DELIVERABLE REPORT D5.7



DELIVERABLE REPORT D5.7

D5.7 Final report on User Applications

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| | Douglas Connect, GmbH (DC) | | | | |
|-------------------------|---|--|--|--|--|
| | National Technical University of Athens (NTUA) | | | | |
| | In Silico Toxicology (IST) | | | | |
| Partner Organisations | • Ideaconsult (IDEA) | | | | |
| | Karolinska Institutet (KI) | | | | |
| | • European Bioinformatics Institute (EMBL-EBI) | | | | |
| | Maastricht University (UM) | | | | |
| | • Misvik Biology (MB) | | | | |
| Authors | Lucian Farcal, Philip Doganis, Georgia Tsiliki, Haralambos Sarimveis, Nina Jeliazkova, Egon Willighagen, Linda Rieswijk, Penny Nymark, Micha Rautenberg, Christoph Helma, Maja Brajnik, Barry Hardy | | | | |
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1. EXECUTIVE SUMMARY

Deliverable 5.7 reports on the Tasks 5.3 and 5.9 on the user applications achievements. The application infrastructure developed within eNanoMapper project aims to support the data management in the area of nanosafety research and to enable an integrated approach for the risk assessment of nanomaterials. To achieve these, eNanoMapper developed an ontology, a data infrastructure and modelling tools with applicability in risk assessment of nanomaterials. eNanoMapper developed resources and tools for predicting toxicity of nanomaterials and worked towards improving the standards in risk assessment of nanomaterials.

The testing phase aimed to provide the basis for test-driven development, ensure the interoperability of services and the developing ontology and alert developers about bugs and interoperability problems. Moreover, the tools and functionalities development followed as much as possible the prioritized use cases identified within WP1.

- The ontology includes common vocabulary terms used in nanosafety research and aims to provide a clear explanation of nanostructures based on information relating to their characterization, relevant experimental paradigms, biological interactions, safety indications and the integration of data from existing nanotoxicology sources.
- To support a collaborative safety assessment approach, an infrastructure for data management was developed, with a database which includes functionalities for data protection, data sharing, data quality assurance, search and interfaces for different needs and usages, comparability and cross-talk with other databases.
- In addition, a collection of descriptors, computational toxicology models and modelling tools were developed, to enable the use and integration of nanosafety data from various sources, via nanoQSAR modelling, read across prediction modelling, experimental design, and interlaboratory testing.

The project provides also a rich source of information and documentation (e.g. tutorials, webinars, publications) to support and guide the users. eNanoMapper dictionary of terms is also available at: http://www.enanomapper.net/library/enm-dictionary



Figure 1. eNanoMapper portal for user applications (http://www.enanomapper.net/applications)

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2. INTRODUCTION

Deliverable 5.7 aims to report on the Tasks 5.3. and Task 5.9 on the user applications achievements (technical options, user interfaces) and link with the prioritized use cases previously identified and described (*see Deliverable 1.2*). The applications followed different steps from the development and optimization phase to testing, before being released for user testing and evaluation. A detailed documentation was recorded for each application.

Within Task 5.3 Integrated Testing, the testing processes were defined and executed, on the prototype or released versions of the applications. The testing aimed to evaluate all applications and it was performed individually or jointly (e.g. within hackathon sessions dedicated to specific applications). Guidance materials were prepared and feedback sections were opened for capturing eventual issues from the users.

The testing phase aimed to provide the basis for test-driven development, ensure the interoperability of services and the developing ontology and alert developers about bugs and interoperability problems.



Figure 2. Integration of ontologies, data and modelling tools towards developing user applications

The aim of Task 5.9 User Application for Prioritised Use Cases, was to guide the development of the user applications based on the case studies identified at the beginning of the project within WP1. As shown in Chapter 4 of this report, most of the prioritised use cases are linked to the user applications, which cover one or more of these cases:

• A comprehensive **ontology** was developed for the nanosafety domain, encompassing nanomaterials and all information relating to their characterization, as well as information describing relevant experimental paradigms, biological interactions, and safety indications. The eNanoMapper ontology includes common vocabulary terms in use in nanosafety research with a classification hierarchy and other relationships. The ontology includes a refinement of the NanoParticle Ontology and incorporates terms from other high quality ontologies (e.g. OBI, ENVO etc.).





• A data infrastructure and search capabilities was developed, supporting all aspects of nanomaterials characterization, environmental and health hazards assessment, and high throughput and high content datasets. The eNanoMapper database is a public database hosting nanomaterials composition and characterization data and biological and toxicological information. The database software is open source, and download / installation instructions are available. The database provides various possibilities to search and explore information, and to download data in different formats as a web application or service.

The import and upload functionality currently supports a variety of NSC templates and OECD Harmonized Templates. The importer is easily extensible to support more spreadsheet formats through configuration.

- Modelling infrastructure and services were developed to analyse nanomaterials-related descriptors and experimental data. The online platform Jaqpot Quattro uses data available from data.enanomapper.net and allows building predictive nanoQSAR models enriched by multiple validation schemes, as well as predictive read across models. Additional functionalities include experimental design and interlaboratory testing techniques. Datasets can be preprocessed or undergo PMML transformations before modelling. Users can upload their own models or algorithms to the system, or seamlessly integrate models and algorithms hosted elsewhere. A user-friendly interface is now available that enables access to eNanoMapper Jaqpot Quattro tools and applications, but also to a repository of validated models. Other developed applications are also available, i.e. the Image descriptor Calculation Tool, a systematic framework for the automated analysis of microscopy images of nanomaterials and the calculation of morphology and population-related nanoparticle descriptors, the RRegrs R package, a collection of R regression tools aiming to find optimal and well validated nanoQSAR models with applications to chemoinformatics and nanotoxicology data, and the Gene Ontology descriptors tool, a framework to group omics NP data to descriptors that would easily summarize the biological data.
- The modelling service links the eNM database with the modelling platform, e.g.:
- It transforms experimental data into a modelling-friendly format, and produces standardized datasets.
- Raw data of nanomaterials such as images, crystallographic data and proteomics data, are processed by descriptor calculation services to produce compact and informative numerical descriptors.
- Data modelling and analysis services implement computational experimental design methods, tools for interlaboratory proficiency testing and non-testing approaches for predicting toxicity and for filling data gaps (NanoQSAR and read-across methods), offering the option of evaluating a model's accuracy and robustness.
- A number of mechanistic modelling tools combine experimental data with information from public biological databases and tools to perform pathway and network analysis.





3. USER APPLICATIONS

3.1. ONTOLOGY



An ontology is a controlled vocabulary built on the hierarchical relationships between terms, used, for example, to harmonize data from several sources to one database or analyze the relationships between terms and categories of terms.

The eNanoMapper ontology is developed by the eNanoMapper team. The ontology includes and defines common vocabulary terms in use in nanosafety research with a classification hierarchy and other relationships. In parts it is an extension and refinement of the <u>NanoParticle Ontology</u>.

- Download the ontology in .owl from: <u>http://purl.enanomapper.net/onto/enanomapper.owl</u>
- Download and explore on Bioportal: <u>http://bioportal.bioontology.org/ontologies/ENM</u>
- Download and explore on Aber-OWL: <u>http://aber-owl.net/ontology/ENM</u>
- Download and explore on Ontology Lookup Service: <u>http://www.ebi.ac.uk/ols/beta/ontologies/enm</u>
- Feedback: <u>https://github.com/enanomapper/ontologies/issues</u>

3.1.1. ONTOLOGY VIEWER APPLICATIONS

3.1.1.1 ENANOMAPPER ONTOLOGY VIEWER

Web application and graphical interface for the eNanoMapper triple store:

- Viewer: <u>https://purl.enanomapper.net/enm-viewer</u>
- Development: <u>https://github.com/enanomapper/enm-ontoviewer</u>
- Feedback: <u>https://github.com/enanomapper/enm-ontoviewer/issues</u>
- Technology: Web application, Library / Ruby, JavaScript
- License / Waiver: GPL3





| in silico toxicology | |
|---|-------------------|
| Problems, bugs, ideas for improvements ? Please report at our issue tracker or send us an email 🖂 (version 1.0.2). | Ƴ 8⁺ in Fi |
| Viewer Sparql Help | |
| PREFIX rdf: <http: 02="" 1999="" 22-rdf-syntax-ns#="" www.w3.org=""> PREFIX rdfs: <http: 01="" 2000="" rdf-schema#="" www.w3.org=""> SELECT DISTINCT ?root_name ?parent_name ?child_name WHERE { VALUES ?root_name { "endpoint" } ?root rdfs:label ?root_name . ?child rdfs:subClassOf{,5} ?root . ?child rdfs:subClassOf ?parent . ?child rdfs:label ?child_name . ?parent rdfs:label ?parent_name . }</http:></http:> | |
| Query - | |

Figure 3. eNM ontology viewer application (search interface)

The eNanoMapper ontology viewer application (Figure 3) visualises SPARQL query results from eNM ontologies and stored in a triple-store database¹. Data in the triplestore is mirrored in RDF format from the eNanoMapper ontology and database (<u>https://data.enanomapper.net/</u>). The eNanoMapper ontology viewer application is publicly available at <u>http://purl.enanomapper.org/enm-viewer</u>. Details about graphics and file output options with screenshots can be found in Annex 6.2.

3.1.1.2. ONTOLOGY VISUALISATION

Access: https://search.data.enanomapper.net/treedemo/

Study summary statistics:

- data.enanomapper.net
- ambitlri.ideaconsult.net

Ontology visualisation:

- Chemical substance (CHEBI59999)
- eNanoMapper ontology
- eNanoMapper ontology (subclasses of BFO_0000040)
- BioAssay ontology (BAO)
- Gene ontology (GO)

Feedback: https://github.com/enanomapper/data.enanomapper.net/issues/59

¹ The SPARQL endpoint triplestore is described in Deliverable D3.3 eNanoMapper 604134 10 December 2016





3.1.2. USER EVALUATION OF ONTOLOGY

In order to determine the appropriateness of the ENM ontology, a <u>survey</u> was created using Google Forms. The survey focuses on evaluating the ontology for users within the nanosafety domain. The eight questions within the survey asks users to access the ENM ontology online either via <u>BioPortal</u> or using <u>Aber-OWL</u> and explore its use with keeping example terms in mind. It also refers to the <u>tutorial</u> which has been created to browse the eNM ontology. When the user has been looking for the example terms in the eNM ontology they are asked about the appropriateness of the closest match of the example term in the eNM ontology. The outcomes of the survey will be used for the external evaluation of the ENM ontology. Screenshots of the survey are listed in Figure 4.

| Determining the appropriateness of the eNanoMapper ontology | Determining the appropriateness of the eNanoMapper ontology Feedback on the eNanoMapper ontology With this form we would like to acquire feedback from the potential usars of the eNanoMapper ontology. Reace if it in the quantities below which we will use to improve the crimet version of the element of the element of the detail of the ontol of the element on the detail of the ontol of the element on the element of the element on the element of the element on the elemen |
|---|--|
| Please try and use the eNanoMapper ontology yourself and tell us if the ontology is ready for your domain. Use BioPortal (<u>bioportal bioontology.org/ontologies/ENM</u>) or Aber-OWL(<u>http://aber-owl.net/ontology/ENM</u>) to look up terms and find definitions. Also see <u>http://enanomapper.net/library/browsing-ontology</u> for an extensive step-by-step tutorial. | Were you able to find the term? Your answer 4. Do you agree with the definition provided within the eNanoMapper ontology? instrained and the second |
| The questions in this survey assume you will take one specific term in mind. The first two questions are about this term. The following questions are about what the eNanoMapper ontology tells you about this term. That is where the survey will ask your feedback on the appropriateness of the closest match of your term in the eNanoMapper ontology. | Principles of hierarchy of an ontology Super Your term Sub class |
| 1. Choose a term which is relevant for your field Your answer | A B C F |
| 2. Please give a brief definition of the term | 5. Do the super classes make sense to your field (if applicable)? A super class is a class from which your term of interest is derived. Your answer |
| Your answer | Courterent C. Do the sub classes make sense to your field (if applicable)? A subclass is actiss which is derived from your term of interest Your answer |
| NEXT Page 1 of 2 | 7. Do you agree with the logical structure leading towards the term of interest? Your answer |
| Never submit passwords through Google Forms. | 8. Additional comments Your answer |
| | BACK SURRAT Page 2 of 2 |

Figure 4. The survey to evaluate the appropriateness of the eNM ontology





3.1.3. DOCUMENTATION ON ONTOLOGY

<u>~ Ontology</u>

- Development
 - <u>
 AnoParticle Ontology</u>
 - o <u>~ Ontologies</u>
 - Feedback
 - Licences
 - Basic Formal Ontology
 - o <u>~ Slimmer</u>
 - o <u>~ Test suite</u>
- Applications
 - <u>~ Download .owl</u>
 - <u>~ Bioportal</u>
 - <u>Aber-OWL</u>
 - <u>Contology Lookup Service</u>
 - <u>
 [~] Ontology Viewer</u>
 - <u>Contology Visualisation</u>
- User guidance
 - $\circ \quad \text{Tutorials} \quad$
 - Browsing the eNM ontology with bioportal, aberowl and protege
 - Webinars
 - <u>Closed</u> Using the eNanoMapper ontology
 - \circ Publications
 - <u>~ Hastings et al., 2015, Journal of Biomedical Semantics</u>
 - Hastings et al., 2014, JBMS supplement: Bio-Ontologies meeting
- <u>~ DoW</u>

 - Reporting
 - <u>~ D2.1 Framework and Infrastructure for Ontology development, versioning and dissemination</u>
 - <u>~ D2.2 Ontology Content Types and Existing Community efforts</u>
 - <u>~ D2.3 Ontology initial release</u>
 - D2.4 Ontology final release





3.2. DATA MANAGEMENT APPLICATIONS



3.2.1. ENANOMAPPER DATABASE DEMO

data.eNanoMapper.net is a public database demo hosting nanomaterials characterization data and biological and toxicological information. The database provides various possibilities to search and explore information, and to download data in various standard formats. The database supports data upload in various formats, including configurable Excel templates. The server contains data from various sources.

- Database technologies available: SQL databases; supported formats: IUCLID5 , ISA-TAB, CSV, Excel spreadsheet, RDF, JSON
- Types of NMs involved: various
- Link: data.enanomapper.net
- Source and download: <u>http://ambit.sourceforge.net/enanomapper.html</u>
- License / Waiver: various Open Source licenses

3.2.2. SEARCH APPLICATION

The search engine integrates data.enanomapper.net and caNanoLab.

- Access: <u>https://search.data.enanomapper.net/</u>
- Search application dedicated to NANoREG data (*under development*) <u>https://sandbox.ideaconsult.net/search/nanoreg1</u>

3.2.3 PROTOCOL SERVICE

The protocol service is available at <u>https://apps.ideaconsult.net/enmprotocol</u> Source code: <u>https://github.com/enanomapper/toxbank-api-server</u>





3.2.4. DATA MANAGEMENT DEVELOPMENT TOOLS

3.2.4.1. ENANOMAPPER TRIPLESTORE AND SPARQL ENDPOINT

Aggregation of eNanoMapper data and ontologies in RDF for SPARQL queries. A virtuoso RDF triplestore wrapped in a ruby webservice with graphical interface and machine accessible SPARQL endpoint.

- Access: <u>https://purl.enanomapper.net/enm-viewer</u>
- Endpoint: <u>https://purl.enanomapper.net/sparql</u>
- Technology: Virtuoso / Ruby

3.2.4.2. AMBIT.JS

JavaScript client library for the eNanoMapper / AMBIT API.

- Status: beta
- Technology: Library / JavaScript
- Access: https://github.com/enanomapper/ambit.js/
- Demo: <u>http://enanomapper.github.io/ambit.js/</u>
- License: MIT License

3.2.4.3. NM DATAPARSER

A command line, which can convert different formats

3.2.4.4. NANO-LAZAR ENM PARSER

lazar (<u>https://github.com/opentox/lazar</u>) comes with command line tools and scripts to mirror, parse and import eNanoMapper data, based on the eNM REST API.

3.2.4.5. R ENANOMAPPER CLIENT PACKAGE

R client library for the eNanoMapper / AMBIT API.

- Status: beta
- Technology: Library / R
- Access: https://github.com/enanomapper/renm/
- Demo: http://enanomapper.github.io/ambit.js/
- License: MIT License





3.2.5. DOCUMENTATION ON DATA MANAGEMENT APPLICATIONS

<u>~ Data</u>

- Development
 - o <u>~ API</u>
 - <u>AMBIT web services</u>
 - <u>Triplestore and SPARQL endpoint</u>
 - o <u>~ AMBIT.JS</u>
 - NM Dataparser
 - o <u>Nano-lazar parser</u>
 - <u>**~** R eNanoMapper client package</u>
- Applications
 - Database
 - Data access
 - Search
 - Data sources
 - Protocol Service
- User guidance
 - \circ Tutorials
 - <u>~ Entering and analysing nanosafety data</u>
 - AMBIT user guide
 - \circ Webinars
 - A substance database to support a safe innovation approach
 - <u>
 [~] Data visualization with AMBIT.JS and D3JS
 </u>
 - o Publications
 - Jeliazkova et al., 2015, Beilstein Journal of Nanotechnology
 - <u>~ Jeliazkova et al., 2014, Bioinformatics and Biomedicine (BIBM)</u>

• <u>~ DoW</u>

- <u>Sue tracker</u>
- Reporting
 - <u>~ D3.1 Technical Specification and initial implementation of the protocol and data management web services</u>
 - <u>~ D3.2 Data Management System with extended search capabilities</u>
 - D3.3 Modules and services for linking and integration with third party databases
 - D3.4 ISA-Tab templates for common bioselected set of assays





3.3. MODELLING APPLICATIONS AND DESCRIPTORS



3.3.1. JAQPOT QUATTRO



Figure 5. JaqPot Quattro user interface

JaqPot Quattro can be considered as an extendable suite of computational tools under a common framework (see also <u>Deliverable 4.3</u>, Deliverable 4.5, Deliverable 4.6). Current functionalities include:

- Data preprocessing algorithms
- Computing descriptors from images and crystallographic and omics data
- Integrating diverse data and creation of datasets suitable for modelling
- Training and validation of nanoQSAR models using a rich selection of machine learning and data mining algorithms (which will be further extended)
- Predictive modelling using the read across method
- Repository of predictive models as ready to use web applications
- Integration with R, Python, Weka and access to JaqPot services through Knime
- Factorial and Optimal experimental design
- Interlaboratory testing implementing ISO 13528
- Reporting results in automatically created and downloadable pdf files (including QPRF OECD reports)
- Saving models in PMML format for easy transfer to other platforms

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- Allowing users to create and store in the cloud their own resources (datasets, models, reports) which

they can access and manage at any time and place through a web browser

- Authorisation and authentication services
 - Architecture of tool / Technology: REpresentational State Transfer (REST) / Java, Python, R
 - API: <u>http://app.jaqpot.org:8080/jaqpot/swagger/</u>
 - Source code: <u>https://github.com/KinkyDesign/JaqpotQuattro</u>
 - Access / download: <u>http://www.jaqpot.org</u>
 - License/waiver: GPL3

3.3.2. IMAGE DESCRIPTORS CALCULATION TOOL

Tool for automated calculation of descriptors from images of nanomaterials. The tool provides the user with a systematic framework for the automated analysis of microscopy images of nanomaterials and the calculation of nanoparticle descriptors (see also <u>Deliverable 4.2</u>).

- Architecture of tool / Technology: Web application / Java
- Source code: <u>https://github.com/enanomapper/imageAnalysis</u>
- Access: <u>http://app.jaqpot.org:8880/imageAnalysis/</u>
- License/waiver: GPL3

3.3.3. RREGRS

RRegrs is an R package for computer-aided model selection for multiple regression methodologies by means of an extensive cross-validation scheme. It is used to find the best regression models for any numerical dataset. The main use of the script is aimed at finding optimal and well validated QSAR models for chemoinformatics and nanotoxicology.

- Architecture of tool / Technology: R
- Source code, access, download: <u>https://github.com/enanomapper/RRegrs</u>
- License/waiver: MIT / BSD

3.3.4. TOXFLOW

toxFlow is a shiny web application for enrichment analysis and predictive read across modelling. If physicochemical and omics NP data are available both techniques can be applied in a sequential order. The tool has been developed by Dimitra D. Varsou during her undergraduate degree project.

- Architecture of tool / Technology: R
- Source code, access, download: <u>http://147.102.86.129:3838/</u>
- License/waiver: GPL3

3.3.5. CHIPSTER FOR NANOMATERIAL-BASED OMICS DATA ANALYSIS

Chipster is an open source user-friendly analysis software for high-throughput data analysis. It offers over 350 bioinformatics tools and it is constantly updated according to the latest state-of-the-art tools and scripts. Users can analyse and visualize data interactively, and share complete analysis sessions and automatic workflows with colleagues. Chipster supports the analysis of over 120 different microarray

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platforms, including the most common types by Affymetrix, Agilent and Illumina. In addition, Chipster has extensive functions and tools for the analysis of NGS data.

Chipster's client software uses Java Web Start to install itself automatically and connects to computing servers to perform the actual analyses. Chipster server can be also installed (free of charge) in the <u>EGI infrastructure</u> for European researchers. EGI and ELIXIR are currently planning to set up also a ready-made Chipster server for end users.

- eNanoMapper resources: <u>http://www.enanomapper.net/library/chipster-tool-analysis</u>
- Chipster website: <u>http://chipster.csc.fi/</u>
- Contact developers: <u>chipster@csc.fi</u>





3.3.6. NANO-LAZAR

lazar is a modular framework for read across predictions of chemical toxicities. Within the eNanoMapper project lazar was extended with capabilities to handle nanomaterial data, interfaces to other eNanoMapper services (databases and ontologies) and a stable and user-friendly graphical interface for nanoparticle read-across predictions. See also Annex 6.1 for nano-lazar prediction results output.

- Access: <u>https://nano-lazar.in-silico.ch</u>
- Development: <u>https://github.com/enanomapper/nano-lazar</u>
- Feedback: https://github.com/enanomapper/nano-lazar/issues
- Technology: Web application, Library / Ruby
- License / Waiver: GPL3



| Select an endpoi | lt. | |
|--|---|---|
| 1. Physchem 2. Phys | hem & Proteomics | |
| Model: Name: Protein Corona Finge Fype: regression Source: https://data.enanom Species: A549 human lung e fraining nanoparticles: 121 Endpoint: log2(Net cell asso Jnit: log2(ug/Mg) Prediction algorithm: local pl Prediction algorithm parame Veighbor algorithm paramet | ithelial carcinoma cells iation) yschem regression er: random forest n neighbors | articles log2(Net cell association) |
| ndependent crossvalidati Num folds: 10 Num instances: 121 Num unpredicted 0 RMSE: 1.81 MAE: 1.334 q2: 0.535 2MRF report download | Num folds: 10 Num instances: 121 Num unpredicted 0 RMSE: 1.848 MAE: 1.388 R ² : 0.515 | Num folds: 10 Num instances: 121 Num unpredicted 0 RMSE: 1.765 MAE: 1.352 R ² : 0.558 |
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| ntensity Mean Hydrodynam | Diameter / Human serum (Sigma #H4522) | |
| 109.21 | | |
| | | |

Figure 6. Nano lazar application

eNanoMapper





3.3.7. DESCRIPTORS AND MODELLING DEVELOPMENT TOOLS

3.3.7.1. GENE ONTOLOGY DESCRIPTOR (GO DESCRIPTOR) CALCULATION TOOL

An R package that calculates biological descriptors derived by clustering methodology of omics and Gene Ontology pathway data (see <u>Deliverable 4.2</u>).

- Technology: R
- License / Waiver: GPL3

3.3.7.2. NANO-LAZAR REST INTERFACE

The nano-lazar API Rest interface provides a Restful webservice and an interactive SWAGGER documentation to obtain OpenBabel, CDK and JoeLib descriptors for core and coating structures, QMRF reports and information on nano-lazar model, validation, dataset, feature and nanoparticles. Unit testing for nano-lazar rest is done with MiniTest library scripts.

- Access and API: https://enm.in-silico.ch/swagger
- Code: https://github.com/opentox/lazar-rest
- Feedback: https://github.com/opentox/lazar-rest/issues
- Testing: https://github.com/opentox/lazar-rest/tree/master/test
- Technology: Web application, Ruby
- License / Waiver: GPL3

3.3.7.3. CHEMISTRY DEVELOPMENT KIT DESCRIPTORS (STRUCTURAL DESCRIPTORS)

Nanomaterial descriptors implemented as part of the Chemistry Development Kit.

- Status: released
- Code: <u>https://github.com/cdk/cdk</u>
- Technology: Java
- License / Waiver: LPGL 2.1 or later





3.2.8. DOCUMENTATION ON MODELLING APPLICATIONS

Analysis and modelling

Applications

- <u>~ JaqPot Quattro</u>
 - API
 - Feedback
 - Source code
 - <u>Image Descriptor Calculation Web Tool</u>
 - Source code
 - <u>RRegrs Package</u>
 - ToxFlow Package
 - <u>Chipster for nanomaterial-based omics data analysis</u>
 - <u>Nano-lazar toxicity predictions</u>
 - Feedback
 - Descriptors and development tools
 - Gene Ontology descriptors
 - <u>~ Openbabel, Cdk and Joelib</u>
 - <u>Chemistry Develop Kit descriptors (structural descriptors)</u>
- User guidance
 - Tutorials
 - Modelling Services
 - JaqPot Quattro UI
 - JaqPot Quattro API
 - Image descriptor
 - RRegrs package
 - <u>Chipster tool for analysis</u>
 - Pathway analysis
 - <u>~ How to make a pathway</u>
 - Statistics analysis
 - AFFYQC web tool
 - o Webinars
 - <u>Cartering Protein corona</u>
 - Publications
 - Kohonen et al., 2014, Basic & Clinical Pharmacology & Toxicology
 - Tsiliki et al., 2015, Journal of Cheminformatics

• <u>~ DoW</u>

- <u>Sue tracker</u>
- Reporting
 - D4.1 Analysis and Modelling Specifications
 - <u>
 [•] D4.2 Descriptor Calculation Algorithms and Methods
 </u>
 - <u>~ D4.3 nQSAR Modelling infrastructure</u>
 - D4.4 Mechanism-of-action Modelling Tools
 - D4.5 Design of experiments and inter-laboratory testing facilities
 - 4.6 Tools for generating QMRF and QPRF reports





3.4 SUPPORT APPLICATIONS

3.4.1. AUTHENTICATION & AUTHORIZATION INFRASTRUCTURE

During the whole project the infrastructure for authentication and authorization, user management and user registration was maintained and updated to newest security standards. User registration, authentication and authorisation was fully described in Deliverable D5.2.

3.4.2. SUMMIT APPLICATION

The web-based application was created as a collaborative and support tool for nano-safety related events, with possible extension to other areas.

- Version 1.0 (<u>https://nanoehs.enanomapper.net/</u>) was used to support the U.S-EU NanoEHS workhop and the scrimmage (Arlington, 2016)
- Version 2.0 (<u>https://summit.enanomapper.net/</u>) was used to support the EU-U.S. NanoEHS workshop and breakout session (Rheinfelden 2016)

The functionalities of the summit application facilitate the interactions before, during and after the event:

- Add and create content and resources (e.g. publications, guidance documents, tools)
- Add topics and questions to be discussed
- Add comments and answers related to the topics
- Gather information and capture the discussions
- Support the reporting



Figure 7. Summit application functionalities





3.4.3. DOCUMENTATION ON USER APPLICATIONS, DISSEMINATION AND TRAINING

<u>User application development, integration & testing</u>

- DoW
 - o <u>~ Issue tracker</u>
 - o Reporting
 - <u>2 D5.1 Integrated Issue Management and Testing system</u>
 - <u>~ D5.2 User registration, authentication and authorisation</u>
 - <u>
 [~] D5.3 User application for importing NanoWiki data
 </u>
 - <u>~ D5.4 User application for importing NanoSafety Cluster data</u>
 - <u>~ D5.5 User application for searching and downloading eNanoMapper</u> <u>data</u>
 - D5.6 User application for conformance to reporting and curation standards
 - D5.7 Final report on User Applications
- Applications
 - o Summit

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- <u>Version 1.0</u>
- <u>~ Version 2.0</u>
- <u>~ GitHub</u>

<u>
 Dissemination & Training
 </u>

- <u>~ Publications</u>
- <u>~ Presentations</u>
- <u>~ Tutorials</u>
- <u>~ Webinars</u>
- <u>~ Events</u>
- DoW
 - o <u>~ Issue tracker</u>
 - o Reporting
 - <u>
 [~] D6.1 eNanoMapper Year 1 Dissemination Report</u>
 - <u>2 D6.2 eNanoMapper Year 2 Dissemination Report</u>
 - D6.3 eNanoMapper Tutorials
 - D6.4 eNanoMapper Community Development Report
 - D6.5 eNanoMapper Exploitation Report
 - D6.6 eNanoMapper Final Dissemination Report





4. PRIOTIZED CASE STUDIES

| Use case | Ontol ogy | Data base | Data Sear ch | Proto col Servi ce | JaqP ot Quat tro | RReg rs | Image Descri ptor Tool | toxFl ow | Chip ster | Nano- lazar | Modell ing descrip tors | SPARQ L endpoi nt |
|--|--------------|--------------|--------------------|-----------------------------|---------------------------|------------|---------------------------------|-------------|--------------|----------------|----------------------------------|----------------------------|
| 02. Design protocol | | | | | | | | | | | | |
| 04. Upload protocol | | | | Х | | | | | | | | |
| 05. Upload dataset | | Х | | | Х | | Х | Х | | | | |
| 06. Design study | | | | | Х | | | | | | | |
| 07. Search protocol | | | | Х | | | | | | | | |
| 08. Search dataset | | Х | Х | | Х | | | | | | | |
| 08. Search ENM | | | Х | | | | | | | | | Х |
| 10. Download dataset | | х | | | x | | | | | | | |
| 13. ISA-TAB creation and/or export | | х | | | | | | | | | | |
| 14. Build QSAR | | | | | Х | Х | Х | | | Х | Х | |
| 17. Validate model | | | | | Х | Х | | Х | | х | | |
| 20. Create template (xls etc) | | | | | | | | | | | | |
| 21. Map nanomaterial to biological pathway | х | | | | | | | x | x | | x | |
| 23. Search for all knowledge of nanomaterial X | х | | X | | | | | | | | | |
| 27. Find/ link related data sources | | х | | | | | | Х | | | х | |
| 29. Save my data in format X | х | х | | | Х | х | | Х | | | | |
| 33. What URI to use for X | | | | | | | | | | | | |
| 34. Give me all names for ontology term A | х | | | | | | | | | | | |
| 36. Harmonize Terminology | х | | | | | | | | | | | |
| 38. Find ontological contradiction | х | | | | | | | | | | | |
| 39. Comp aided ENM design | | | | | X | | | | | | х | |





| 44. Find producer of eNM C | | X | | | | | | | |
|--|---|---|---|---|--|---|--|---|--|
| 45. Find QC data of eNM C | | | | | | | | | |
| 49. Map nano material found in DB 'A' to an entry in DB 'B' | | x | | | | | | | |
| 50. Find all DB's with data of Paper X | | | x | | | | | | |
| 52. Register and get access (public) | | X | | x | | | | | |
| 53. Map existing used schemas to ontology IDs (e.g. OECD harmonized templates) | х | | | | | x | | х | |
| 54. Annotation of data with ontology IDs (e.g. experimental data in ISA-Tab) | x | | | | | | | | |
| 55. Experimental design | | | | x | | | | | |





5. CONCLUSION

A modular infrastructure was developed in order to achieve the main goal of the project in offering viable solutions to the nanosafety community regarding the data management (e.g. sustainable data storage) and data use (e.g. modelling). Therefore, eNanoMapper worked on developing of tools for data storage and analysis, information exchange and reporting of research (nano) data, but also towards creating a community framework for interdisciplinary collaboration in the area of nanosafety.

Therefore, the eNanoMapper team have: i) developed a nano ontology for the categorization and characterization of nanomaterials, ii) developed and implemented a modular infrastructure for data storage, sharing and searching, based on open standards and semantic web technologies, and iii) created and tested different computational modelling tools and services for nanomaterials safety assessment.

Overall, the application infrastructure developed within eNanoMapper is able to offer reliable data management solutions and facilitate the integration of experimental data into risk assessment by using different computational models.

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Figure 8. eNanoMapper documentation map





6. ANNEXES

6.1 NANO-LAZAR RESULTS OUTPUT

Nano-lazar presents predictions in tabular form with the query nanoparticle on top followed by similar nanoparticles for the local QSAR model. Each nanoparticle is characterised by its similarity to the query compound, endpoint measurements and the properties relevant for the particular endpoint. If the query nanoparticle is part of the training data (as in this example) all information from this substance is removed from the training set before making the prediction. In this case the measured value is displayed for comparison purposes.

| ID \$ | Similarity v | Composition \$ | Toxicity Net cell association ≎ [mL/ug(Mg)] | Localized Surface Plasmon Resonance (LSPR) index / Human serum (Sigma #H4522) | Intensity Mean Hydrodynamic Diameter / Human serum (Sigma #H4522) | ZETA POTENTIAL / Human serum (Sigma #H4522) | ZETA POTENTIAL [‡] | Autot (ICP-AES) / Human serum (Sigma #H4522) | Core size ♀ |
|-----------------|-------------------------|--|---|--|--|--|--------------------------------|---|----------------|
| G15.Ser-SH | 1 | Core: [Au] | Prediction: -4.813 95% Prediction interval: -6.093.53 Measurement: -5.224 | 0.406 | 83.08 | -8.73 | -20.4 | 253.215 | 14.9 |
| G15.Asn-SH | 0.832 | Core: [Au] Coating: Thiolated L-asparagine | Measurement: -5.676 | 0.327 | 68.92 | -8.29 | -20.27 | 240.177 | 14.9 |
| G15.Gly-SH | 0.796 | Core: [Au] Coating: Thiolated L-glycine | Measurement: -4.975 | 0.403 | 74.16 | -5.68 | -17.77 | 243.954 | 14.9 |
| G15.NT@PSMA-EDA | 0.765 | Core: [Au] Coating: 2-Naphthalenethiol | Measurement: -5.403 | 0.363 | 87.24 | -7.57 | -18.3 | 237.624 | 14.9 |
| G15.Ala-SH | 0.747 | Core: [Au] Coating: Thiolated | Measurement: -5.505 | 0.275 | 63.72 | -6.73 | -24.08 | 247.019 | 14.9 |

6.2 ENM ONTOLOGY VIEWER GRAPHICAL AND FILE OUTPUT FORMATS

The eNM Ontology Viewer application is a three page, tab-structured interface. The "Viewer" page has a SPARQL interface contains a query template that collects all corresponding triples by the keyword "endpoint". The user has the possibility to choose between two types of graphical representation of the query results. "Dendrogram" and "Sunburst" (Figure 10).







Figure 10. Select option for rendering results.

The output option "Dendogram" is a tree based vector graphic representing the relations of nodes in the triples of the query result (Figure 11). The request is handled in real-time by the client browser.



Figure 11. Dendrogram corresponding nodes

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The "Sunburst" option generates an interactive pie chart vector graphic (Figure 12), that allows us to navigate through the levels of the result by clicking the colored fields in the graphic (Figure XY). Each color represents a binding of a node. By click on a colored field the graphic will zoom in so that this field gets the center of the graphic.



Figure 12. Sunburst interactive pie chart.







Figure 13. Click on colored fields brings up a deeper level of the pie chart

The "SPARQL" page contains a user interface (Figure 13) to execute SPARQL queries and download the result in various formats as a file. Furthermore, it contains some examples to select. "text/html" selected as output format also allows to render the result direct to the page. In this HTML table eNanoMapper ontology URIs link direct to the specific entry in the Bioportal service (http://bioportal.bioontology.org/ontologies/ENM). On Bioportal all visits to the eNanoMapper ontology get counted and visualized in a diagram.





| VIEWER SPARQL HELP | | | | |
|---|--|--|-----------------|-----------------|
| PREFIX chebi: <http: chebi_="" obo="" purl.obolibrary.org=""> PREFIX npo: <http: obo="" purl.obolibrary.org=""></http:> PREFIX obo: <http: obo="" purl.obolibrary.org=""></http:> PREFIX bao: <http: bao#="" www.bioassayontology.org=""> PREFIX sio: <http: bao#="" www.bioassayontology.org=""> PREFIX sio: <http: resource="" semanticscience.org=""></http:> SELECT DISTINCT ?resource ?epLabel ?value ?unit WHERE { ?resource a chebi:59999 . OPTIONAL { ?resource obo:BFO_0000056 ?feature . ?feature a ?featureType ; obo:OBI_0000299 ?endpoint . ?endooint sio:has-value ?value : text/html</http:></http:></http:> | Example Physico-Chemia • Particle Size • All ENMs ha • Surface cha | cal Characte (Distribution) ve at least of | eristics on) | mical component |
| resource | epLabel | value | unit | |
| https://data.enanomapper.net/substance/NWKI-71060af4-1613-35cf-95ee-2a039be0388a | PARTICLE SIZE | 76.0 | nm | |
| https://data.enanomapper.net/substance/NWKI-895a506b-c331-3576-bf9e-cbcde5822c11 | PARTICLE SIZE | 73.0 | nm | |
| https://data.enanomapper.net/substance/NWKI-895a506b-c331-3576-bf9e-cbcde5822c11 | PARTICLE SIZE | 63.0 | nm | |

Figure 14. Graphical user interface to write SPARQL queries

A variety of output formats can be selected by a drop-down menu that is divided into SELECT and CONSTRUCT parts (Figure XY). The result clause (SELECT or CONSTRUCT) determines the associated output format that can be used.

| SELECT application/json | | |
|--|-----------------------|--|
| application/rdf+xml | | |
| application/sparql-results+json | | |
| application/sparql-results+xml | | |
| application/vnd.ms-excel | D2/22-rdf-syntax-ns#> | |
| text/csv | /01/rdf-schema#> | |
| text/html | | |
| text/n3 | | |
| text/plain | | |
| text/tab-separated-values text/turtle | | |
| CONSTRUCT | | |
| application/ld+json | | |
| application/microdata+json | | |
| application/odata+json | | |
| application/rdf+json | | |
| application/rdf+xml | | |
| application/turtle | | |
| application/x-turtle | | |
| application/json | ✓ download | |

Figure 15. Select output format by SPARQL result clause

| eNano | Ларрег |
|-------|--------|
|-------|--------|