### OpenRiskNet

RISK ASSESSMENT E-INFRASTRUCTURE

# AOPLink

Identification and Linking of Data related to AOP-Wiki

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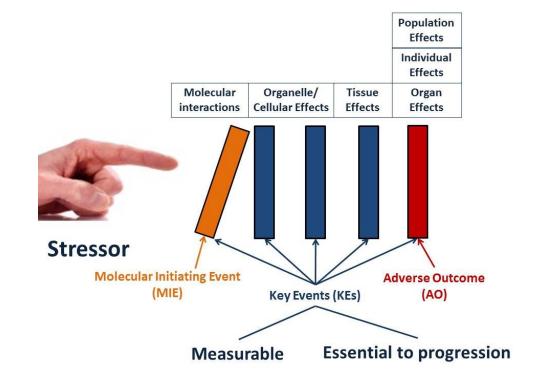
OpenRiskNet: Open e-Infrastructure to Support Data Sharing, Knowledge Integration and *in silico* Analysis and Modelling in Risk Assessment

Project Number 731075



## Central concept: Adverse Outcome Pathways

Framework that captures mechanistic knowledge of toxicological processes to support decision making in risk assessments





## Case study objectives

Q1: For an AOP, which experimental data is available to support the AOP?

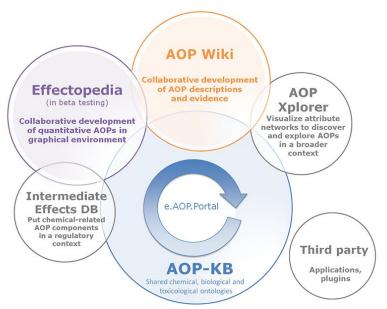
Q2: Can this experimental data support an existing AOP?





## Central repository: AOP-Wiki

- The main qualitative AOP repository of the AOP-KB
- Joint effort between EC-JRC and US EPA

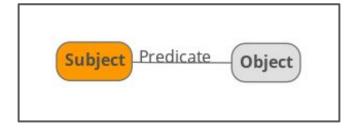


https://aopwiki.org



## Resource Description Framework (RDF)

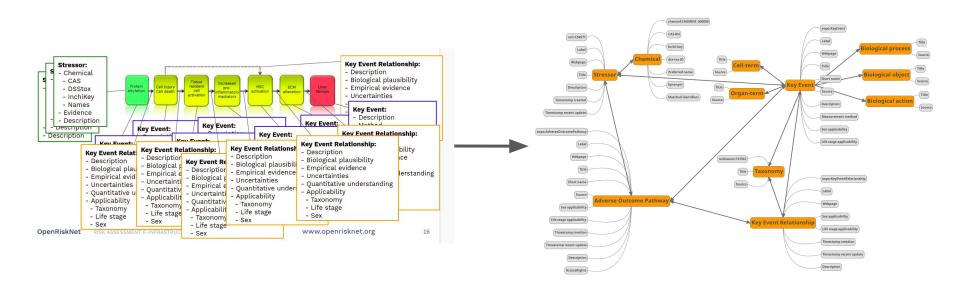
- Standard to describe information in web resources
- Information stored in triples



- Generally used in databases
- Large number of libraries and tools



## Semantic modelling of AOP-Wiki





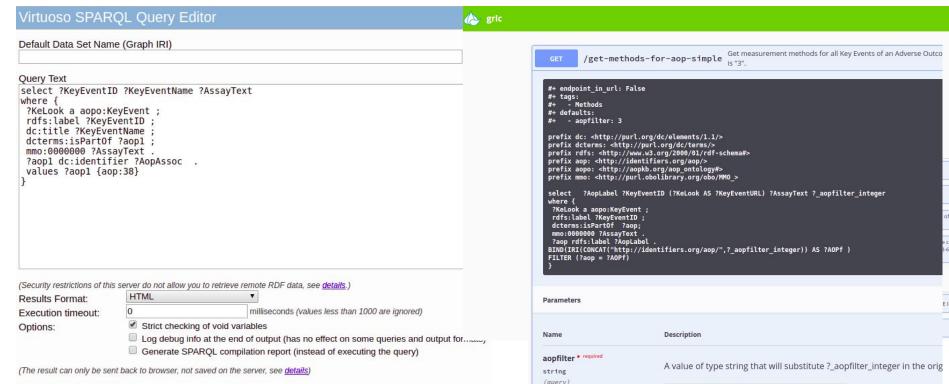
### How to access the AOP-Wiki RDF

Through the SPARQL endpoint

Through the REST API

http://aopwiki-rdf.prod.openrisknet.org/sparql/

http://grlc.io/api/marvinm2/AOPWikiQueries



## Integration of the AOP-DB

Winners of the OpenRiskNet implementation challenge

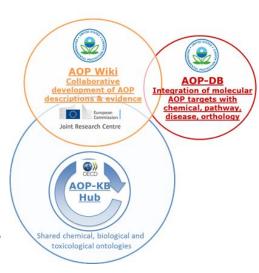


Database of AOPs linked to external data sources for (among others:

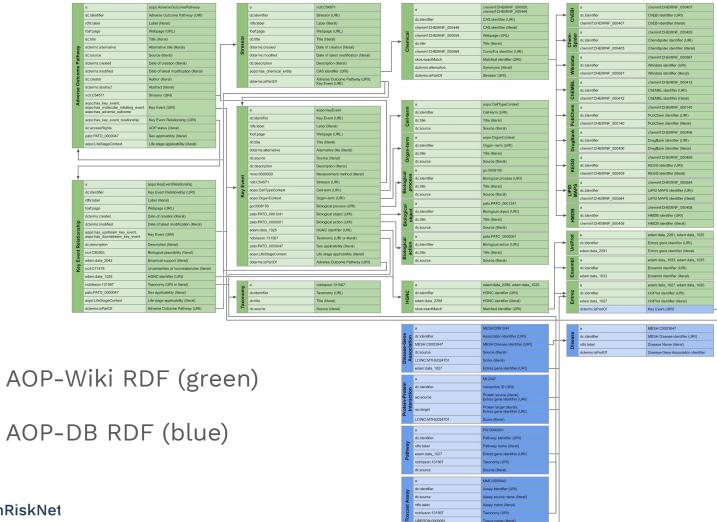
- Genes
- Pathways
- ToxCast assays
- Diseases

Parts of AOP-DB converted into RDF and exposed in a SPARQL endpoint

AOP-DB webinar: <a href="https://openrisknet.org/events/60/">https://openrisknet.org/events/60/</a>







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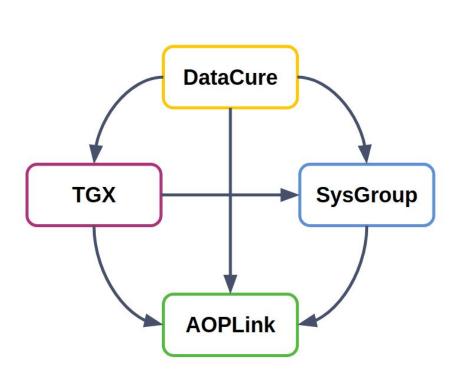
OpenRiskNet

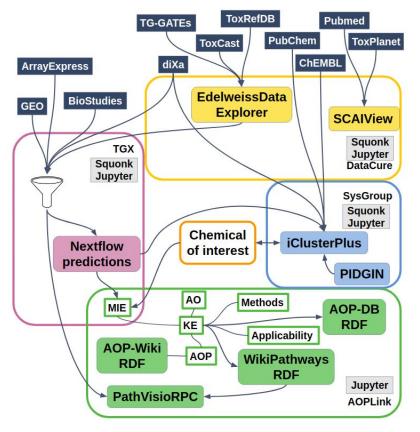
```
MDS - SELLIL
   KERs = set[[])
    for result in results["results"]["bindings"]:
        MIEs.add(result["MIE ID"]["value"])
        AOs.add(result["AD ID"]["value"])
        KEs.add(result["KE ID"]["value"])
       KERs.add(result["KER_ID"]["value"])
       KEtitle[result["KE ID"]["value"]]=result["KE Title"]["value"]
#list all NEs. MIEs and AOs separately
KEs2 - []
for item in KEs:
   if item not in MIEs and item not in AOs:
        KEs2.append(item)
net- Network(height="188%", width="188%")
for MIE in MIES
   net.add node(MIE, color = 'Lightgreen', size = 58, shape = 'circle', font = '28px arial black', title = KEtitle[MIE])
for KE in KEs2:
   net.add node(KE, color = 'khaki', size = 50, shape = 'circle', font = '29px arial black', title = KEtitle[KE])
for AD in ADS
   net.add node(AO, color = 'salmon', size = 50, shape = 'circle', font = '20px arial black', title = KEtitle[AO])
for KER in KERs:
    sparglquery = ""
   SELECT 7KE UP ID 7KE DOWN ID
    TKER URI a appo:KeyEventRelationship; rdfs:label TKER ID; appo:has upstream key event TKE UP URI; appo:has downstream key event TKE DOWN UR
    7KE UP URI rdfs:label 7KE UP ID.
    7KE DOWN URI rdfs:label 7KE DOWN ID
   FILTER (7KER ID = " +KER+" + ")
    appwikisparql.setQuery(sparqlquery)
    appwikisparql.setReturnFormat(JSON)
    results = appwikispargl.guery().convert()
    for result in results["results"]["bindings"]:
       met.add edge(result["KE UP ID"]["value"], result["KE DOWN ID"]["value"], width = 2, color = 'black', label = KER, arrows = "to')
net.show('mygraph.html')
IFrame(src='./mygraph.html', width=788, height=688)
                     KE 1214
                                                                             765
                                         KE 716 -HER-780- KE 77
                           KE 1170
                                              KE 787
                                                                  KE 209
                                                                KER 703
                          KE 724 HER-YEA KE 726
```

```
[25]: Assays = pd.DataFrame(columns=['Assay ID', 'Assay title', 'Entrez', 'Tissue', 'Spe
       for gene in Genes:
           sparqlquery = '''
           SELECT ?Assay title ?Assay ID ?Tissue ?Species name WHERE{
           SELECT * WHERE{
           ?Assay a mmo:0000441; bao:BAO 0003064 ?Entrez URI; rdfs:label ?Assay title; fo
           SERVICE <a href="http://aopwiki-rdf.prod.openrisknet.org/sparql/">http://aopwiki-rdf.prod.openrisknet.org/sparql/</a>
           ?Species URI dc:title ?Species name.
           FILTER (?Entrez URI = ncbigene: '''+gene +''')}}
           aopdbsparql.setQuery(sparqlquery)
           aopdbspargl.setReturnFormat(JSON)
           results = aopdbspargl.query().convert()
           for result in results["results"]["bindings"]:
               Assays = Assays.append({'Assay ID' : result["Assay ID"]["value"],
                                          'Assay title' : result["Assay title"]["value"],
                                          'Tissue'
                                                         : result["Tissue"]["value"],
                                                              : result["Species name"]["valu
                                          'Species name'
                                          'Entrez'
                                                           : gene}, ignore index=True)
       display(Assays)
```

Assay_ID		Assay_title	Entrez	Tissue	Species_name
0	269	NVS_NR_hPPARa	5465		Homo sapiens
1	6	ATG_TRANS	5465	liver	Homo sapiens
2	6	ATG TRANS	5465	liver	Homo saniens

### AOPLink links with other case studies









## Identification and Linking of Data related to AOP-Wiki [AOPLink]

CS leader: Marvin Martens, Egon Willighagen, Chris Evelo (UM)

Involved: EwC, UoB, CRG

#### **Outcome:**

- Discoverable annotated BridgeDb API
- Development of the AOPLink RDF (AOP-Wiki + WikiPathways + AOP-DB), and loaded and exposed as Virtuoso SPARQL endpoints
- Implementation challenge service: AOP-DB RDF
- Workflows utilizing the AOPLink RDF, linking knowledge repositories and experimental data to AOPs.

#### To do:

- Improved linking of AOPs with WikiPathways via KE genes.
- Development of pathway analysis Jupyter notebook with gene expression data related to AOP stressor chemicals.
- Knowledge base linking nanomaterials to MIEs

### **Risk Assessment Framework**

Tier 0.3, 0.4 (Support Data), 1.6 (MOA)

### **Databases**

- AOP-Wiki, AOP-DB: AOP knowledgebase (AOP-KB);
- WikiPathways, Reactome: biological pathway database;
- eNanoMapper, EPA Chemistry Dashboard, NORMAN Network: experimental data.

### Tools / APIs

- BridgeDb, ChemIdConverter: identifier mapping;
- PathVisioRPC: pathway analysis;
- eNanoMapper database test instance

#### Results

- BridgeDb service, AOP-Wiki and AOP-DB SPARQL endpoints, operational in VRE
- Report on AOPWiki<>WikiPathways linking options

### **Activities**

- Continued development identifier mapping databases
- Semantification of AOPWiki
- AOP Portal (<a href="http://aop.wikipathways.org">http://aop.wikipathways.org</a>)
- Exploration of APIs around semantic web technologies

https://openrisknet.org/development/case-studies/case-study-aoplink/

