

# **FSK-ML**

## **Food Safety Knowledge Markup Language**

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# Federal Institute for Risk Assessment



<b>Established</b>	November 2002 (predecessor founded in 1876)
<b>Annual budget</b>	Ca. 65 Mio €
<b>Research budget</b>	Ca. 6 Mio €
<b>Staff</b>	Ca. 750 employees (550 scientists)
<b>Location</b>	Berlin

## BfR - Areas of work

- Microbiological and substance-chemical safety and assessment of foods
- Safety and assessment of substances (chemicals, plant protection products, biocides)
- Selected products (commodities, cosmetics, tobacco products, textiles, ...)
- Risk communication
- Research
- Alternatives to animal experiments where the safety of substances can be determined



Available online at [www.sciencedirect.com](http://www.sciencedirect.com)

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International Journal of Food Microbiology

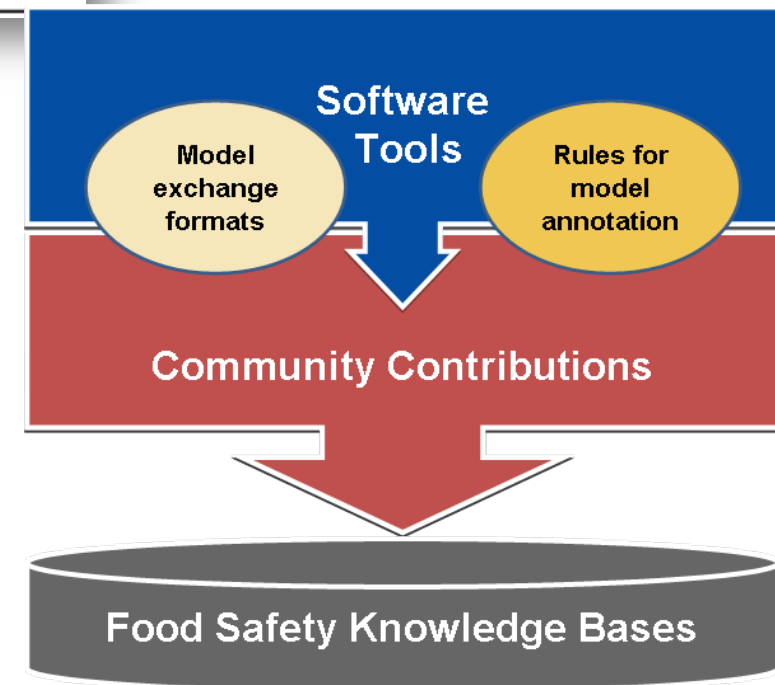
INTERNATIONAL JOURNAL OF  
Food Microbiology

[www.elsevier.com/locate/ijfoodmicro](http://www.elsevier.com/locate/ijfoodmicro)

## A strategy to establish Food Safety Model Repositories

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[http://www.researchgate.net/publication/273791203\\_A\\_strategy\\_to\\_establish\\_Food\\_Safety\\_Model\\_Repositories](http://www.researchgate.net/publication/273791203_A_strategy_to_establish_Food_Safety_Model_Repositories)

# Step 1.: Standardized Data format for Models

## Predictive Modelling in Food Markup Language (PMF-ML)

Software Developer Guide  
Version 1.0

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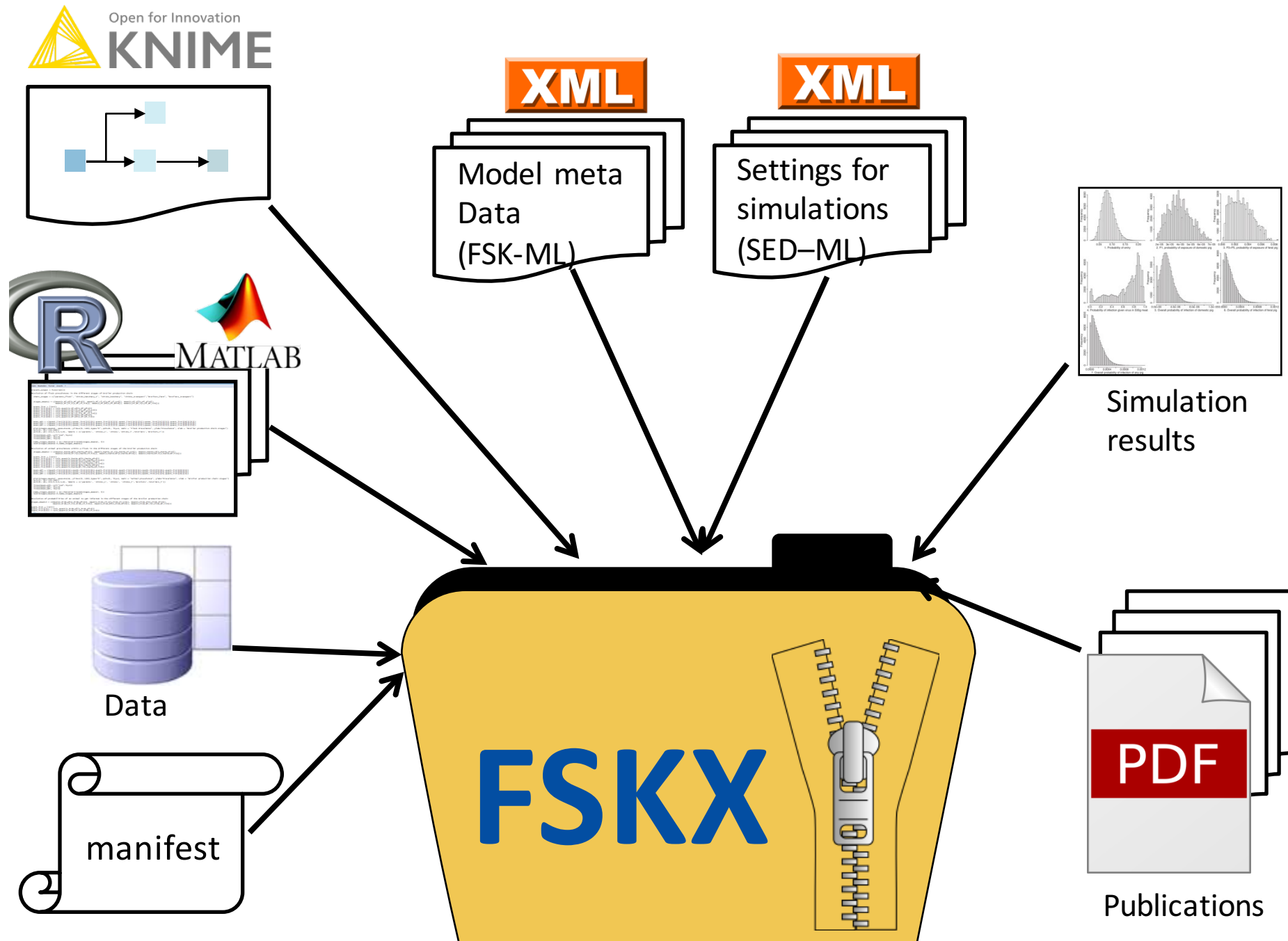
- ✓ Based on SBML v3
- ✓ Mathematical expressions encoded as MathML
- ✓ Meta data encoded using domain-specific controlled vocabularies

The screenshot displays an SBML model editor interface. On the left, a 'Tree View' shows the hierarchical structure of the model, including elements like 'sbml', 'model', 'listOfSpecies', 'species', 'listOfParameters', and 'parameter'. On the right, the 'XSL Output' shows the corresponding XML representation of the model. The XML includes metadata such as version, encoding, and standalone status, as well as model-specific data like compartment names, species names, and parameter values.

```
<?xml version="1.0" encoding="UTF-8" standalone="no">
  <!-- Created by SBML Writer node version 1.0 on 2015-09-10 at 14:09:10 MEZ with JSBML version... -->
  <sbml xmlns="http://www.sbml.org/sbml/level3/version1/core" level="3"
    xmlns:comp="http://www.sbml.org/sbml/level3/version1/comp/version1"
    comp:required="true" version="1">
    <annotation>
      <salml25>
        Three-Phase Linear Model (Buchanan et al., 1997) - 1PMP Full Growth Models Eq 8 log10()...
      </salml25>
    </annotation>
    <model>
      <id>
        <name>
          culture_broth_broth_culture_culture_medium
        </name>
      </id>
      <listOfUnitDefinitions>
        <unitDefinition>
          <constant>
            <name>
              culture broth, broth culture, culture medium
            </name>
          </constant>
        </unitDefinition>
      </listOfUnitDefinitions>
      <listOfSpecies>
        <species>
          <id>
            <constant>
              <name>
                salmonella spp
              </name>
            </constant>
          </id>
          <boundaryCondition>
            <false>
              log10_count_g
            </false>
          </boundaryCondition>
          <substanceUnits>
            <value>
              culture_broth_broth_culture_culture_medium
            </value>
          </substanceUnits>
          <compartment>
            <name>
              culture_broth_broth_culture_culture_medium
            </name>
          </compartment>
        </species>
      </listOfSpecies>
      <listOfParameters>
        <parameter>
          <id>
            <constant>
              <value>
                0
              </value>
            </constant>
          </id>
          <units>
            <h>
              k
            </h>
          </units>
          <value>
            <true>
              0.014365402911347337
            </true>
          </value>
          <units>
            <dimensionless>
            </dimensionless>
          </units>
        </parameter>
      </listOfParameters>
    </model>
  </sbml>
</pre>
```

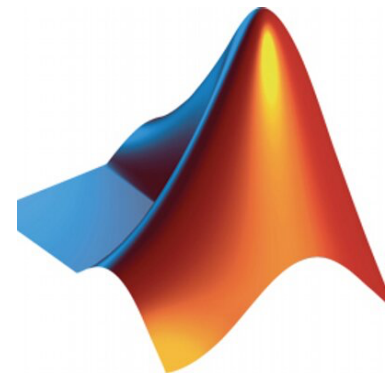
<http://sourceforge.net/projects/microbialmodelingexchange/>

## Step 2: Standardized Data Format for Script-based Models



## Step 2: Standardized Data Format for Script-based Models

- PMF-ML extended for allowing the exchange of knowledge embedded in script programming languages
- Goal: Harmonization of the exchange of food safety knowledge (like predictive models)
- New COMBINE-based format:
  - Parameterized model + model meta data
  - No more rules: Math no longer in SBML but a script
  - Model meta data in PMF-ML
- Software dependent
- Introduce a COMBINE-based format:
  - Parameterized models + Model metadata
- Parameterized models written in script-based programming languages (R, Matlab or Python)
- Model metadata written in PMF-ML
  - Extended SBML (Predictive Modelling in Food Markup Language)



# FSK Terminology

## Model

- Mathematical description of a system
- May be parameterized → Models may carry predefined values obtained in a parameter fitting process
- Parameter**. Variables with predefined values
- Example**. Parameterized model based on experimental data on the growth of a certain pathogen within a temperature range.

## Simulation

- Model-based predictions generated from different parameterizations of the same model
- Simulation settings in SEDML (parameters values, simulation type, etc.)
- Simulation results in NuML



# FSK types

```
# Examples of scalar data types
pi = 3.14
year = 2016
name = "Miguel, Lord of Westeros"
```

```
# Vectors
```

```
cookies_per_meeting <- c(10, 5, 20, 15, 10)
cookies_per_meeting <- c(10, "fünf", 20, "fünfzehn", 10)
cookies_per_meeting <- c("zehn", "fünf", "zwanzig", "fünfzehn",
                          "zehn")
```

```
# Matrices
```

```
menus = matrix(
  c("Hänschen", "Reis", "Fishfilet", "Geschnezeltes", "Spinach",
    "Boulette"),
  nrow = 2, ncol = 3, byrow = TRUE,
  dimnames = list(
    c("Menu 1", "Menu 2"), c("Montag", "Dienstag", "Mittwoch")))
```

Supported types in FSK	
Numeric	Real numbers
Integer	integer
Character	Strings
Vector	1D array
Matrix	2D array

# FSKX file – model script and libraries

## Model script

Script stored within the FSKX archive that calculates the values of the model.

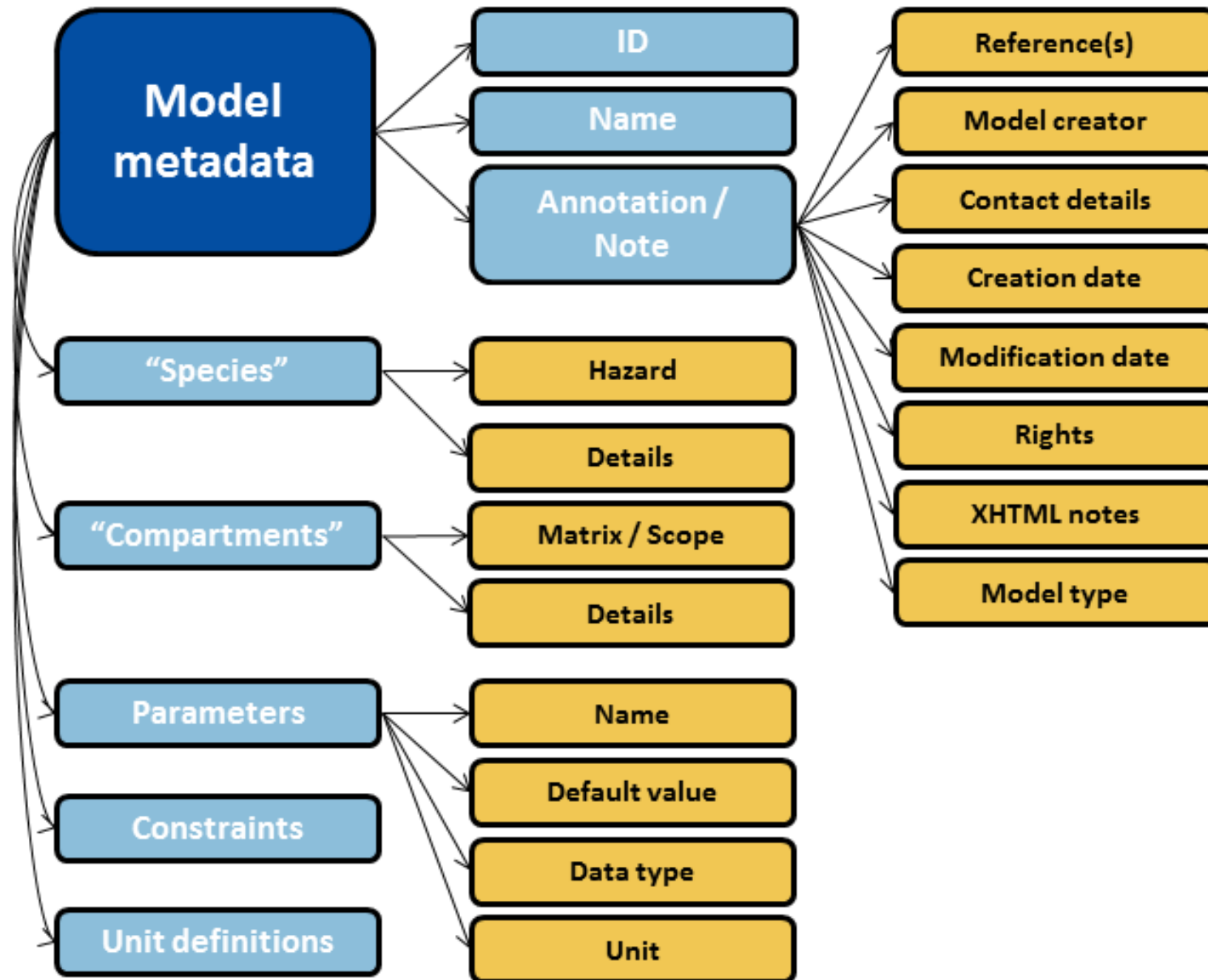
```
#####  
test_model_1 = function(a, b, c){  
  res = 100*(rbeta(a, shape1 = b + 1, shape2 = c - b + 1))  
  return(res)  
}
```

**Model script example**

## (Binary) libraries

- All the required libraries for the model execution must be provided
- The location in the archive is free

## FSKX file – Model meta data (PMFML)



### Model meta data

# Simulation files

## FSK-SED-ML files

- Extended SED-ML describing the simulation of a model
  - Parameter values
  - Type of simulation: deterministic, statistic or probabilistic
  - Output with the simulation results

## Visualization scripts

- Scripts with commands to generate a visualization with the simulation results
- May be referenced or embedded in FSK-SED-ML files

```
hist(test_model_1(200, 20, 100), breaks=50, main="Headline", xlab="Text", col="32")
```

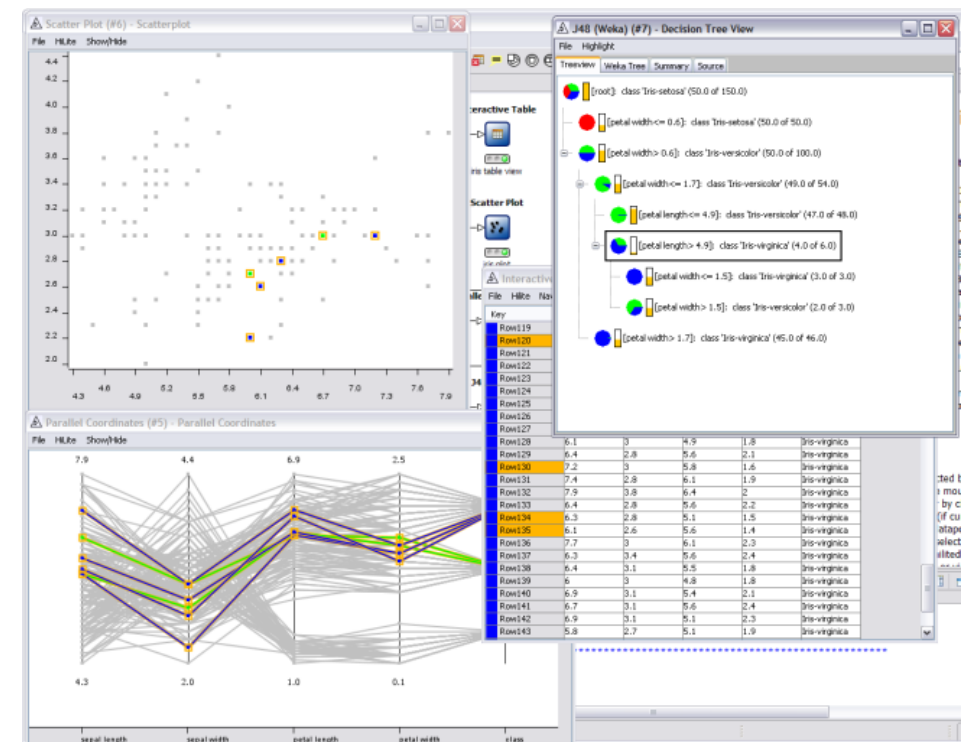
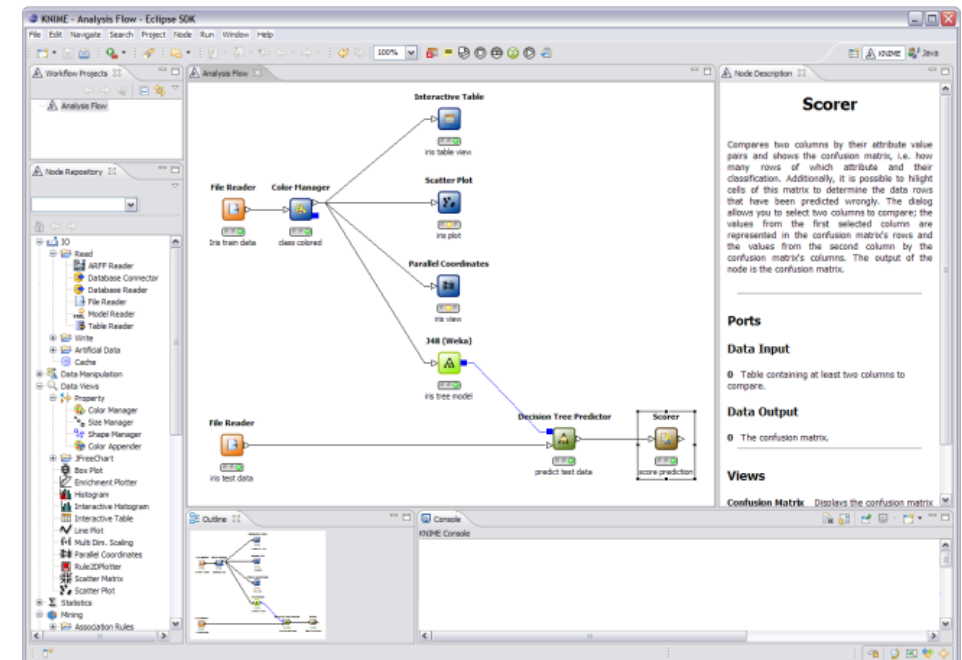
**Example visualization script**

## Results NuML

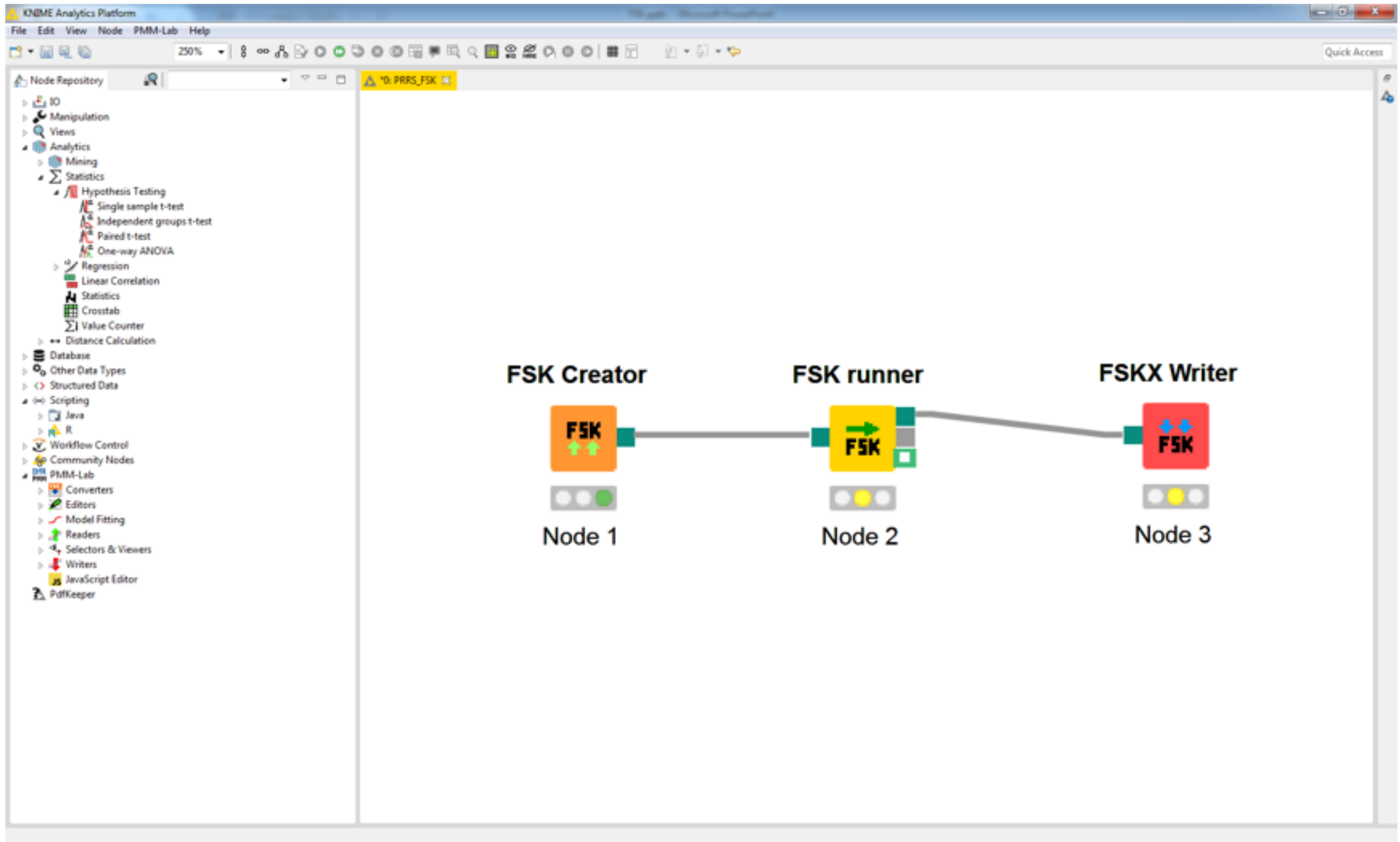
- Results of the model encoded in NuML
- Supported data types: numeric, integer, character, vector and matrix



- Konstanz Information Miner
- Created and hosted by KNIME.com
- 1<sup>st</sup> version released in '06
- Free of charge, OpenSource
- Uses:
  - Data extraction
  - Transformation
  - Modelling
  - Data analysis

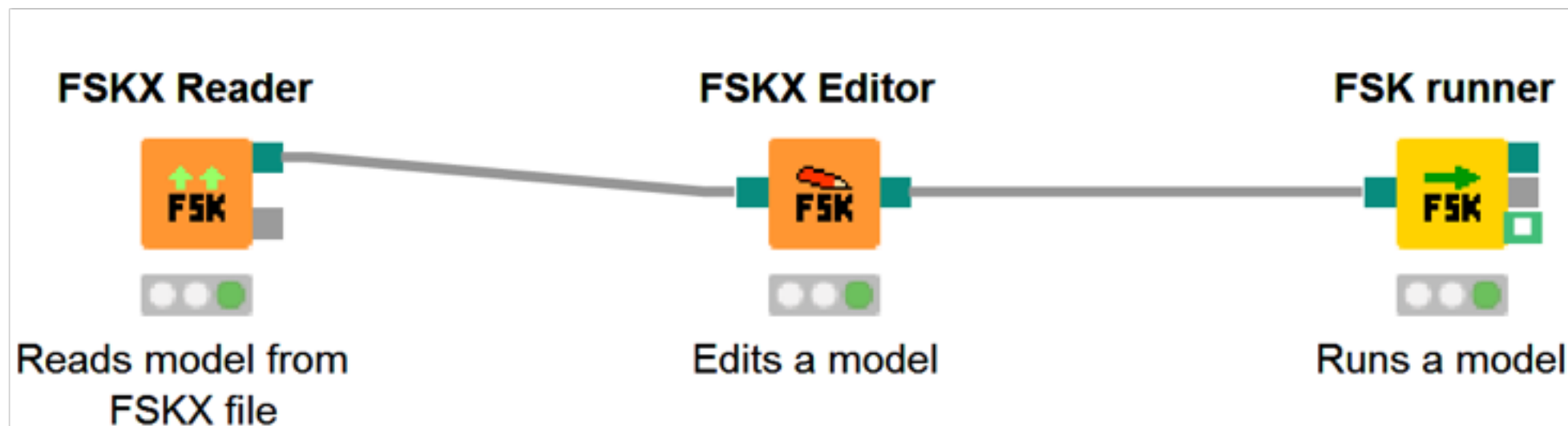
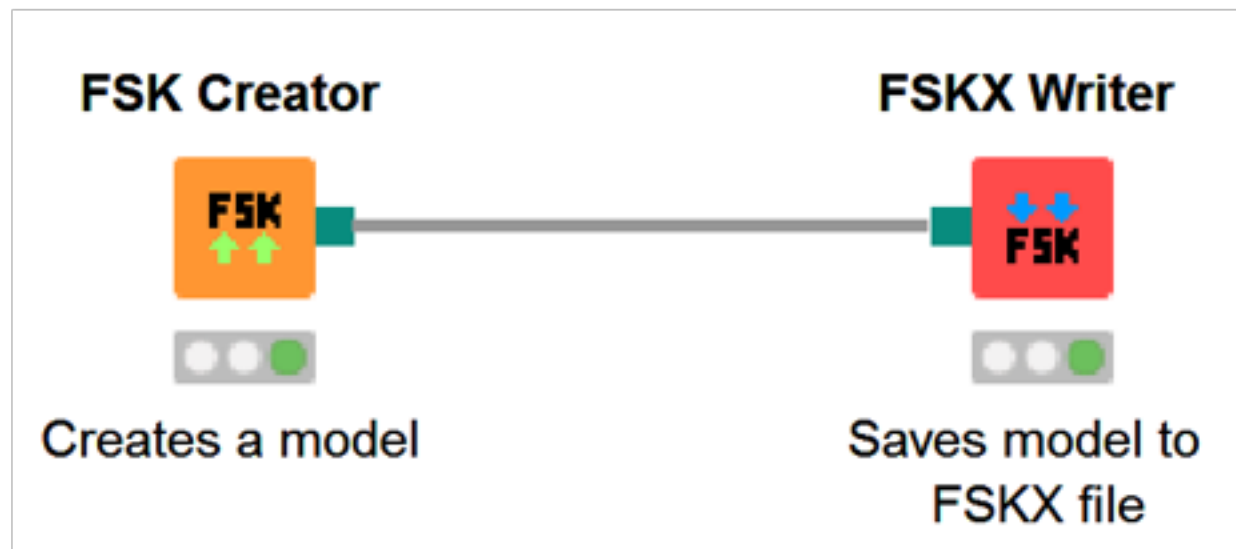
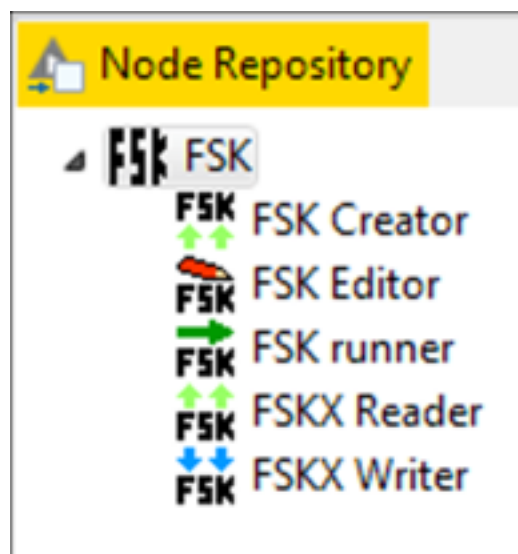


# Implementation in detail



**Basic workflow to create an FSK model, run it and store it into a local file**

# Implementation in KNIME



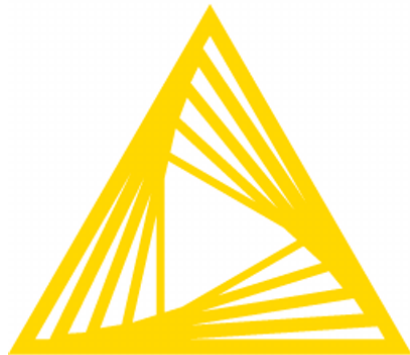
## Implemented FSK KNIME nodes

# Want to play?

**Binary builds available in SourceForge**

<https://sourceforge.net/projects/pmmmlab/>

- KNIME build with PmmLab plugins

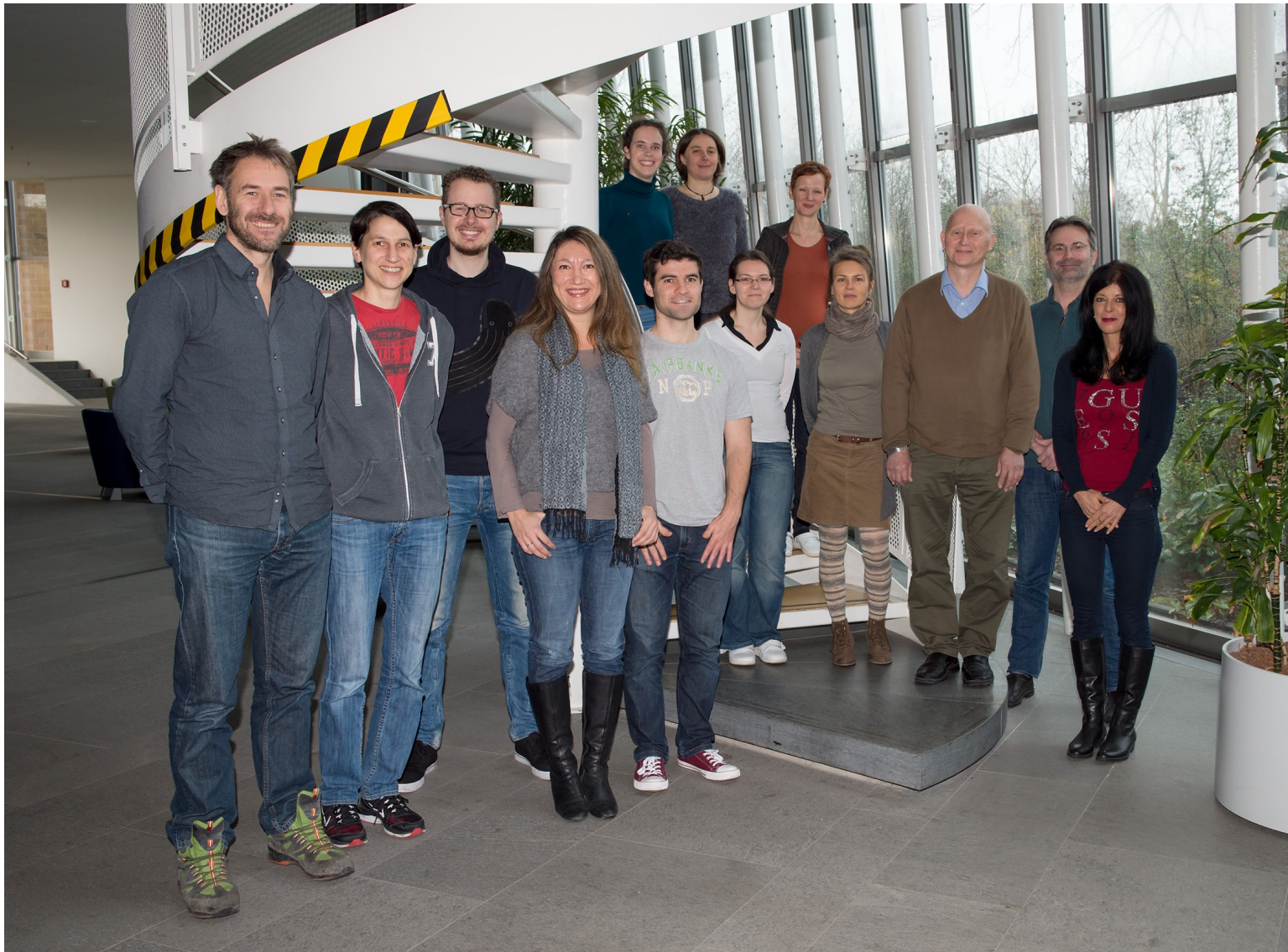


## Vanilla KNIME

- PmmLab is installable with the update site
- <http://dl.bintray.com/silebat/test/>



# Acknowledgments



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- Christian Thöens
- Armin Weiser

**BfR Group 43: Biological Safety**

**Thank you for your attention**

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