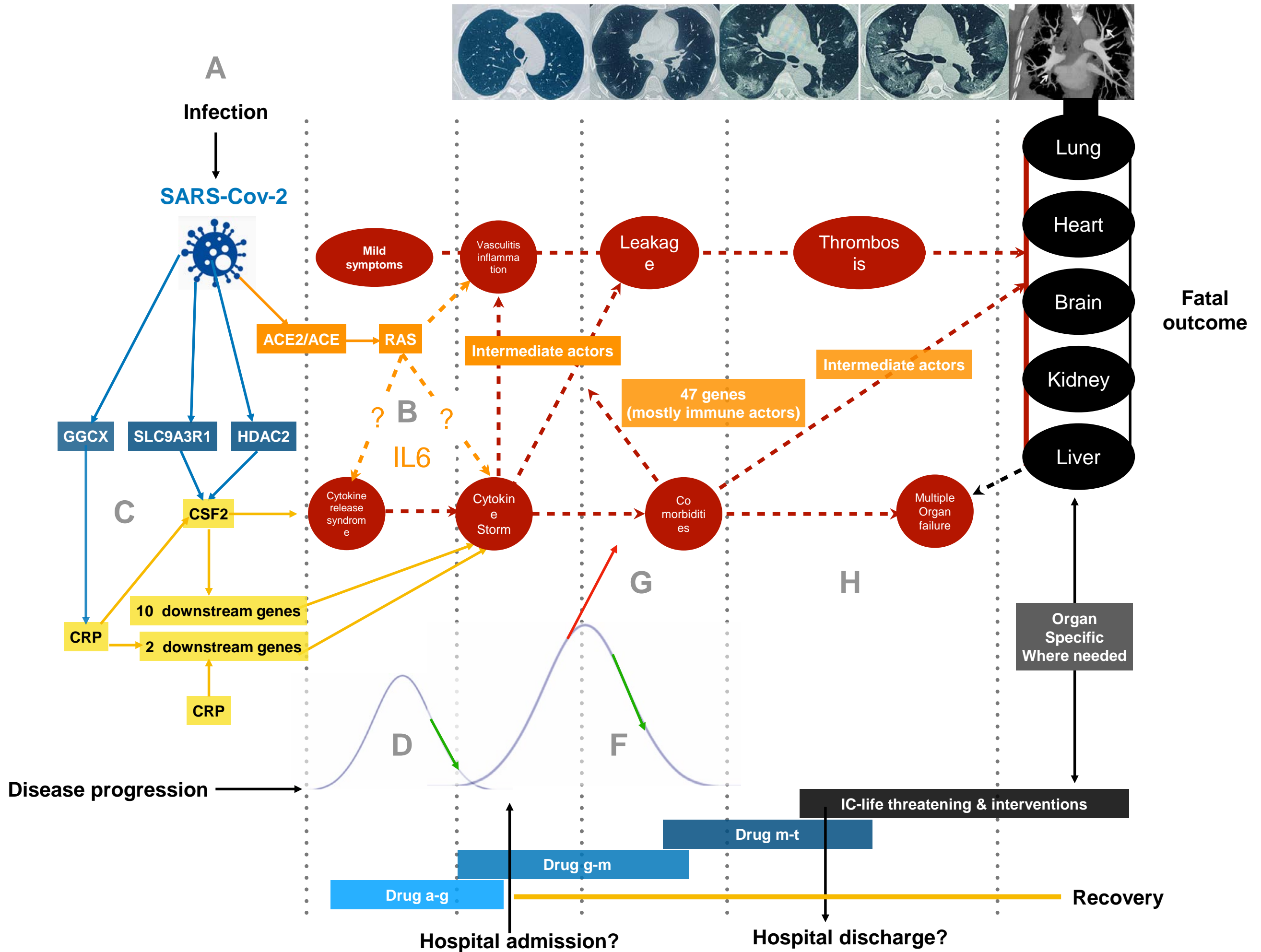
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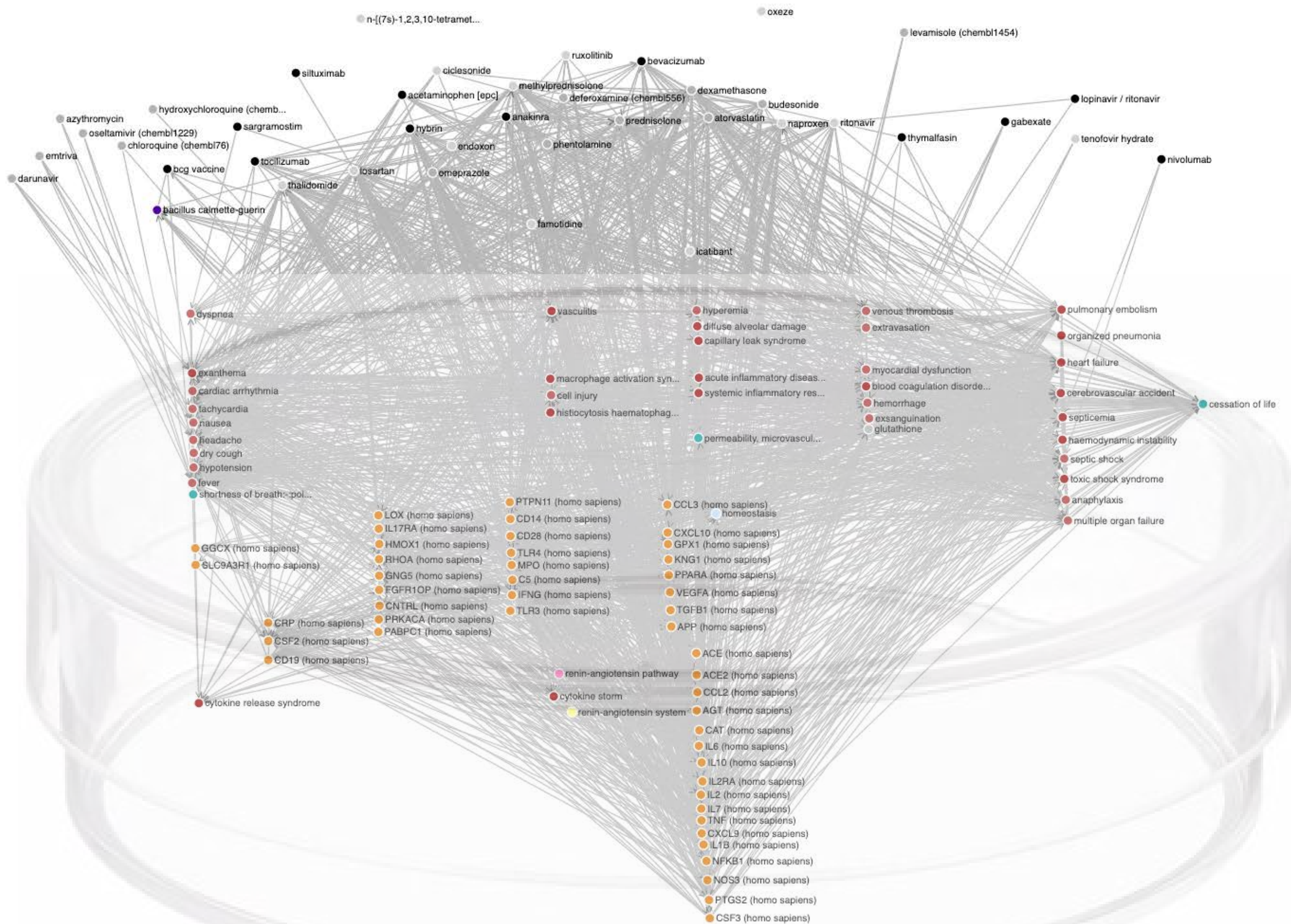
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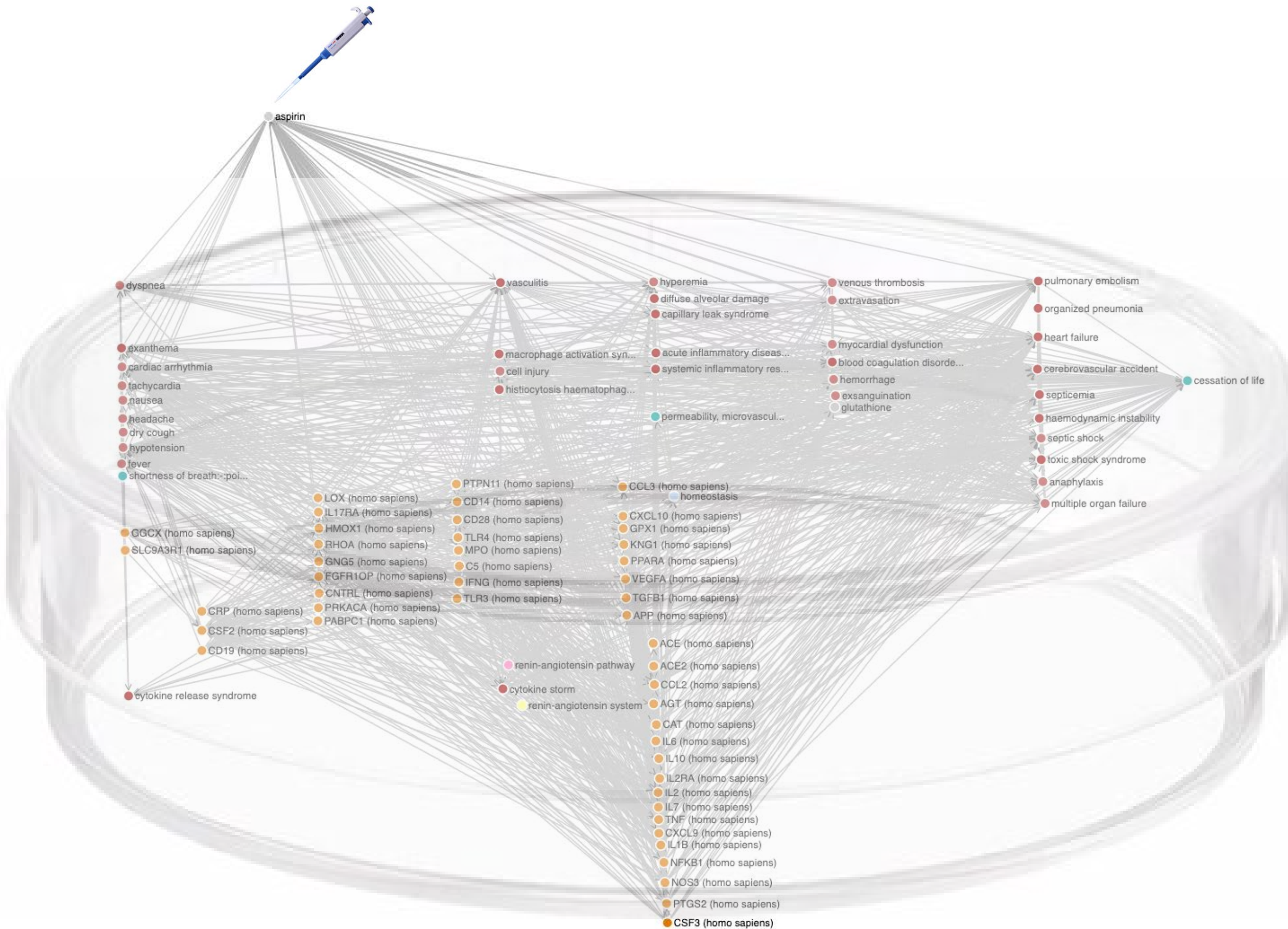
V

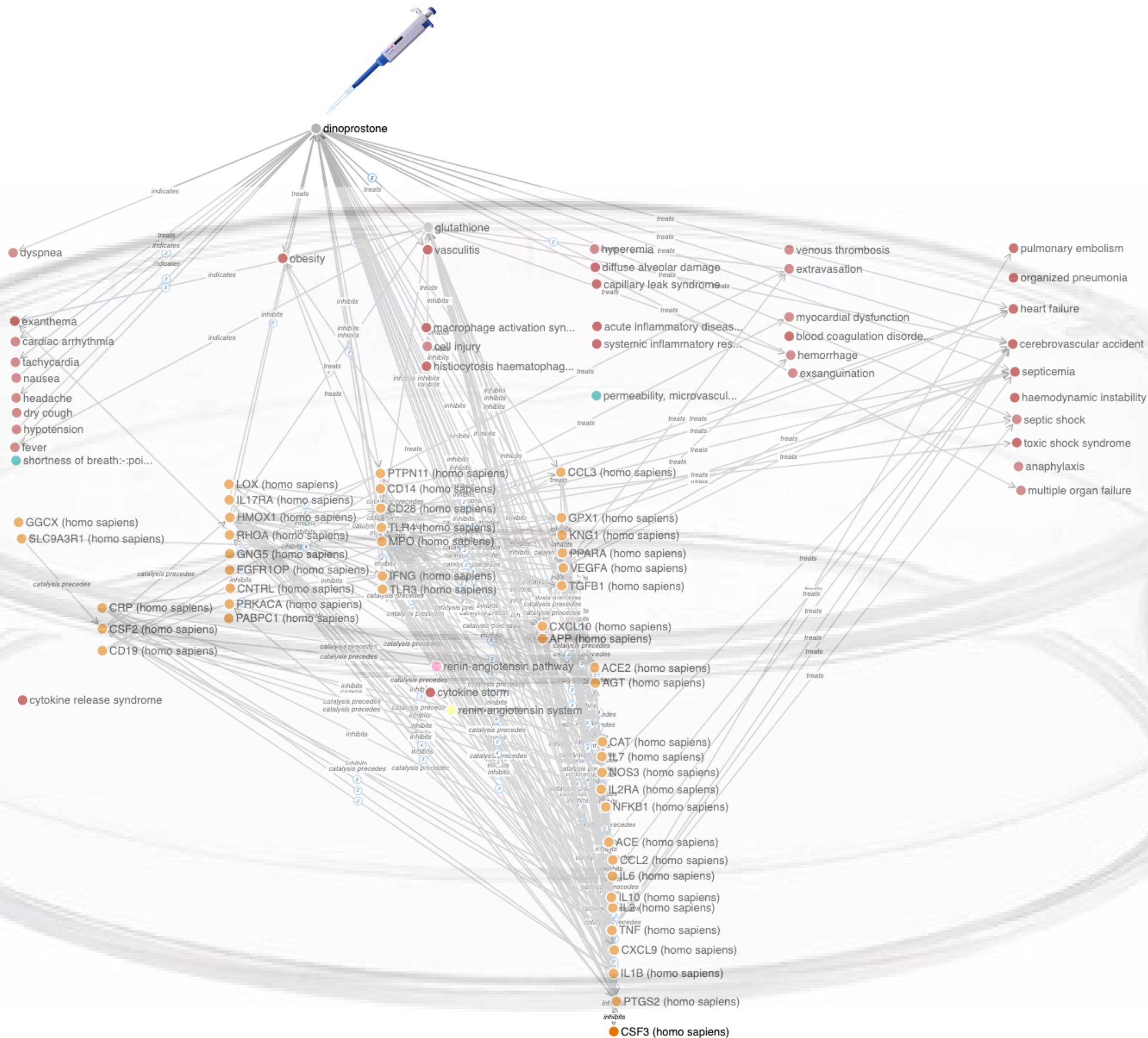
CT characteristics	Normal			Normal	Perfusion defects/GGO/hyperemia	Infarction/GGO (increase)	Interlobular septa, Pulmonary embolism
Phase	Phase 1 (mild symptoms)			Phase II (onset Cytokine storm)	Phase III Early endothelial/vascular disorders	Phase IV Vascular and thrombotic disorders (severe)	Phase V Severe, life threatening manifestations
Lung	Cytokine release syndrome, shortness of breath			endotheliitis/Vasculitis,	Diffuse alveolar damage, microvascular obstruction, Hyperemia, obstruction, Capillary leak syndrome.	Venous thrombosis/permeability disorders, extravasation	Organised pneumonia, pulmonary embolism.
Heart	arrhythmia, tachycardia					Myocardial dysfunction	Heart failure
Brain							Stroke
Kidney							Acute renal failure
General symptoms/manifestations	Nausea, shortness of breath, dyspnea, headache,, tachycardia, exanthema, coughing, fever, hypotension			Macrophage activation syndrome, cell injury, Histiocytosis Hematophagocytic, reactive hemaphagocytic syndrome, Lymphohistiocytosis, hemo...	Acute inflammatory disease, systemic inflammatory response	Thrombus, blood coagulation disorders, hemorrhages	Septicemia, hemodynamic instability, DIC, diffuse hemorrhages, septic shock, toxic shock syndrome, anaphylaxis, multiple organ failure
Direct interaction SARS-COV-2 proteome-human proteome	GGCX, SLC9A3R1, HDCA2			GNG5, RHOA, FGFR1OP, CNTRL, PRKACA, TTGB1, HMOX1, IL17RA, PABPC1, LOX	PTPN11, CD14, CD28, TLR4, MPO, C5, IFNG, TLR3	CCL3, CSF3, CXCL10, GPX1, KNG1, IKL6R, HMOX1, PPARA, VEGFA, TGFB1, APP	
Genes affected in human proteome		CRP, CSF2, CD19			ACE, ACE2, AGT, CAT, IL6, CCL2, IL10, IL2RA, IL2, IL17A, IL7, INFG, TNF, CXCL9, IL1B, CSF2, CFS3, NFKB1 NOS3 PTGS2		
Processes	Viral induction?	Cytokine release syndrome	Transition	Onset cytokine storm	cytokine storm, renin-angiotensin system, angiotensin pathway	Downstream effects renin-angiotensin disturbance	fatal outcome
Small molecules					Glutathione		
					Myeloperoxidase		



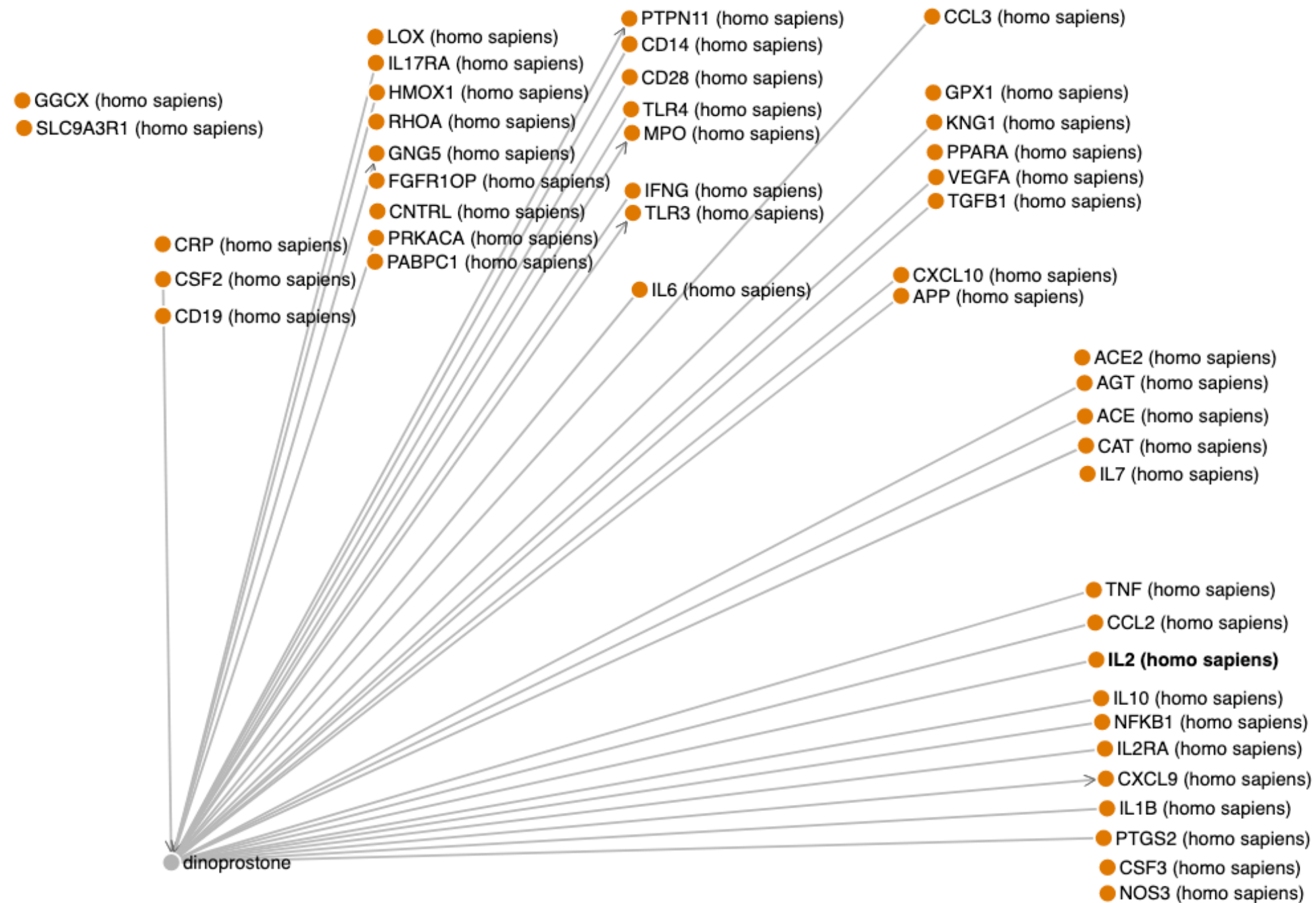




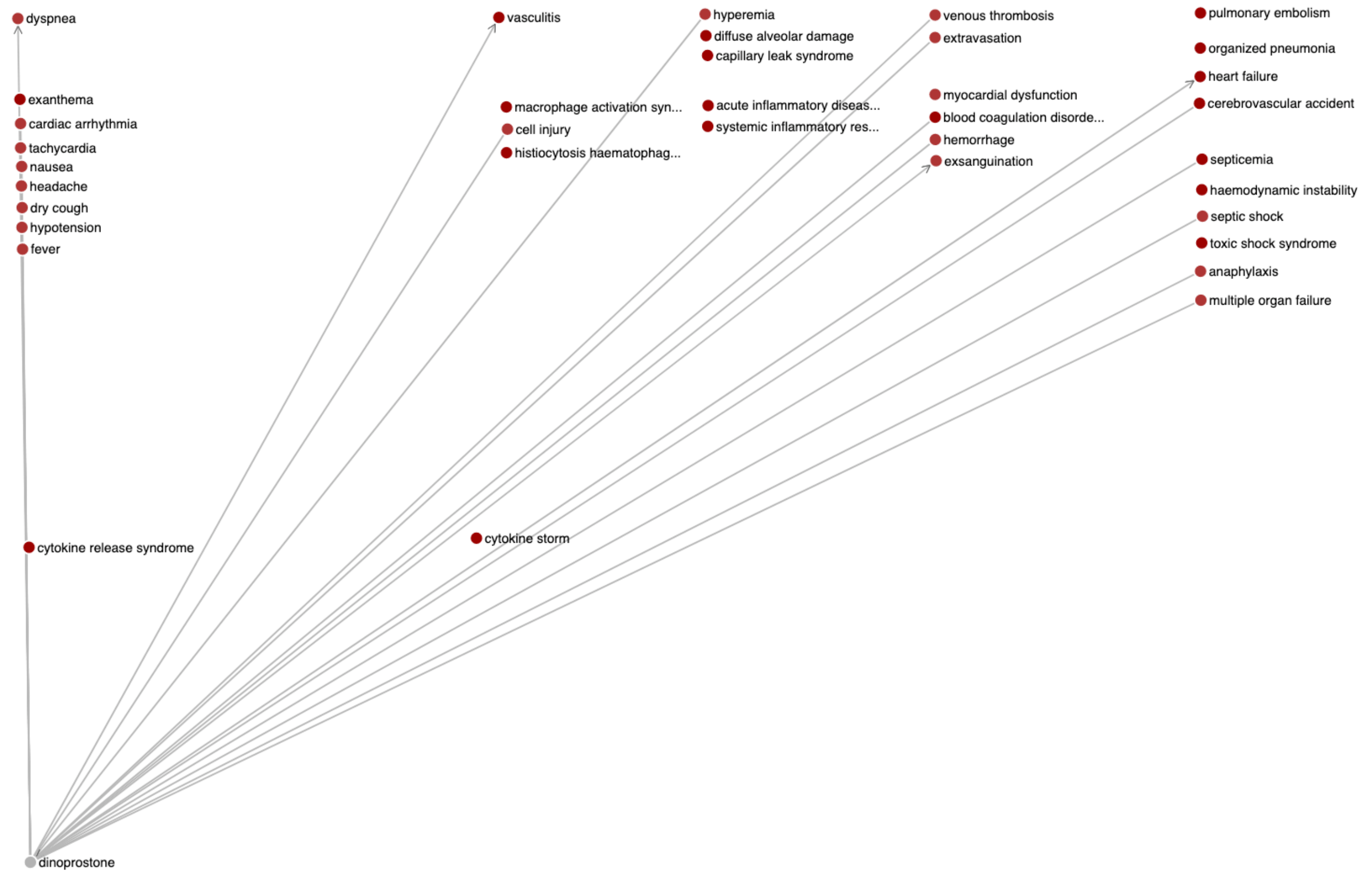


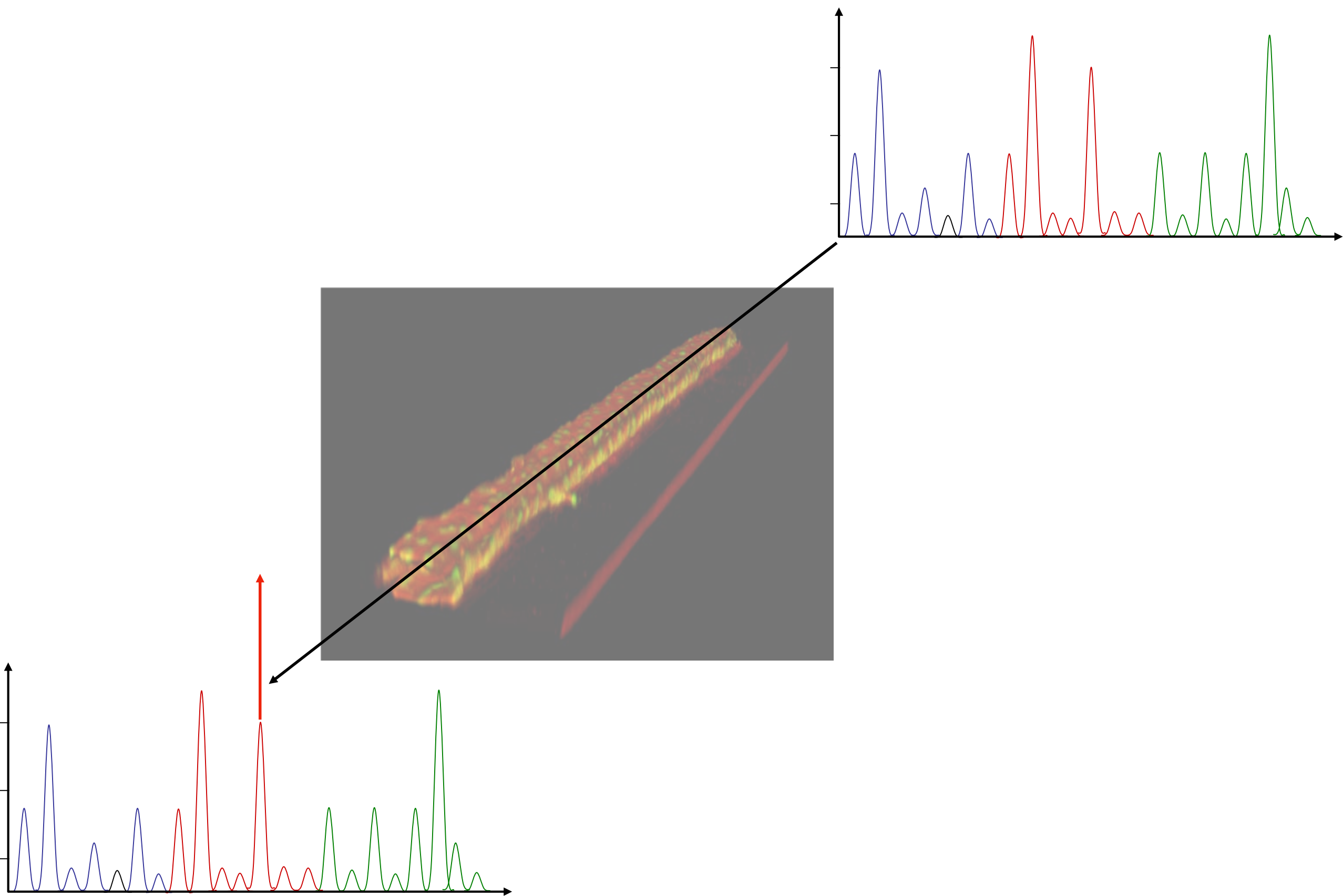


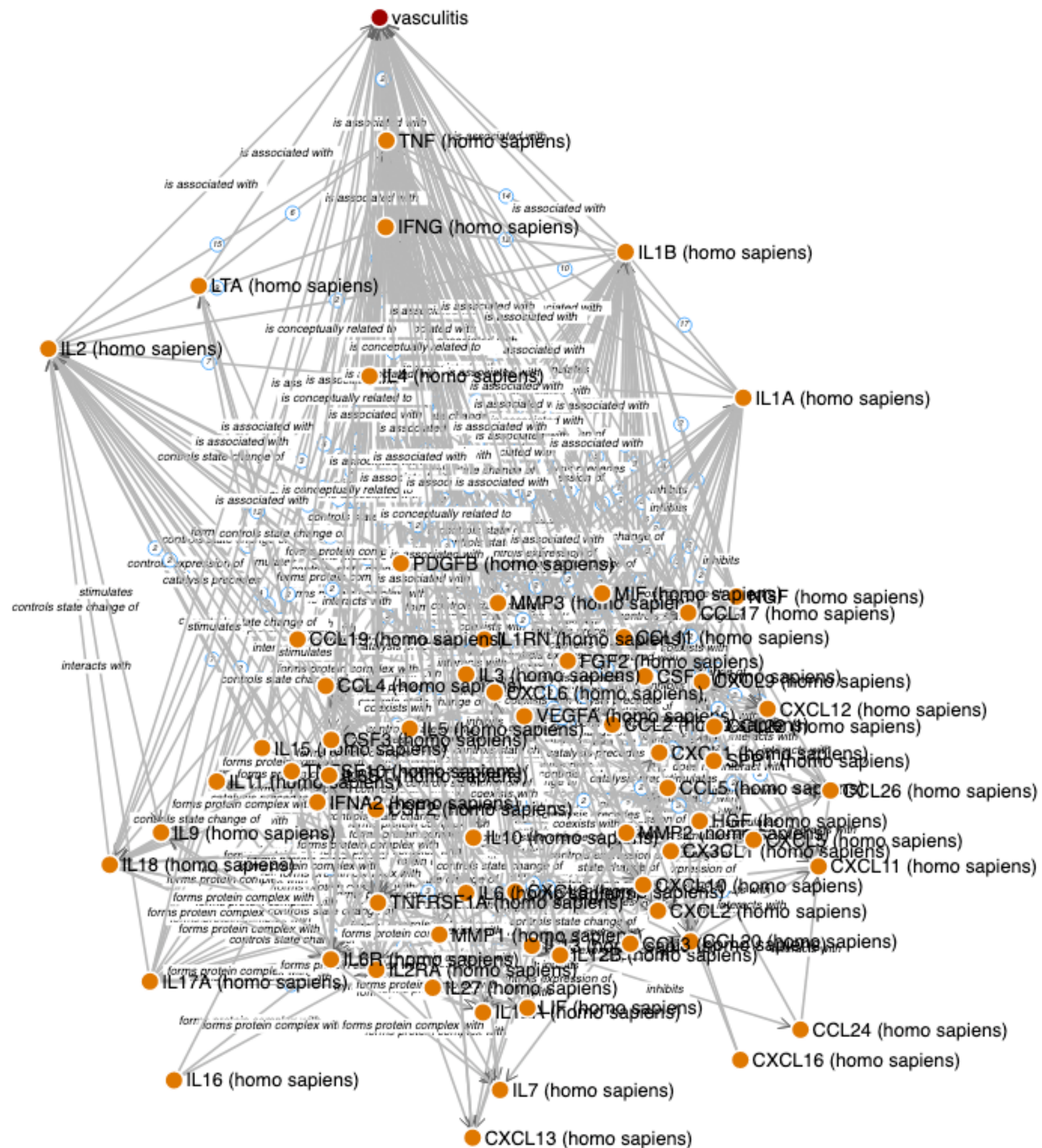
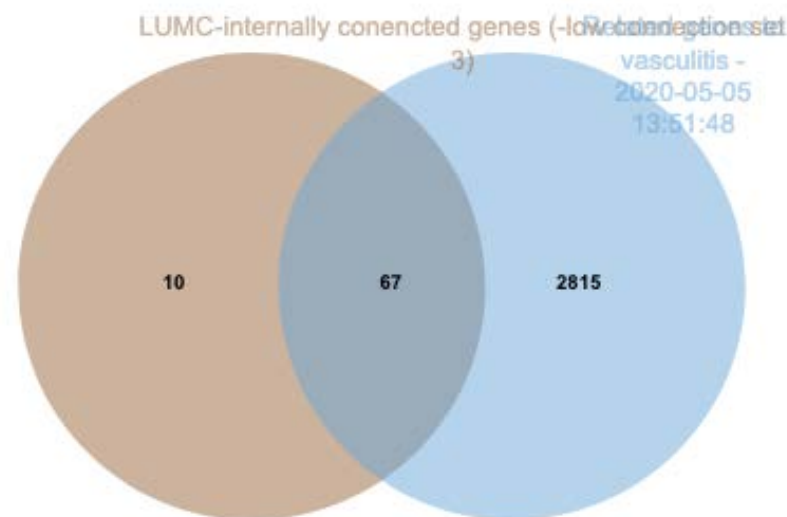
Dinoprostone connectome with disease model: filter: genes only

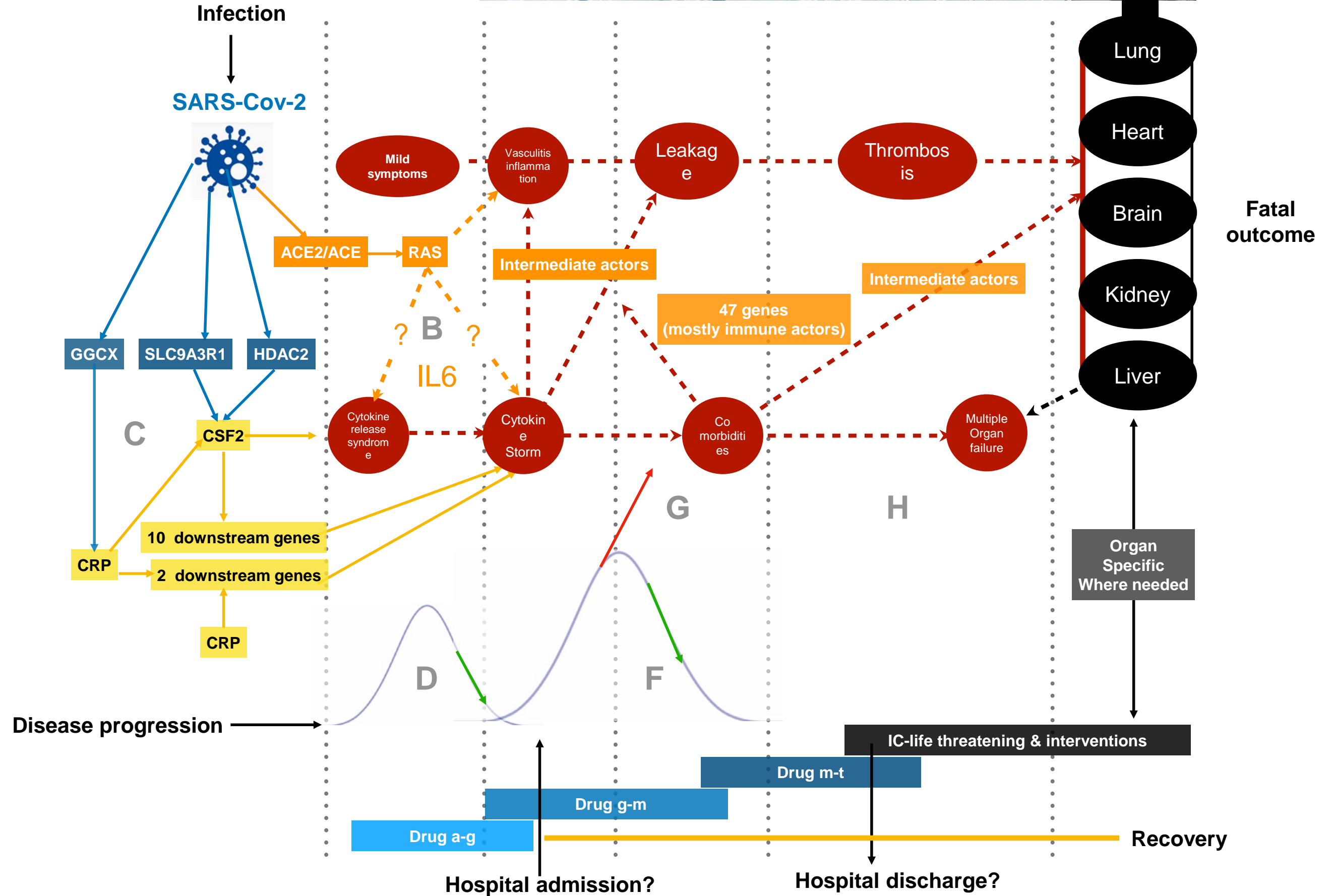
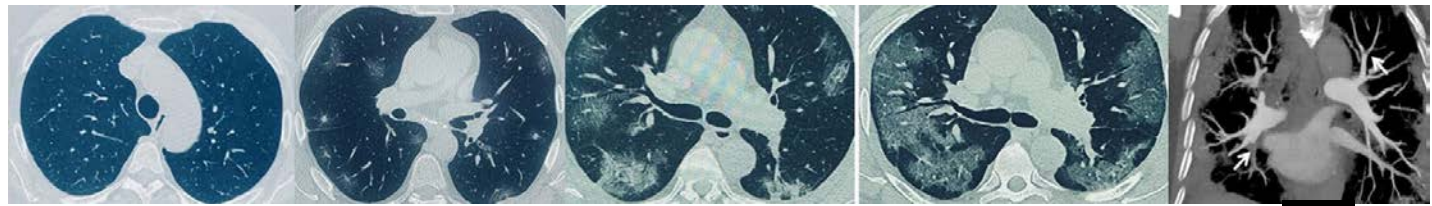


Dinoprostone connectome with disease model: filter: diseases only

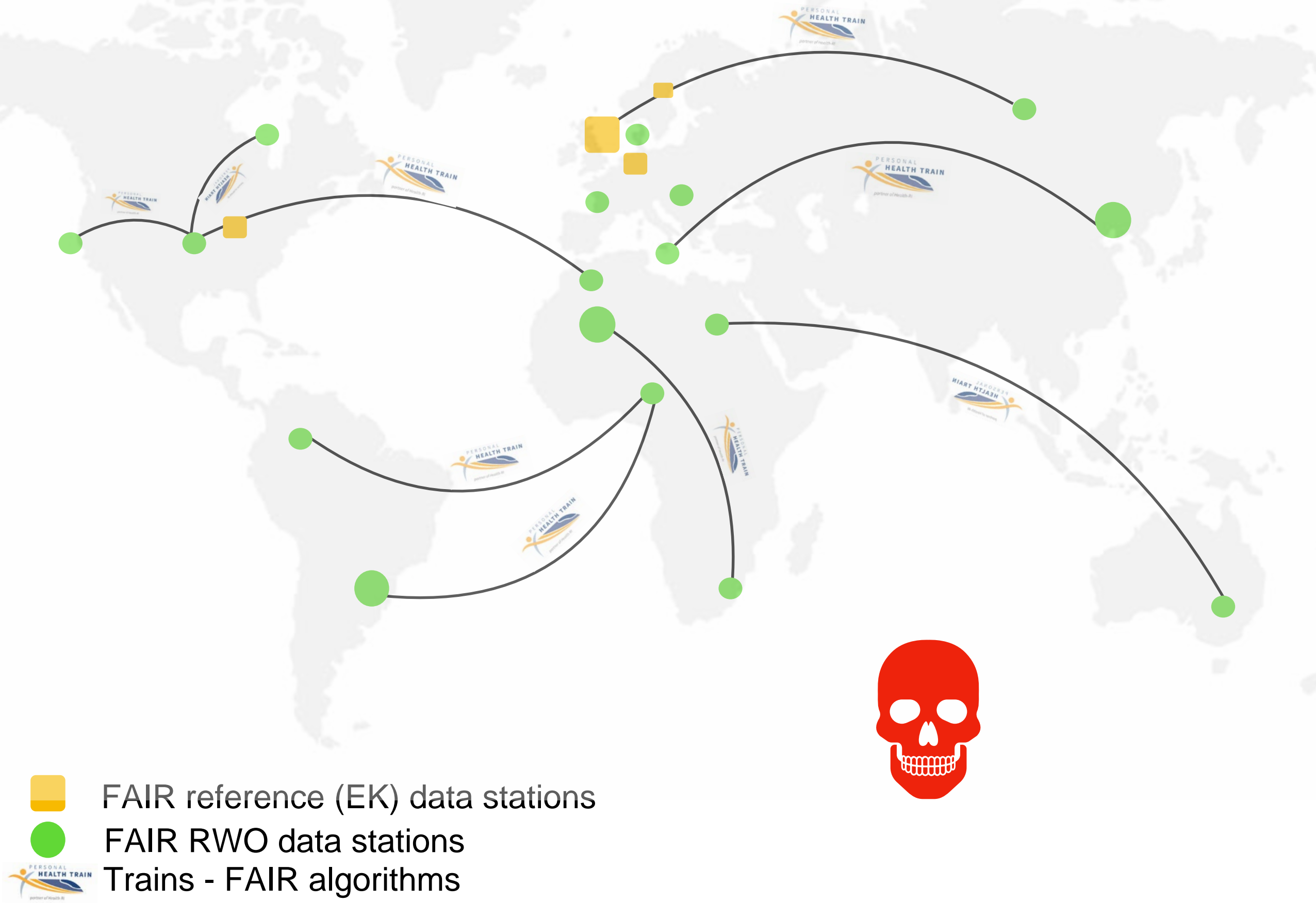








The VODAN-IN approach: distributed analytics over FAIR data



Please.....

