



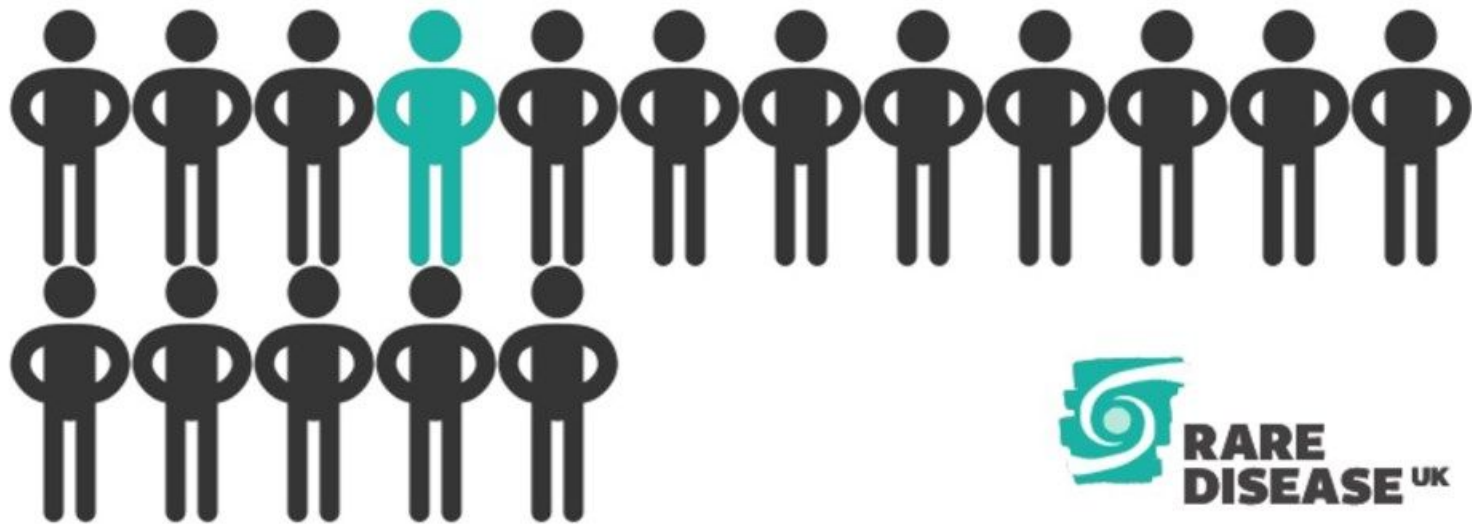
Chris Evelo, Friederike Ehrhart
Science café 28.02.2019

RARE
DISEASE
Day®



Maastricht University

1 in 17 people will be affected by a rare disease at some point in their life.



Objectives (our summary ;-)

- Better diagnosis and better treatments through better research

IRDiRC goals 2017 – 2027

- Patients are **diagnosed within one year** if their disorder is known in the medical literature;
- Undiagnosable individuals will enter a globally coordinated **diagnostic and research pipeline**;
- **1000 new therapies** for rare diseases will be approved, the majority of which will focus on diseases without approved options;
- **Methodologies will be developed to assess** the impact of diagnoses and therapies on rare disease patients.





EUROPEAN JOINT PROGRAMME ON RARE DISEASES

COORDINATION & TRANSVERSAL ACTIVITIES

INTEGRATIVE RESEARCH STRATEGY

SUSTAINABILITY

ETHICAL, LEGAL, REGULATORY & IPR ISSUES

COMMUNICATION & DISSEMINATION

1

**RESEARCH
FUNDING**

2

**COORDINATED
ACCESS TO
DATA &
SERVICES**

3

**CAPACITY
BUILDING &
EMPOWERMENT**

4

**ACCELERATING
TRANSLATION**

Some numbers:

85 partners

33 participating countries

about 100 Mio budget

Started January 2019

Duration 5 years



WP1 COORDINATION & MANAGEMENT

WP2
STRATEGY

WP3
SUSTAINABILITY

WP4
ETHICS, LEGAL, REGULATORY & IPR

WP5
COMMUNICATION & DISSEMINATION



WP6
Joint Transnational Calls

WP7
Networking scheme

WP8
RDR Challenges

WP9
Monitoring of funded projects

WP 10
User-driven strategic planning for P2

WP 11
Virtual Platform for data & resources

WP 12
Enabling sustainable FAIRness

WP 13
Holistic approaches for rare disease diagnostics and therapeutics

WP 14
Training on data management & quality

WP 15
Capacity building and training of patients and researchers

WP 16
Online Academic education course

WP 17
ERN RD training and support programme

WP 18
Development and adaptation of training activities

WP 19
Facilitating partnerships and accelerating translation

WP 20
Validation, use and development of innovative methodologies for clinical studies

Maastricht University
Bioinformatics

Coordinated by

Infrastructural work around the analysis of -omics data

- Pillar 2

WP10: User-driven strategic planning and transversal activities for Pillar 2 data ecosystem

Annual strategic meetings with users (ERNs) & developers to define the priorities – coordination of outputs & needs – technical GDPR implementation – quality, sustainability and scaling up

WP11: Common virtual platform for discoverable data and resources for RD research

Metadata & ontological models – FAIR compliance – data deposition & access to data infrastructure – online tools

WP12: Enabling sustainable FAIRness and Federation at the record for RD data, patients and samples

Alignment of core interoperability standards – software for FAIR ecosystem – FAIRification support

WP13: Enabling multidisciplinary, holistic approaches for rare diseases diagnostics and therapeutics

System biology approaches for RD – biological pathways – variants to function – environmental toxicology – treatment drugs - proof of principle studies

Sub task leaders



Peter-Bram 't Hoen
(Radboud
University Medical
Centre, Nijmegen)

member

ELIXIR and EMBL-EBI

UNIVERSITÄT
TÜBINGEN

UNIVERSITAETS
-KLINIKUM
FREIBURG

Instituto de
Salud Carlos III



Anaïs Baudot
(INSERM-AMU)

That's WP13

WP13 lead



Chris Evelo (Maastricht
University) and **Franz Schäfer**
(University Hospital
Heidelberg)

Acibadem University

University
hospital

Groningen
Ludwig Boltzmann Gesellschaft
GmbH

FUNDACIO CENTRE
DE REGULACIO
GENOMICA



Marco Roos (Leiden
University Medical
Centre)



**Domenica Taruscio, Claudio Carta and
Alberto Mantovani** (Istituto Superiore di
Sanita, Rome)



WP13 - objectives

- WikiPathways rare disease portal (see <http://raredisease.wikipathways.org>)
- **Evaluate omics and other relevant data-availability** e.g. from ERN partners
- **Combine affected pathways into data and knowledge supported rare disease networks**, evaluate these for things like active nodes and make them available on NDEX.
- Allow **extension of these networks with relevant regulatory information** (e.g. transcription factors and miRNAs) and where available evaluate data on such regulatory factors.
- Use the networks to **evaluate drug targets** and thus come up with ideas for drug repurposing with some special interest in orphan drugs (building on our IMI collaborations).
- Evaluate the network for **intrinsic lifestyle factors** (e.g. micronutrients present in or known to affect the networks) or processes known to be affected by exercise (building on our NuGO and other nutrition-related collaborations).
- Allow extension with **external environmental factors** like chemical exposure (toxicology) and evaluate overlap with so-called adverse outcome pathways (building on toxicology collaborations).
- **Create complete workflows and make these available**, including component containers and specific networks resulting from the analysis.

WP13 Holistic approaches

Task 13.1: Gap filling

13.1.1: Pathways created and expert curated.

13.1.2: Mapping to genes.

13.1.3: Mapping genes to function.

13.1.4: Link to external FAIR data.

13.1.5: Network repository.

13.1.6: Environmental lifestyle

13.1.7: Treatment drugs

13.1.8: Environmental toxicology

13.1.9: Workflow leading to understanding of disease mechanisms and diagnosis

13.1.10: Link to Adverse Outcome Pathway approach

13.2 Organise proof of principle studies

[←](#) [→](#) [🔍](#) [📄](#) [⋮](#) [🔖](#) [🌐](#) [🔄](#) [🏠](#)

[https://www.wikipathways.org/index.php/Portal:RareDisease](#)

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Portal:RareDisease

Rare Disease pathways at WikiPathways

This portal highlights WikiPathways content related to rare genetic human diseases, and is designed as a central organizing point for exploring, curating and expanding the collection of rare disease pathways.

A rare or orphan disease is a disease which affects relatively few people. The exact definition varies between 1:1000 and 1:200.000. E.g. it can be 1:1500 (USA) , 1:2000 (EU) or 1:2500 (Japan). Rare diseases are mostly caused by genetic variation making them chronic and hard to cure. The severity depends on the affected gene and its physiological implications.

This portal is funded by:

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activity

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- Statistics

tools

- PathwayWidget
- Tissue expression
- Pathway Finder
- Software tools

community

- Quality control
- Development
- WikiPathways Blog
- AOP portal
- CIRM portal
- CPTAC portal
- Renal Genomics portal
- Disease portal
- ExRNA portal
- Lipids portal
- Micronutrient portal
- Nanomaterials portal
- NetPath portal

Get information

Explore rare disease pathways on WikiPathways:

- MECP2 and Associated Rett Syndrome
- Amyotrophic lateral sclerosis (ALS) SOD1 - CHMP2B MODEL
- Fanconi Anemia Pathway
- The effect of progerin on the involved genes in Hutchinson-Gilford Progeria Syndrome
- Lamin A-processing pathway
- Viral Acute Myocarditis
- Disorders of Phenylalanine and Tetrahydrobiopterin (BH4) Metabolism
- Tyrosine Metabolism
- Sulphur Amino Acids
- Disorders of Folate Metabolism and Transport
- MTHFR deficiency (additional pathway)
- Vitamine B6-Dependent and Responsive Disorders
- Molybdenum (Moco) cofactor biosynthesis
- Cysteine and Methionine catabolism
- Vitamin B12 Disorders
- Thiamine Disorders

Featured Pathway

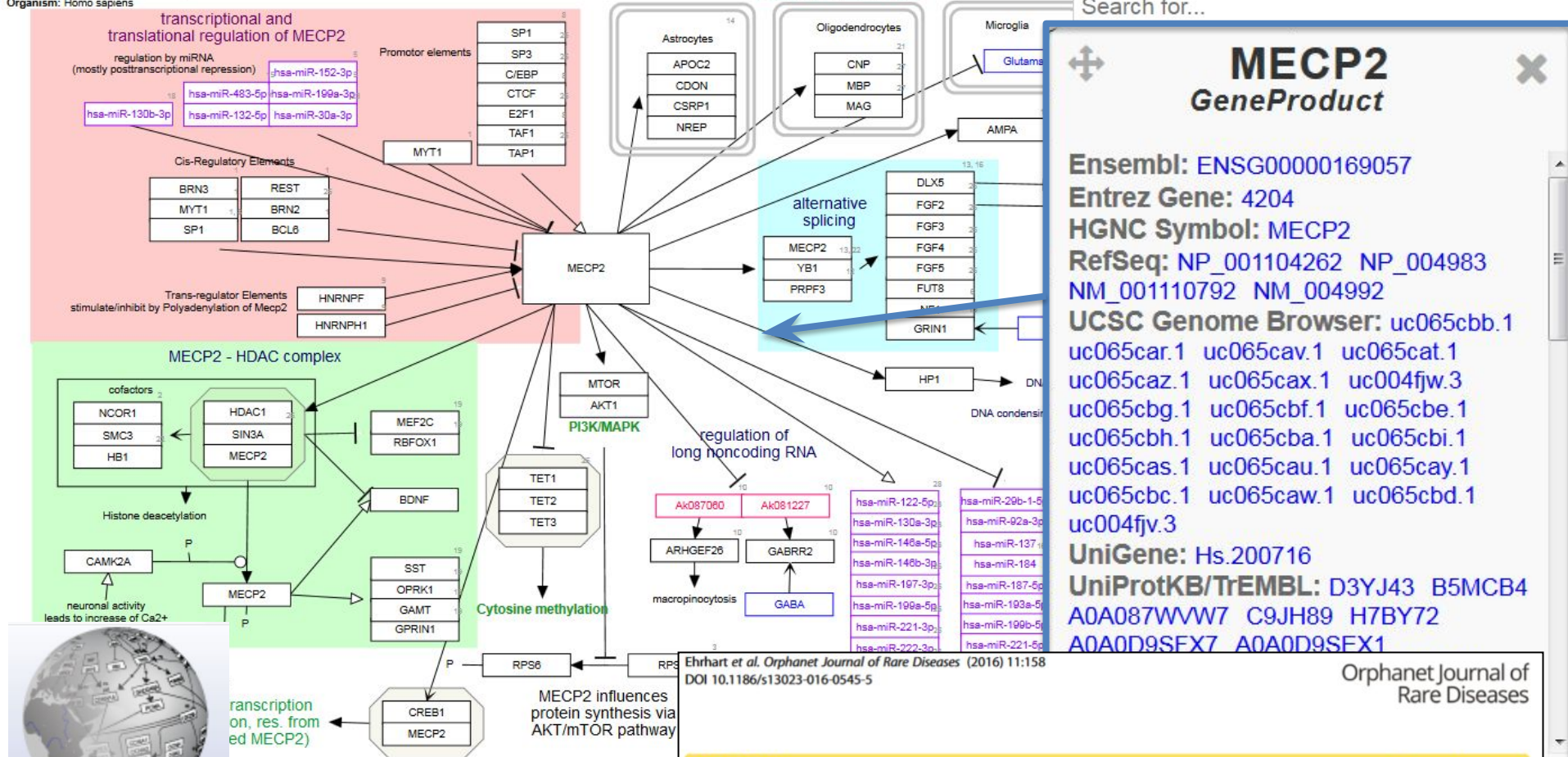
Neurotransmitter Disorders (Homo sapiens)

[View all Featured Pathways for this Portal](#)

Special Issue: Workshop planned

We are currently planning to have a workshop and training event on the making of and curation of rare disease pathways organized by the EJP-RD later this year. The planned date will be in the second half of 2019. Location will be Maastricht University. The

Title: MECP2 and Associated Rett Syndrome
Organism: Homo sapiens



REVIEW

Open Access

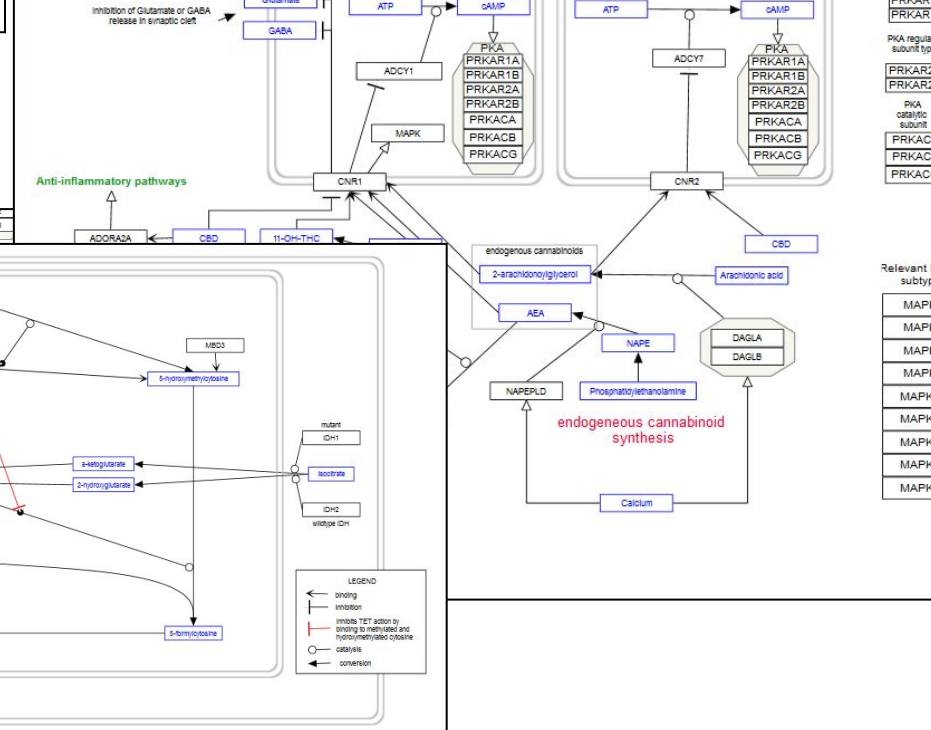
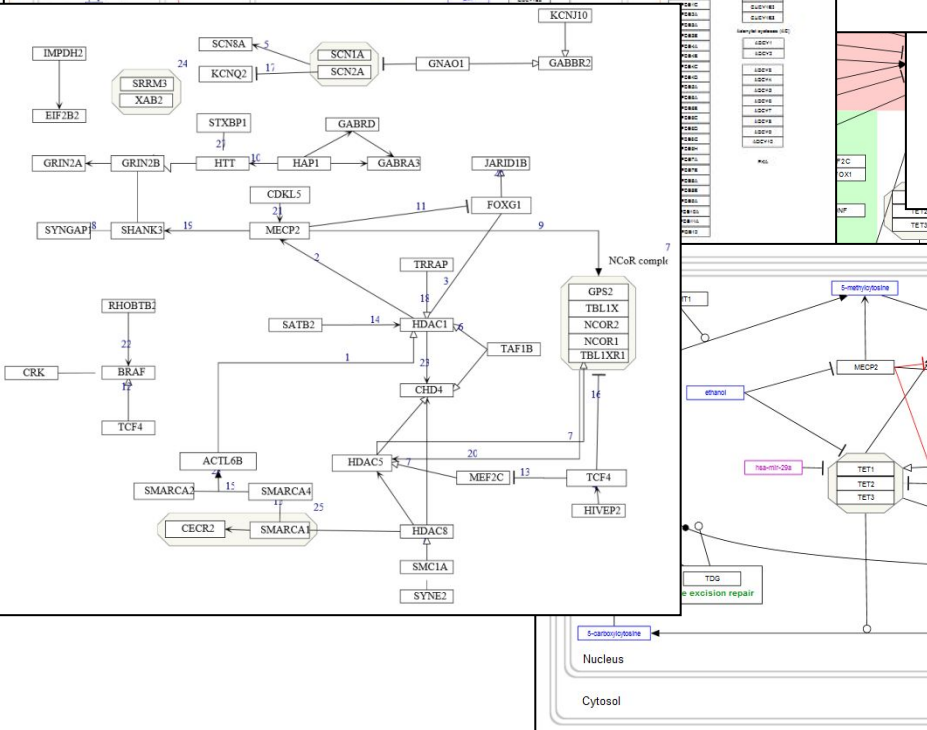
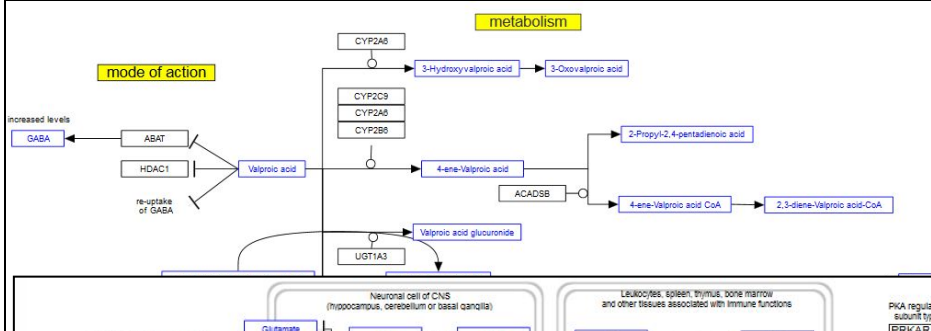
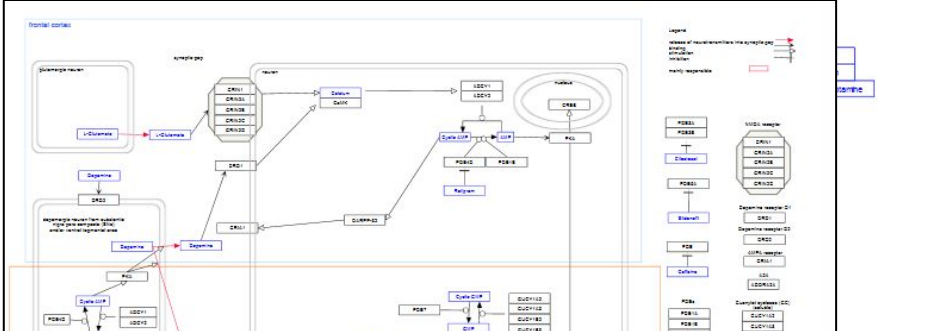
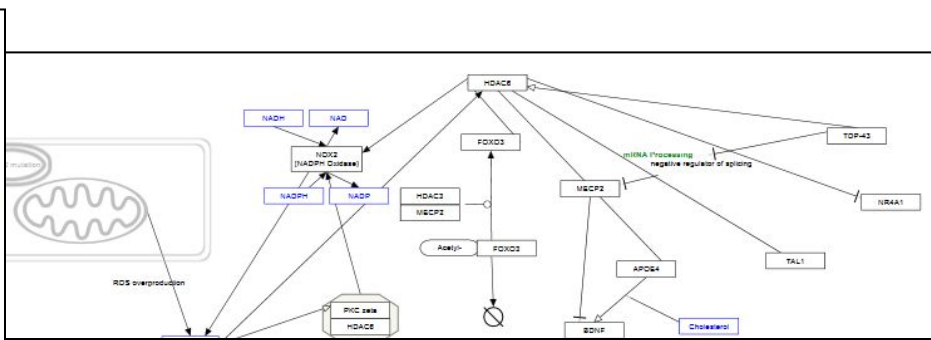
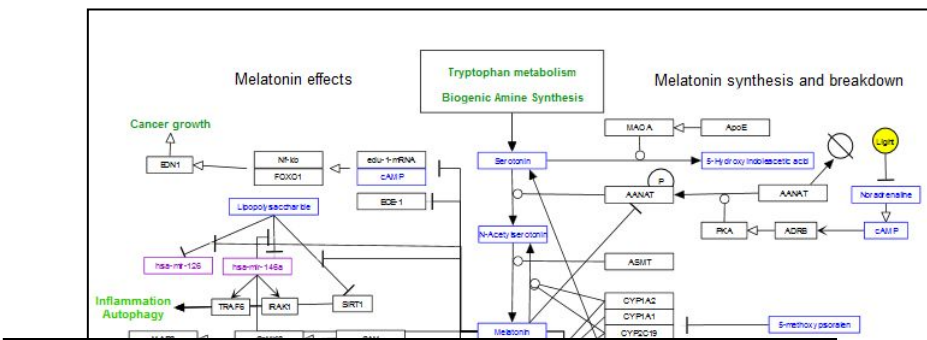
Rett syndrome – biological pathways leading from MECP2 to disorder phenotypes

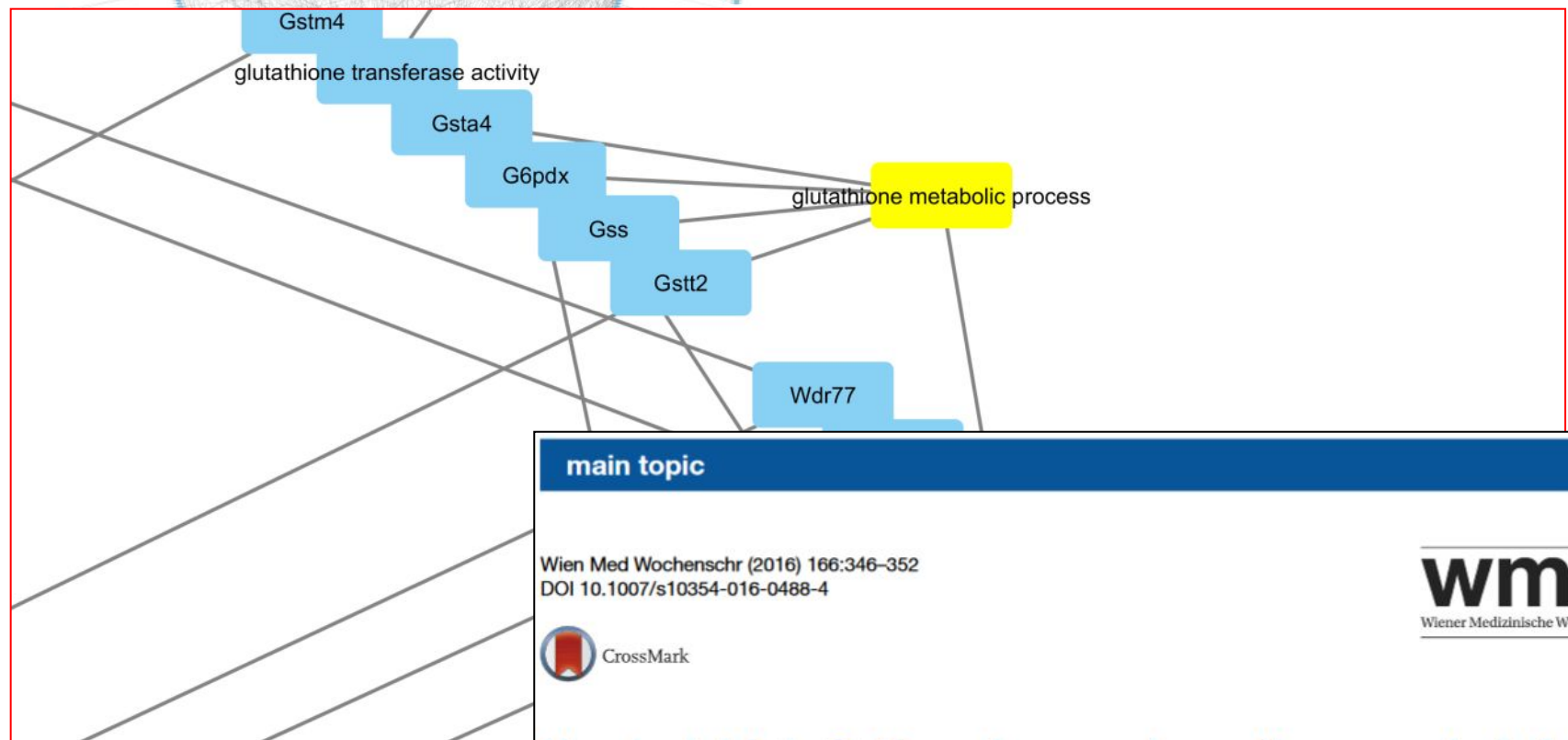
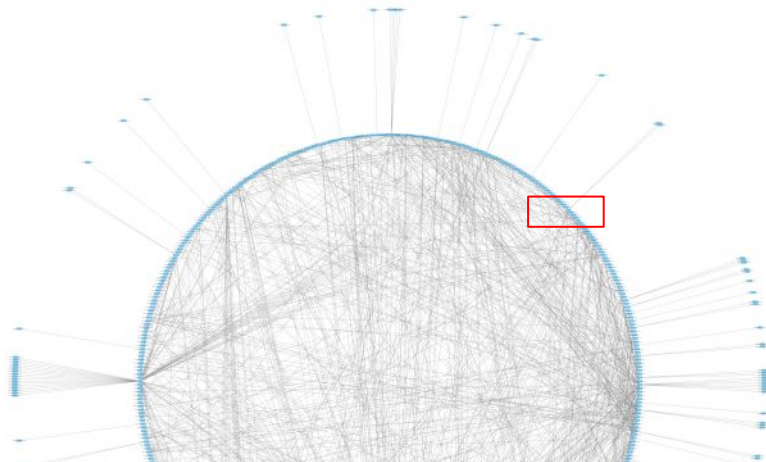
Friederike Ehrhart^{1,2*}, Susan L. M. Coort², Elisa Cirillo², Eric Smeets¹, Chris T. Evelo^{1,2} and Leopold M. G. Curfs¹

Ehrhart et al. Orphanet Journal of Rare Diseases (2016) 11:158 DOI 10.1186/s13023-016-0545-5

Orphanet Journal of Rare Diseases

CrossMark





main topic

Wien Med Wochenschr (2016) 166:346–352
DOI 10.1007/s10354-016-0488-4



wmw
Wiener Medizinische Wochenschrift

New insights in Rett syndrome using pathway analysis for transcriptomics data

Friederike Ehrhart · Susan L. M. Coort · Elisa Cirillo · Eric Smeets · Chris T. Evelo · Leopold Curfs

BridgeDb

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SOFTWARE TOOL ARTICLE

Providing gene-to-variant and variant-to-gene database identifier mappings to use with BridgeDb mapping services. [version 1; referees: 1 approved, 1 not approved]

Friederike Ehrhart

Jonathan Melius

Elisa Cirillo

Martina Kutmon

Egon L. Willighagen

Susan L. Coort

Leopold M.G. Curfs

Chris T. Evelo

Author details

elixir

This article is included in the ELIXIR gateway.

Abstract

Database identifier mapping services are important to make database information interoperable. BridgeDb offers such a service. Available mapping for BridgeDb link 1. genes and gene products identifiers, 2. metabolite identifiers and InChI structure description, and 3. identifiers for biochemical reactions and interactions between multiple resources that use such IDs while the mappings are obtained from multiple sources. In this study we created BridgeDb mapping databases for selections of genes-to-variants (and variants-to-genes) based on the variants described in Ensembl. Moreover, we demonstrated the use of these mappings in different software tools like R, PathVisio, Cytoscape and a local installation using Docker. The variant mapping databases are now described on the BridgeDb website and are available from the BridgeDb mapping database repository and updated according to the regular BridgeDb mapping update schedule.

Keywords

database identifier mapping, gene variant, BridgeDb, interoperability

Metrics

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1. Patrice Godard

UCB (Union Chimique Belge), Belgium

2. Osman Ugur Sezerman

Acibadem University, Turkey

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Available for SNPs (will need maintenance and large file support)

Not yet (operationally) available for:


- InDels (Insertions and Deletions)
- CNVs (Copy Number Variations)

Standardized variant descriptions evaluated at FAIR BYOD in Maastricht
(Where is it? Does it cover CNVs?)

Problems:

- 1) Cluster various variants occurring in close proximity
- 2) See when InDels CNVs and various SNPs occur in same region (e.g. protein domain).

13.1.3: Mapping to genes to function



BLAST/BLAT | VEP | Tools | BioMart | Download

Using this website | Annotation and prediction | Data access | API & software

in this section

- VEP web interface
 - Input form
 - Results
- VEP script
 - Tutorial
 - Download and install
 - Running VEP

Help & Documentation | API & Software

Variant Effect Predictor

VEP determines the effect of your variants

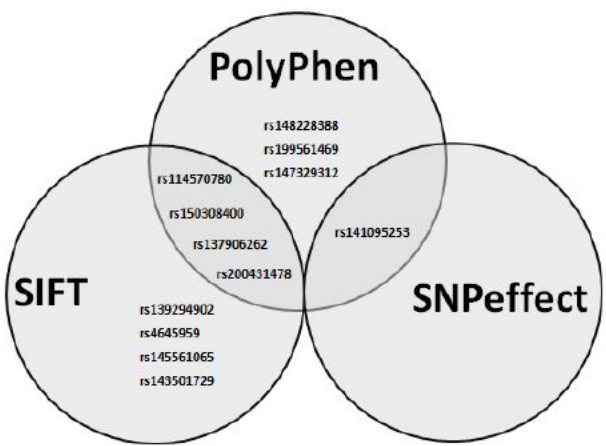
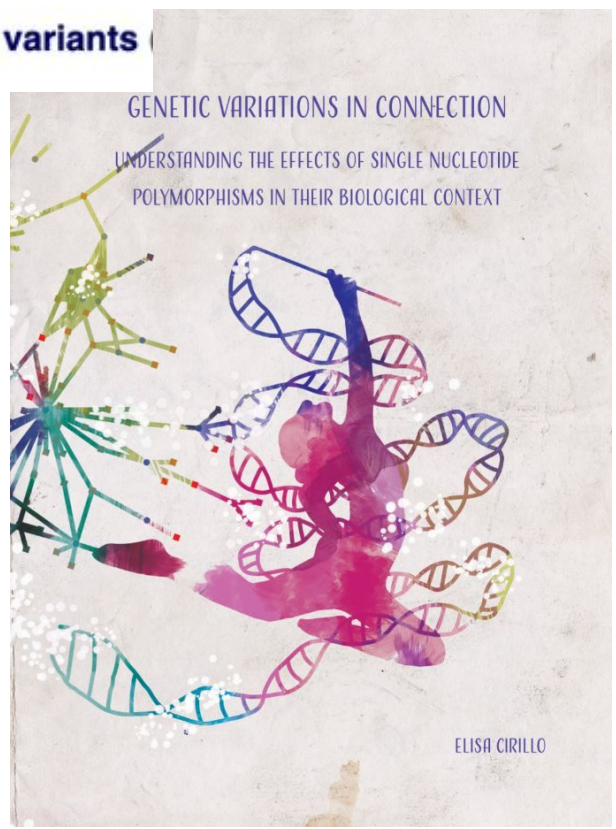
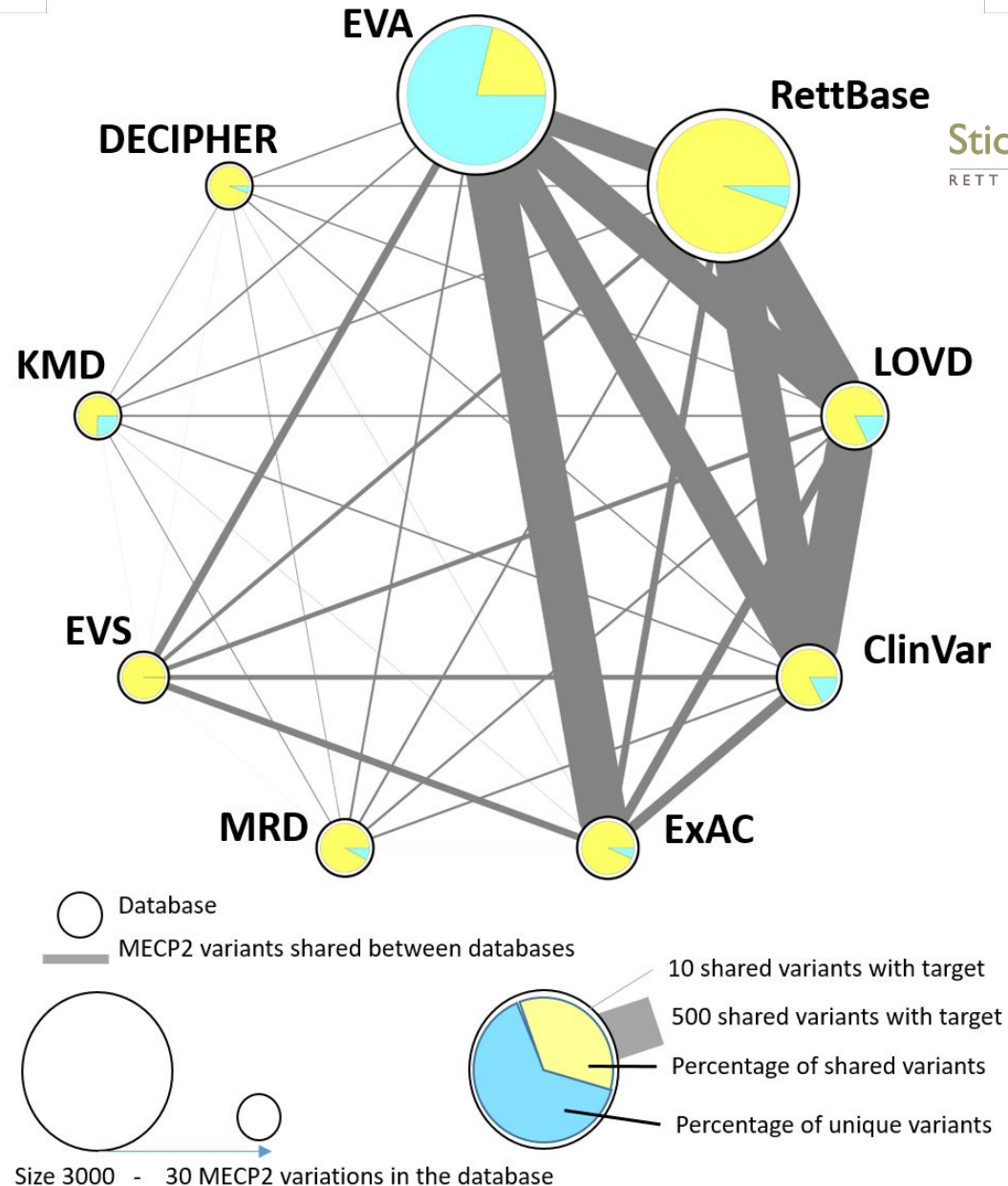


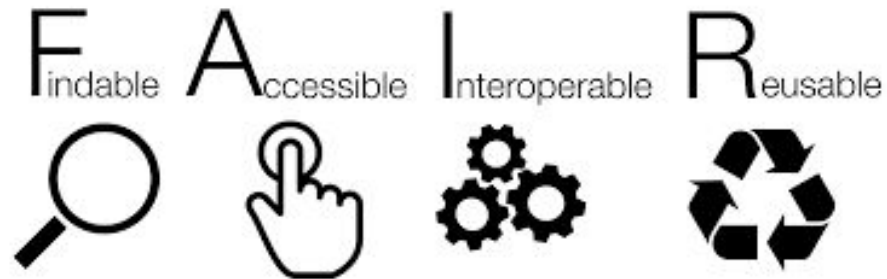
Fig. 4. nsSNPs of human c-Myc1 protein predicted by SIFT, PolyPhen and SNPeffect algorithms to have some biological importance.



The landscape of MECP2 variants in the different databases

Paper in preparation
863 variants of RETT... 2019

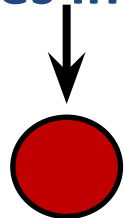




FAIRplus

WP12

A federated Open PHACTS??

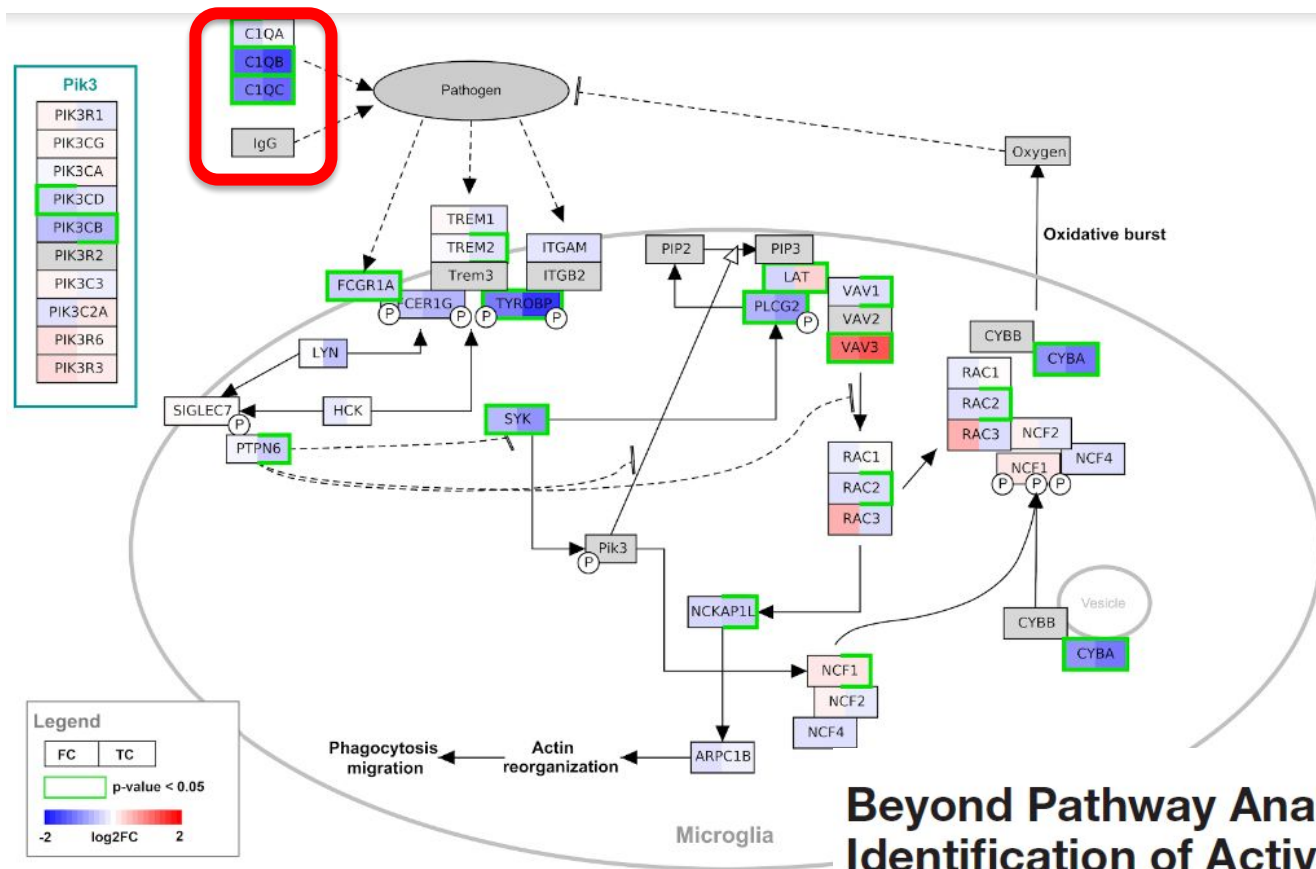


bioRxiv
THE PREPRINT SERVER FOR BIOLOGY

Integrated analysis of human transcriptome data for Rett syndrome finds a network of involved genes

doi: <https://doi.org/10.1101/274258>

Beyond pathway analysis – using of integrated network of ALL pathways



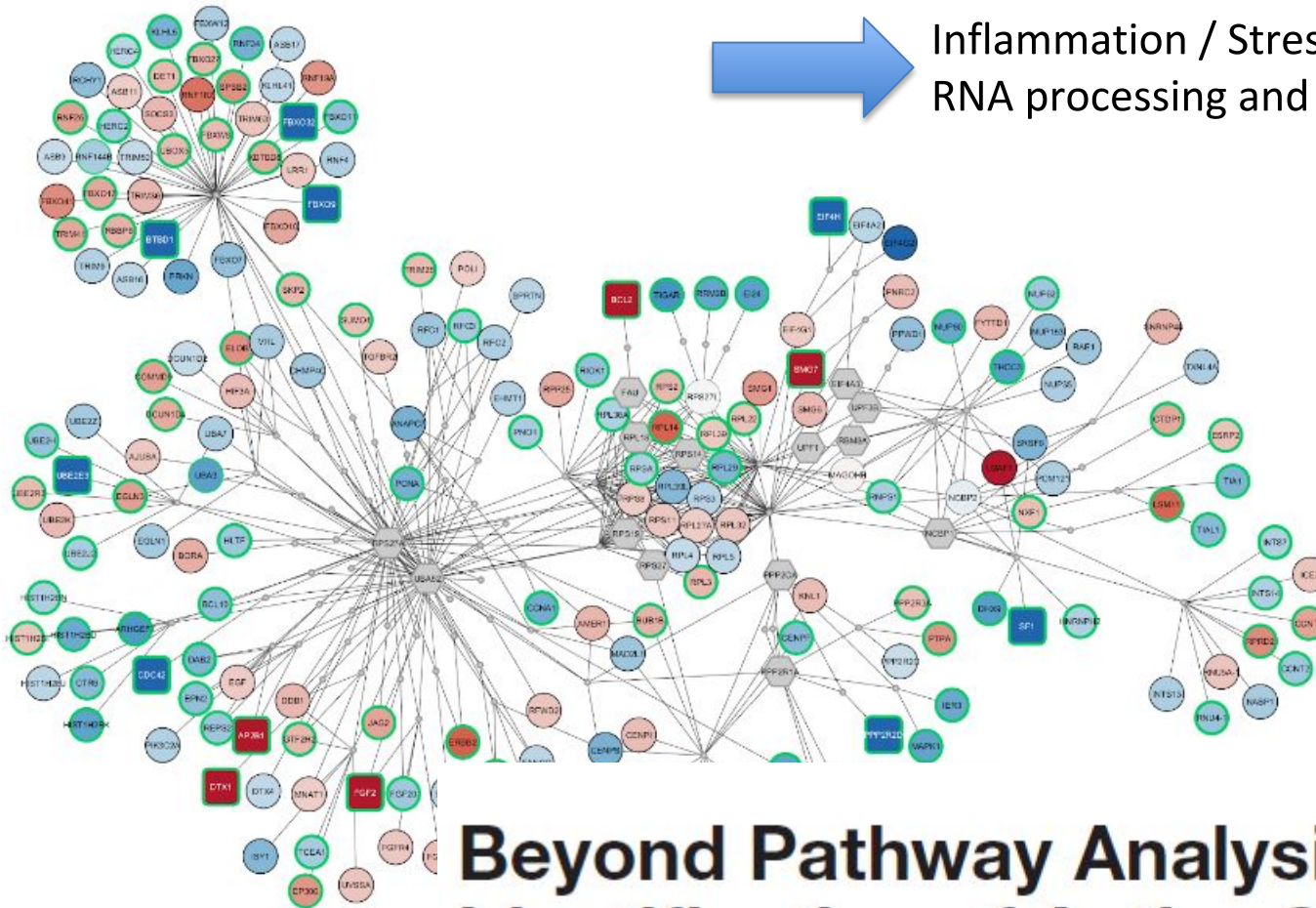
Beyond Pathway Analysis: Identification of Active Subnetworks in Rett Syndrome

Ryan A. Miller^{1†}, Friederike Ehrhart^{1,2†}, Lars M. T. Eijssen^{1,3}, Denise N. Slenter¹, Leopold M. G. Curfs², Chris T. Evelo^{1,2,4}, Egon L. Willighagen¹ and Martina Kutmon^{1,4*}



Inflammation / Stress

RNA processing and translation processes



Beyond Pathway Analysis: Identification of Active Subnetworks in Rett Syndrome

Ryan A. Miller^{1†}, Friederike Ehrhart^{1,2†}, Lars M. T. Eijssen^{1,3}, Denise N. Slenter¹,
Leopold M. G. Curfs², Chris T. Evelo^{1,2,4}, Egon L. Willighagen¹ and Martina Kutmon^{1,4*}

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Featured Content



DisGeNET

DisGeNET is a discovery platform containing one of the largest publicly available collections of genes and variants associated to human diseases.

Find Public Networks

Use the Search Panel above to explore the public networks available in NDEX. Our Featured Networks are a great place to start, examples of high-quality content from different projects and laboratories. If you use Search Term Expansion, common aliases for human gene and protein identifiers will be added to the search. >> [Learn More...](#)

Store and Share Networks

NDEX is for everyday work and collaboration, a Dropbox for networks! When you sign up for an NDEX account, you get 10 GB of free storage, enough for several very large networks or thousands of small networks. Your networks start out as private to you, but you can share them to collaborate with other NDEX users or groups. You can also share a network with anyone using a Shareable URL, just paste it into email or documents! >> [Learn More...](#)

The Cytoscape Cloud

If you use Cytoscape 3.7, you can store your networks in NDEX! Cytoscape is the leading desktop application for network visualization and analysis and NDEX its cloud storage component. The CyNDEX-2 Core App lets you save and display networks in NDEX, including their style and layout information, while networks viewed in the NDEX Web UI can be seamlessly opened in Cytoscape with just one click! >> [Learn More...](#)

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NDEX lets you specify Licenses and Request DOIs for your networks to include in grant proposals or publications thus enabling papers to link directly to your data. Readers can now go from static figures to interactive, actionable data objects in just a few clicks! Vice versa, networks linking out to the papers they support provide you with new opportunities for discovery and citation. NDEX is a recommended repository for Scientific Data, Springer Nature, and PLOS. >> [Learn More...](#)

Access to Data

NDEX supports access to data according to FAIR principles. Individual users and organizations can make networks public, findable and accessible in NDEX. Each public network has its unique, stable URL and can always be downloaded either manually or programmatically, via our REST API.

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The NDEX Project @NDEXProject

HumanNet v2 integrated networks now available in @NDEXProject . Find them here: goo.gl/SWeUQB

For more info, please visit the HumaNet v2 website at: inethio.org/humannet/#networkbiology #ncitcr #compbio @cytoscape @CancerCellMap



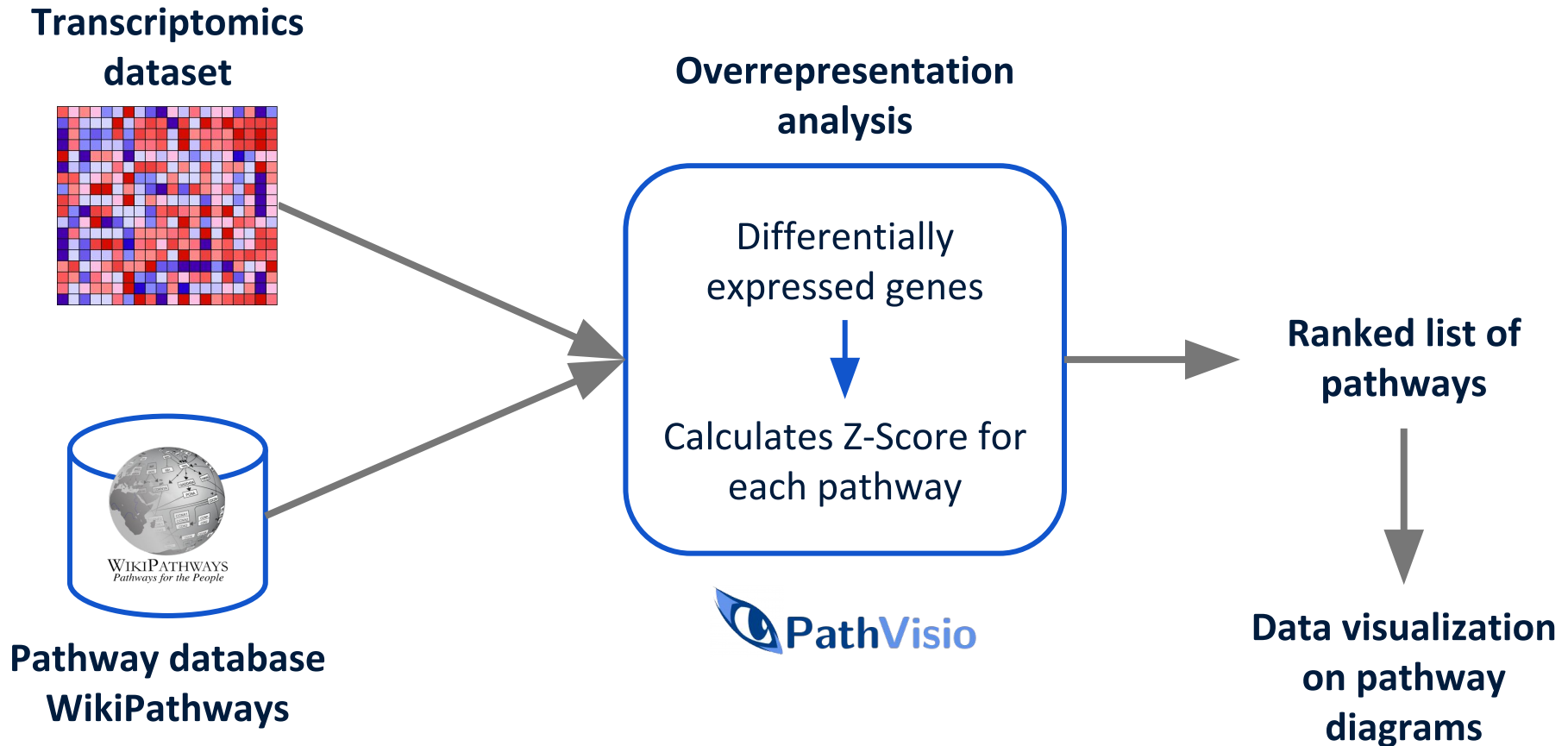
Feb 20, 2019



The NDEX Project @NDEXProject

Up-to-date data from @DrugBankDB v5.1.2 and @DisGeNET v6 now available in NDEX! Access here: goo.gl/WNBjra#networkbiology #ncitcr #compbio @cytoscape @CancerCellMap

Pathway analysis-method



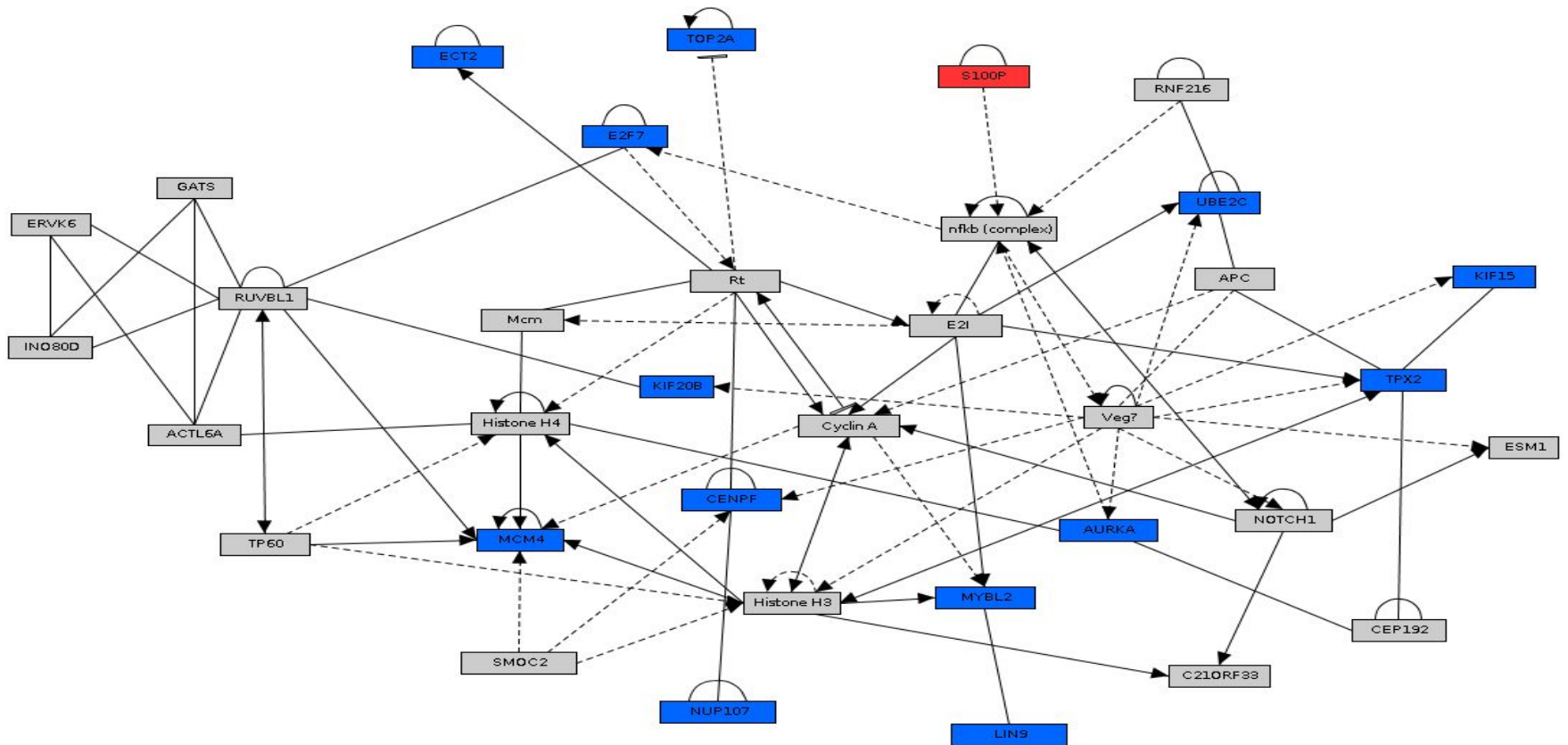
Significantly altered pathways after $1.25(\text{OH})_2\text{D}_3$ treatment in prostate cancer cells

- 8 general cell cycle related pathways
- 7 cancer related pathways

Pathway	Z-Score	Category	Pathway	Z-Score	Category
DNA Replication	11.91	general	Retinoblastoma (RB) in Cancer	12.63	cancer
Cell Cycle	11.04	general	Gastric cancer network 1	10.44	cancer
Histone Modifications	10.44	general	Gastric cancer network 2	5.13	cancer
G1 to S cell cycle control	9.12	general	Integrated Pancreatic Cancer Pathway	4.08	cancer
DNA damage response	5.40	general	Integrated Cancer pathway	3.85	cancer
ATM Signaling pathway	4.87	general	Integrated Breast Cancer Pathway	3.41	cancer
Fluoropyrimidine Activity	4.16	general	Signaling Pathways in Glioblastoma	2.02	cancer
AhR signaling pathway	2.47	general			

Pathway analysis -results

Title: Gastric cancer network 1
Last modified: 10/17/2013 1
Organism: Homo sapiens

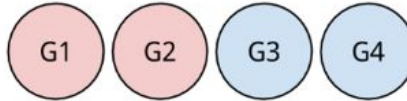


Gastric Cancer Network 1

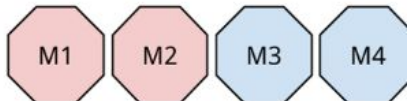
up
down

Workflow

1. mRNA/microRNA expression data

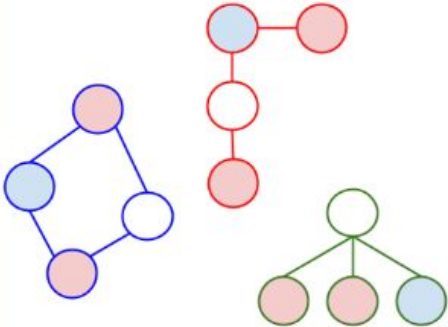


mRNA expression



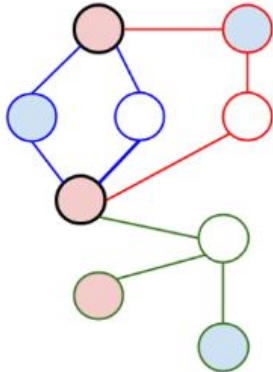
microRNA expression

2. Pathway analysis



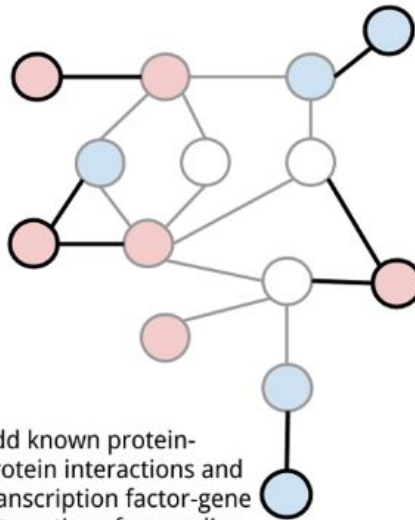
Find significantly altered pathways from mRNA expression data

3. Network building



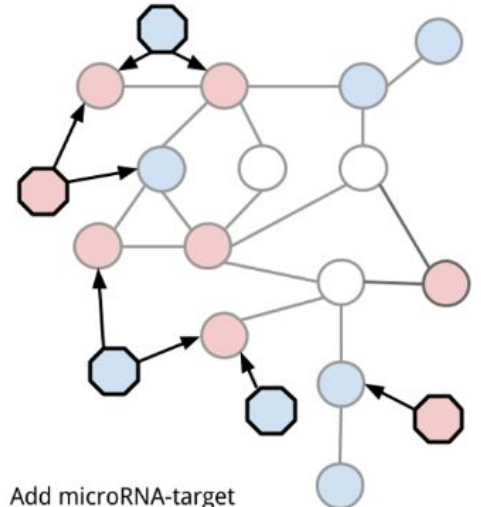
Merge all pathways in one network

4. Network extension



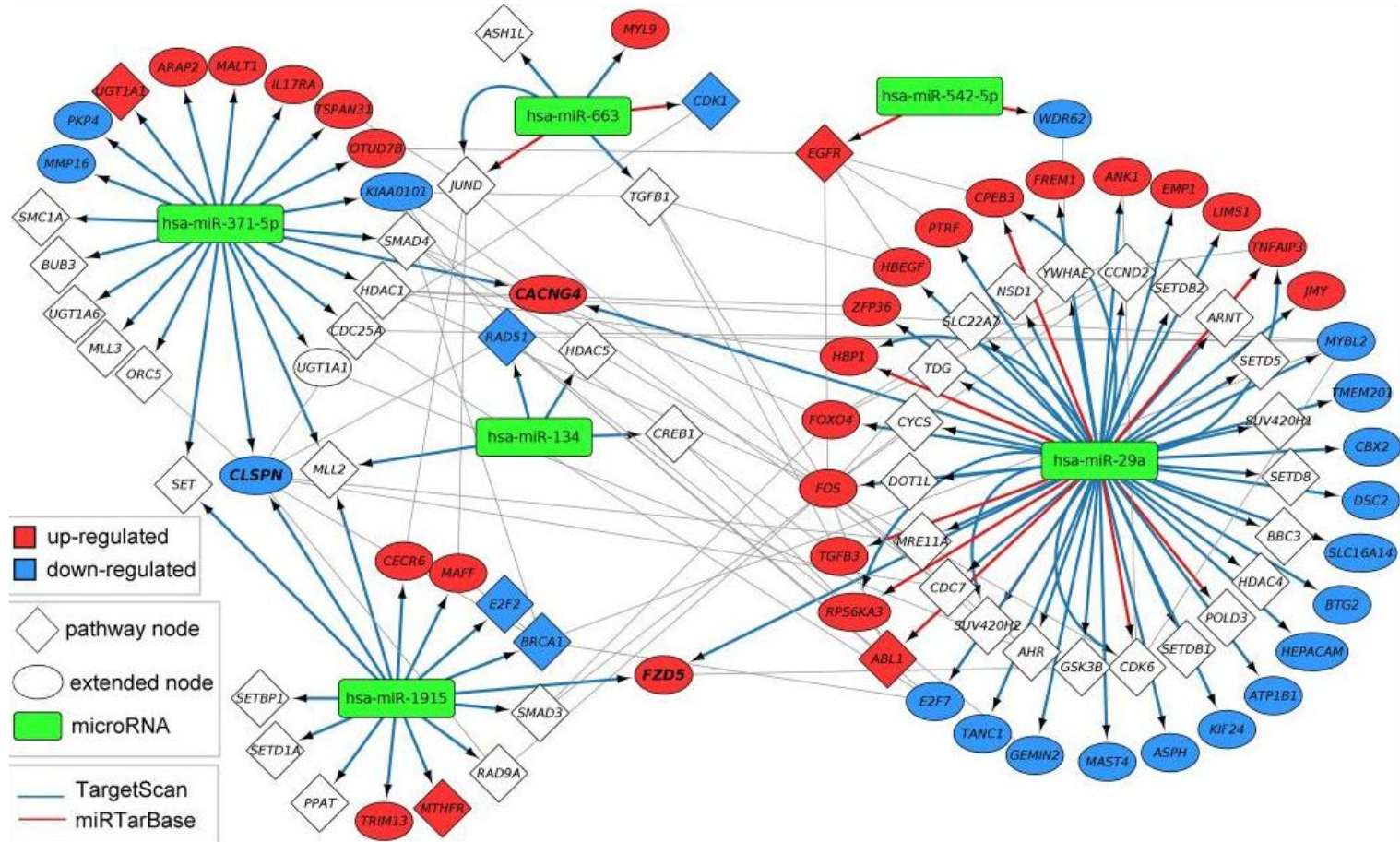
Add known protein-protein interactions and transcription factor-gene interactions from online databases

5 MicroRNA regulation



Add microRNA-target interactions from online databases

Vitamin D-microRNA network



Targeted by multiple microRNAs:

CLSPN - cell cycle

FZD5 - receptor for Wnt proteins

CACNG4 - calcium channel

31 targets up-regulated (3 in pathways)

23 targets down-regulated (4 in pathways)

CyTargetLinker

a Cytoscape app for simple network extension

RECENT POSTS

CyTargetLinker automation feature release

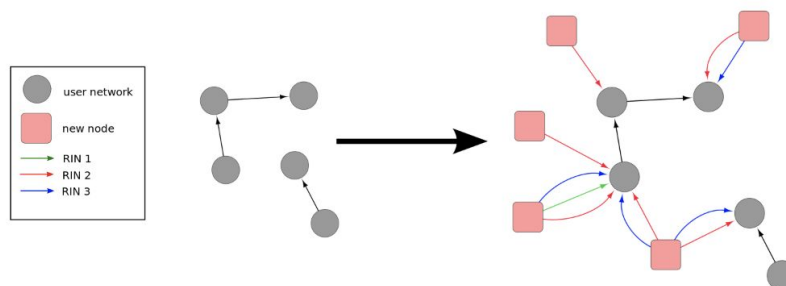
A microRNA Signature Associated with Early Recurrence in Breast Cancer.

CyTargetLinker publication in PLoS One

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WELCOME

Extend your biological networks in Cytoscape with our CyTargetLinker app



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Download CyTargetLinker and the relevant regulatory interaction networks (RINs).

CyTargetLinker

a Cytoscape app for simple network extension

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RECENT POSTS

- CyTargetLinker automation feature release
- A microRNA Signature Associated with Early Recurrence in Breast Cancer.
- CyTargetLinker publication in PLoS One

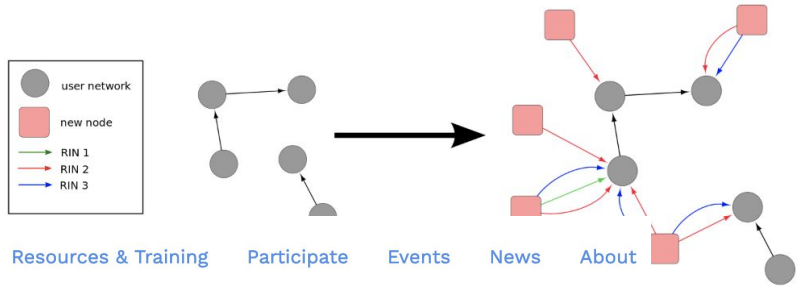
OpenRiskNet

RISK ASSESSMENT E-INFRASTRUCTURE

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WELCOME

Extend your biological networks in Cytoscape with our CyTargetLinker app



Open e-Infrastructure to Support Data Sharing, Knowledge Integration and in silico Analysis and Modelling in Predictive Toxicology and Risk Assessment

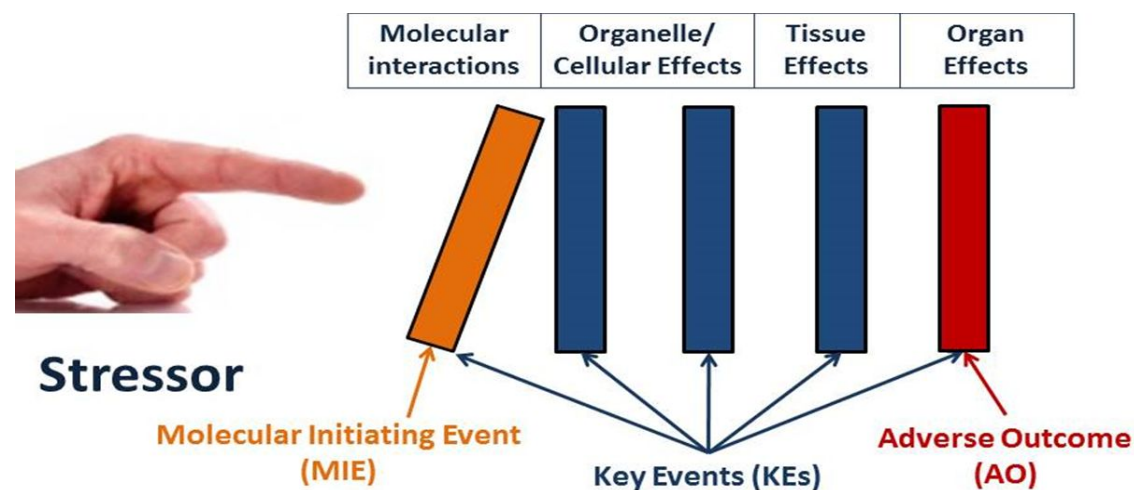
OpenRiskNet is a 3 year project with the main objective to develop an open e-Infrastructure providing resources and services to a variety of communities requiring risk assessment, including chemicals, cosmetic ingredients, therapeutic agents and nanomaterials. OpenRiskNet is working with a network of partners, organized within an Associated Partners Programme.

our tutorials.



eraction networks (RINs).

Adverse Outcome Pathways (AOPs)



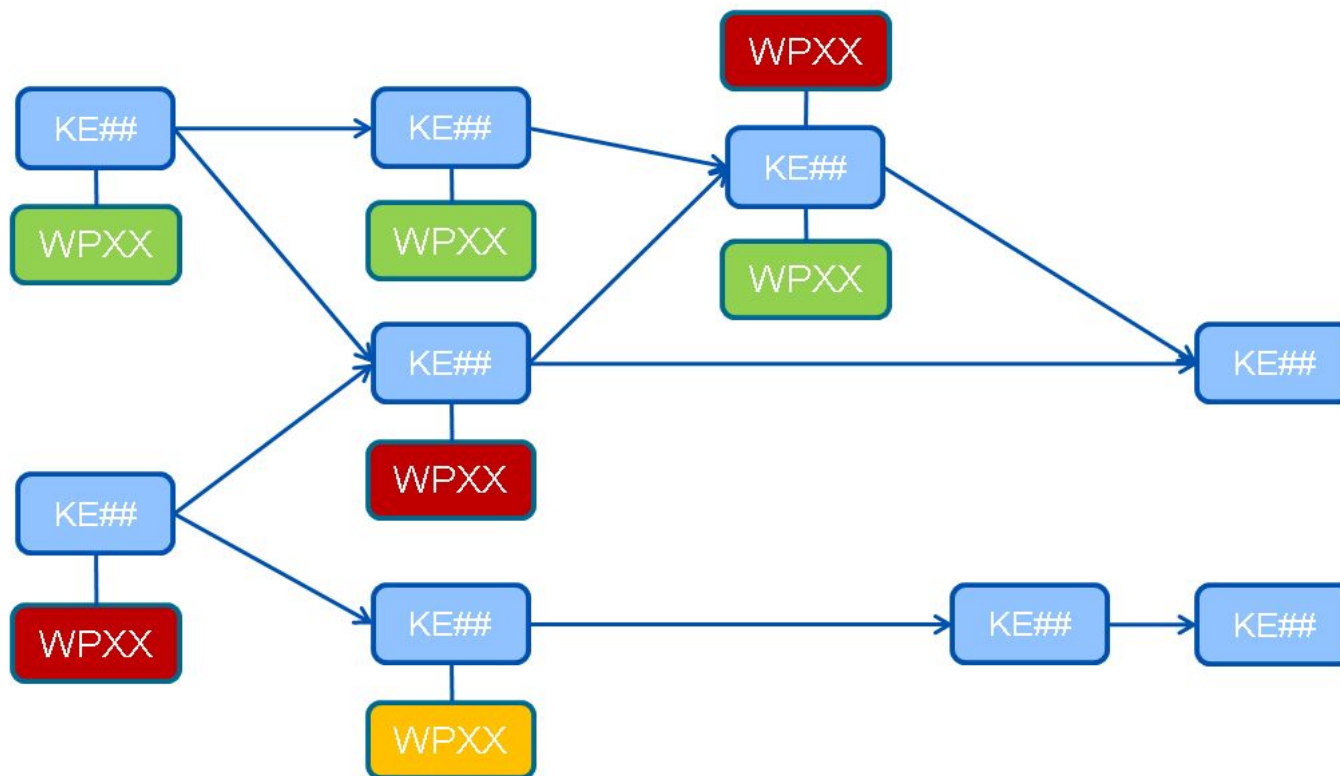
Framework with mechanistic knowledge of toxicological processes to support decision making

Toxicology data

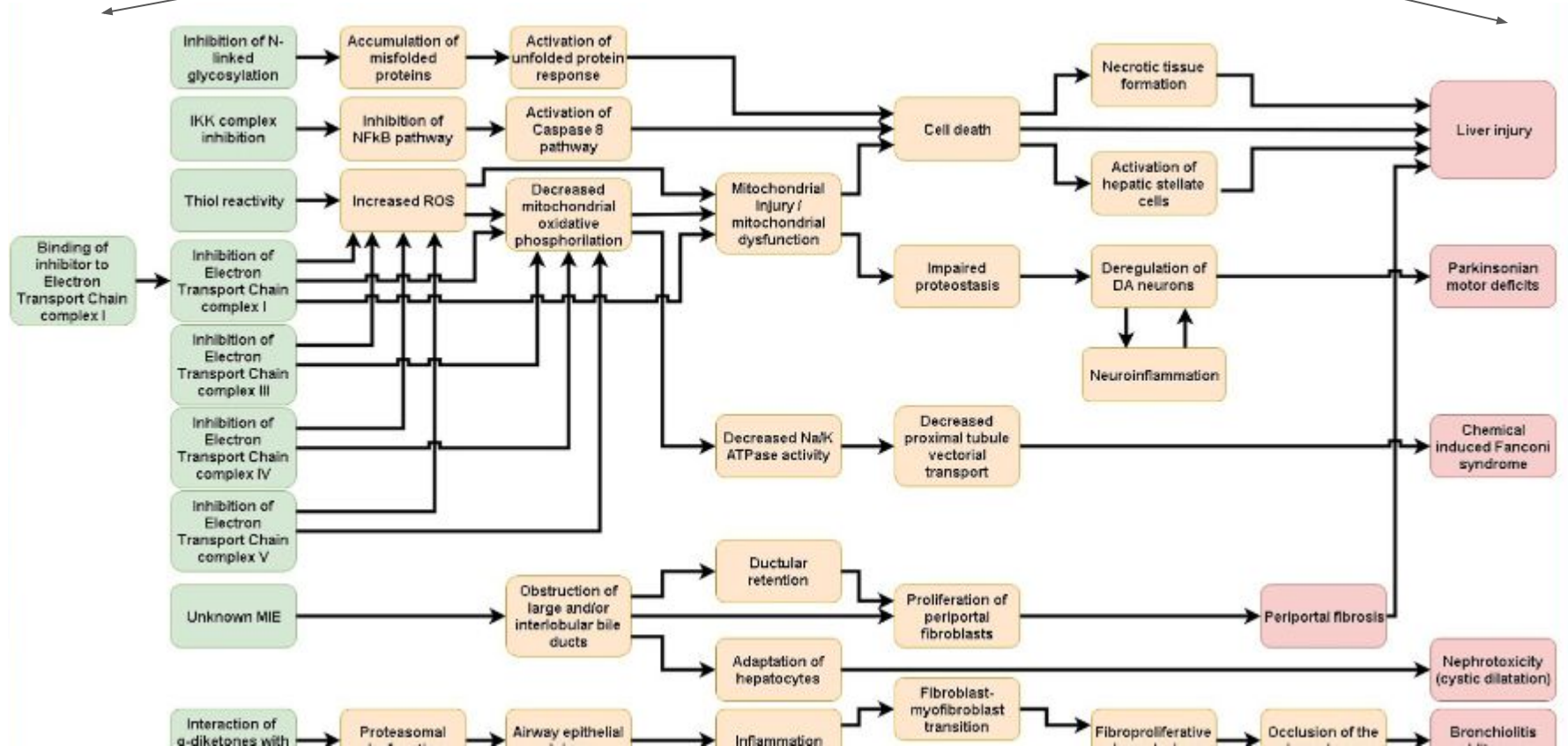


Knowledge-based regulatory risk assessment

Goal: link molecular pathways to AOPs

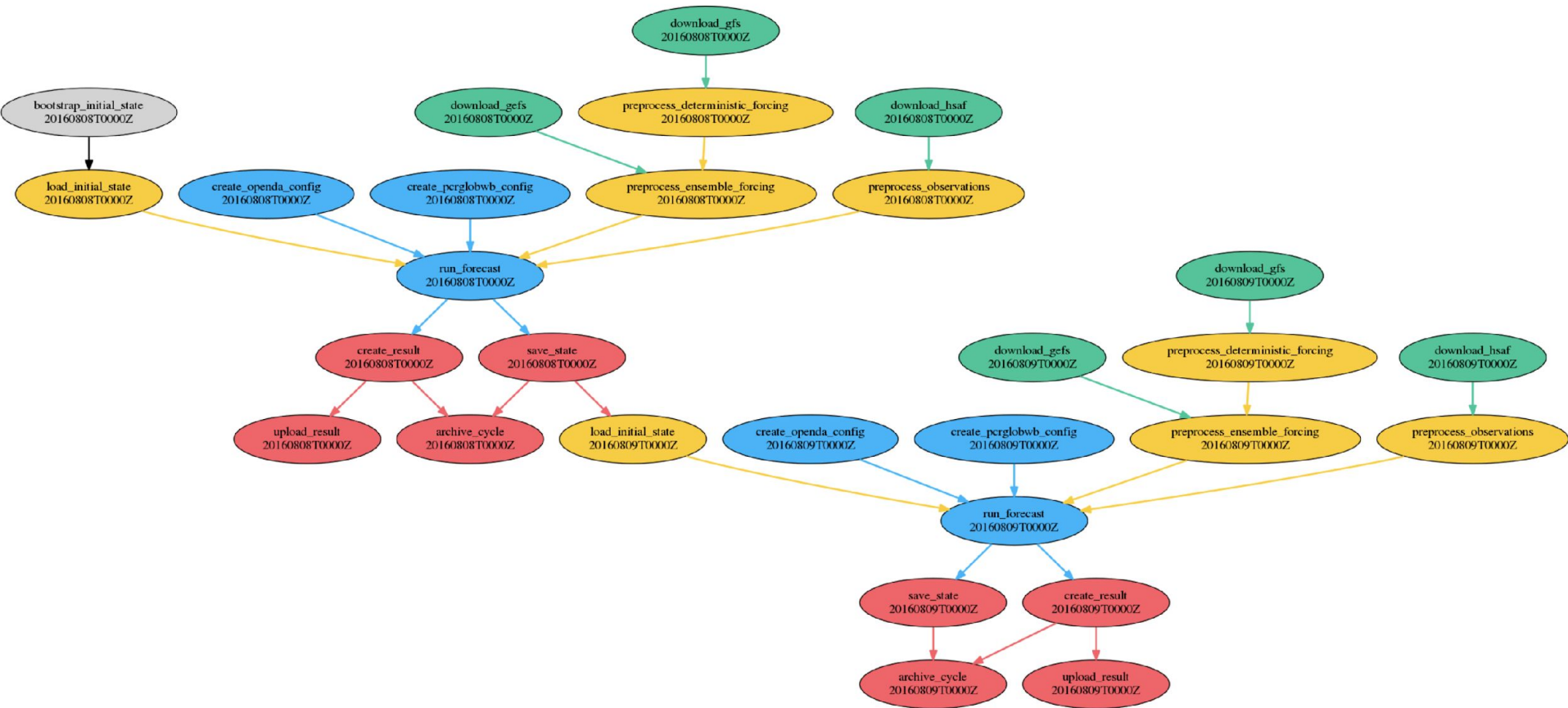


Links to rare genetic diseases?



Reproducible Science: The Common Workflow Language

 Nils Drees [Follow](#)
Mar 11, 2017 · 4 min read



Happy



RARE DISEASE DAY®



Thank you for your attention!

Contact:

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WP 13 Enabling multidisciplinary, holistic approaches for rare diseases diagnostics and therapeutics

Task lead: Chris Evelo



- **System biology approaches for RD**
 - Biological pathways for RD
 - Understanding of disease mechanisms and diagnosis
- **Variants to function mapping**
 - SNP-to-protein function, disease-to-protein function
- **Environmental lifestyle and toxicology**
- **Drugs**
- **Proof of principle studies**
 - E.g. on Rett syndrome