



## Implementing a Cheminformatics Workflow Environment from Scratch in Medium-Sized Pharma Company - Lessons Learned

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**Berlin, November 4th 2021**

# Nuvisan Innovation Campus Berlin

- Fully integrated Science contract research organization specializing in drug discovery and development
- Areas of research:
  - Lead Discovery
  - Life Science Chemistry
  - Therapeutic Research
  - Preclinical Compound Profiling
  - Digital Life Science
- We needed the platform that will:
  - Enable the implementation of different workflows for the processing, analysis and predictive modeling of chemical data
  - Enable sharing of the developed workflows across the organization with ensured data privacy
  - Be budget-friendly

# KNIME at Innovation Campus Berlin: Infrastructure



## KNIME Analytics Platform

- Implementation of project-specific workflows within Digital Life Science

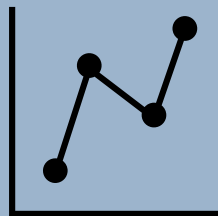
## KNIME Server

- Implementation of various apps that are available to different departments
- Currently accessible through WebPortal, integration with other analytics platforms (e.g., TIBCO Spotfire®) is planned
- Technical details:
  - KNIME Server Large license split into two licenses for development and production server
  - Hosted on Virtual Machine with Ubuntu 20.04.3 LTS

# KNIME at Innovation Campus Berlin: Use cases

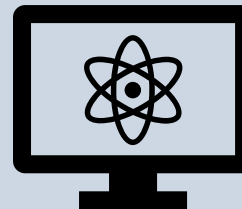
## Data wrangling and analysis

Processing of different file formats, integration of different data sources, generation of user-friendly output,...



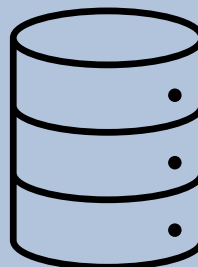
## Cheminformatics-specific application

Prediction of molecular properties, clustering, tools for structure-activity relationship (SAR) analysis,...



## Database mining

Retrieval of the information from the Life Science Database, analysis of the retrieved data and generation of the output in various file formats,...



# Example workflow: Calculation of molecular properties

## Select properties

### Excludes

logD@pH7.5  
Molecular Weight  
TPSA  
Rotbonds  
Solubility@pH6.5(mg/L)



### Includes

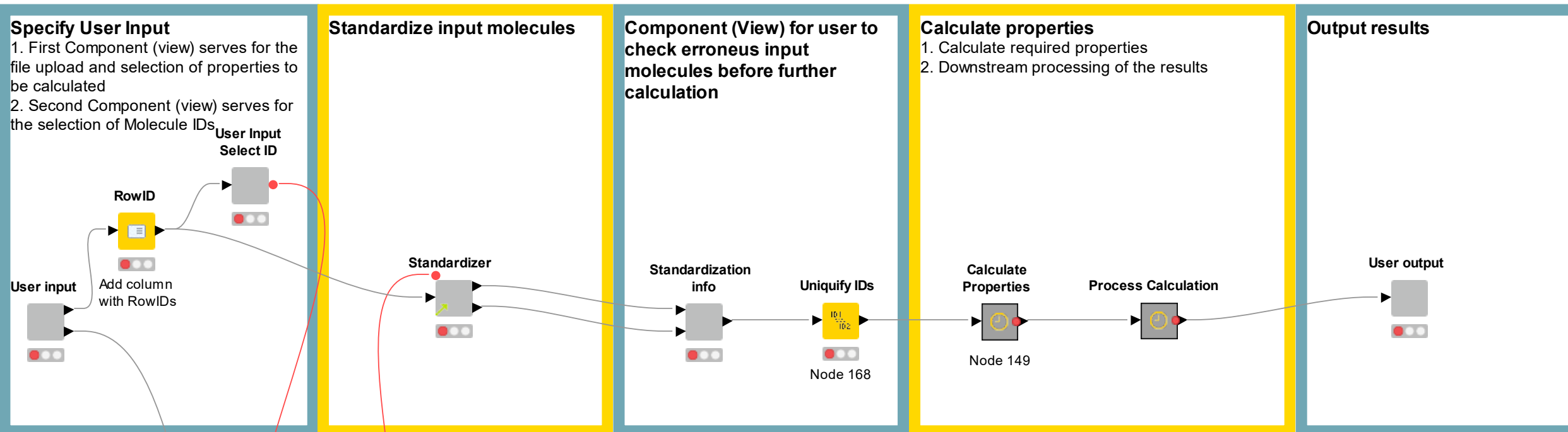
## Upload .sdf file

Select file

sample\_set.sdf

User input: File upload and selection of properties in the WebPortal

# Example workflow: Overview



Helper functionality to handle user selection of the properties for the user output and python environments

Column Select

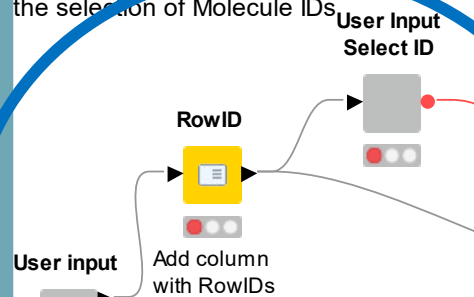
## Calculation of different properties

Calculation of different properties (Molecular Weight, Solubility, LogD, CYP inhibition,...) either directly via various chemistry integrations in KNIME (e.g. RDKit, CDK, Indigo, Vernalis,..) or by implementing machine learning models based on the *in-house* life science data

# Example workflow: User input

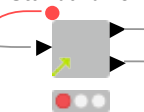
## Specify User Input

1. First Component (view) serves for the file upload and selection of properties to be calculated
2. Second Component (view) serves for the selection of Molecule IDs



## Standardize input molecules

### Standardizer

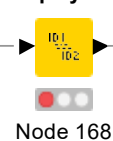


## Component (View) for user to check erroneous input molecules before further calculation

### Standardization info



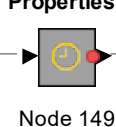
### Uniquify IDs



## Calculate properties

1. Calculate required properties
2. Downstream processing of the results

### Calculate Properties



### Process Calculation



## Output results

### User output



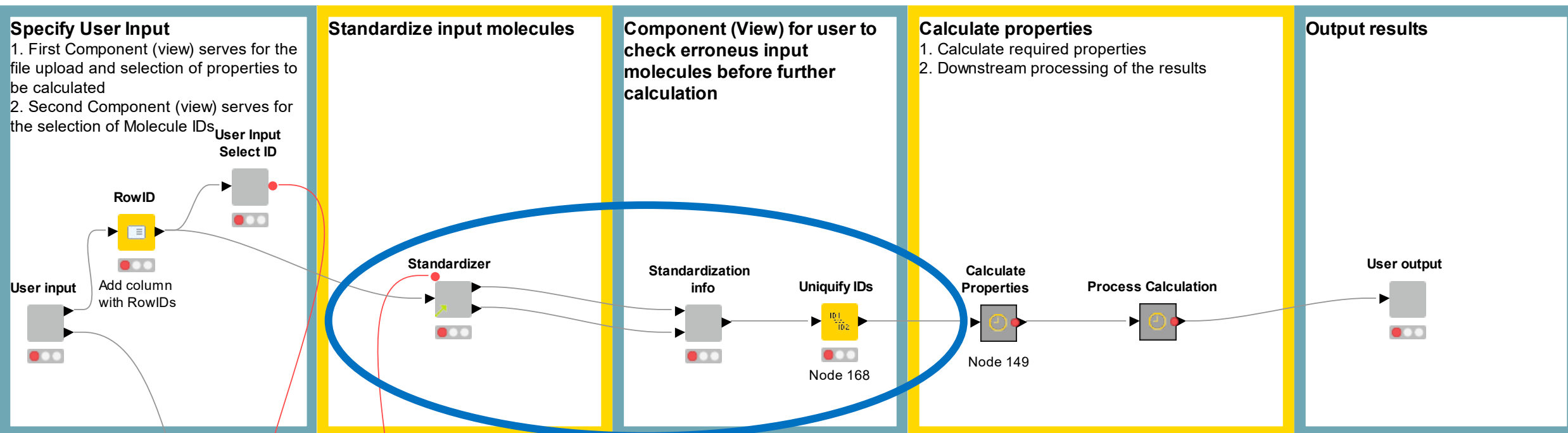
Helper functionality to handle user selection of the properties for the user output and python environments

### Column Select



User Input

# Example workflow: Standardization of the molecules



Helper functionality to handle user selection of the properties for the user output and python environments

Column Select

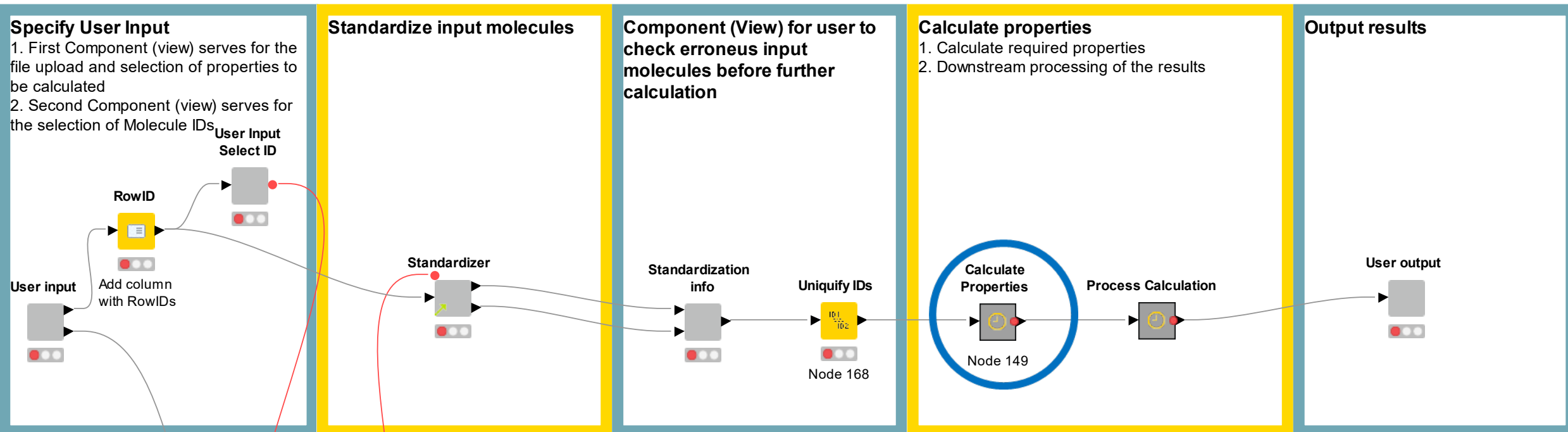
## Standardizer

Structure standardization and check-up is mostly based on this very useful Python package:

[https://github.com/chembl/ChEMBL\\_Structure\\_Pipeline](https://github.com/chembl/ChEMBL_Structure_Pipeline)



# Example workflow: Calculation of properties



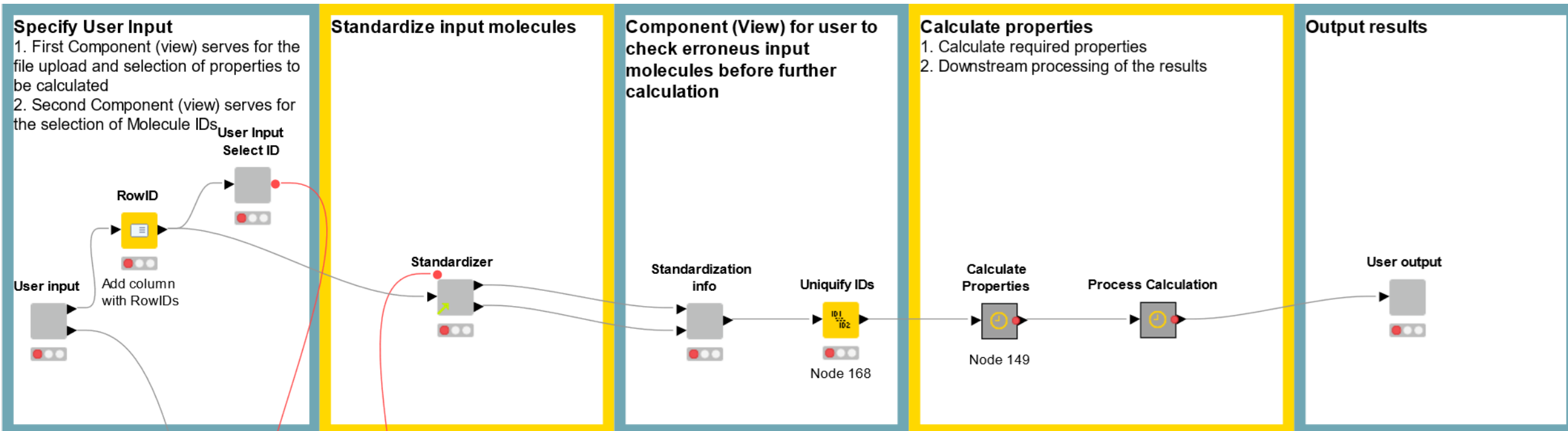
Helper functionality to handle user selection of the properties for the user output and python environments

Column Select

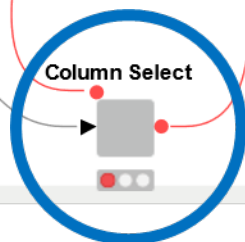
## Integration with other programming languages

Machine learning models and different python-based scripts (or other programming languages) can be implemented easily using Python Integration Nodes

# Example workflow: Specifying different environments



Helper functionality to handle user selection of the properties for the user output and python environments



## Using multiple python environments

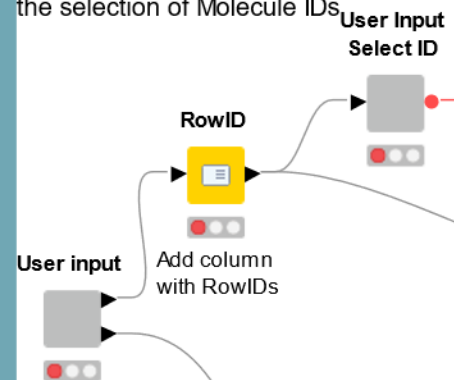
Different environments (e.g conda or pyenv) per each node can be used by specifying the paths using flow variables

[https://docs.knime.com/latest/python\\_installation\\_guide/index.html#configure\\_python\\_integration](https://docs.knime.com/latest/python_installation_guide/index.html#configure_python_integration)

# Example workflow: User output

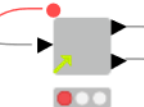
## Specify User Input

1. First Component (view) serves for the file upload and selection of properties to be calculated
2. Second Component (view) serves for the selection of Molecule IDs



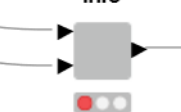
## Standardize input molecules

### Standardizer

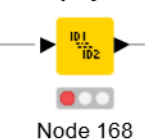


## Component (View) for user to check erroneous input molecules before further calculation

### Standardization info



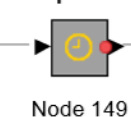
### Uniquify IDs



## Calculate properties

1. Calculate required properties
2. Downstream processing of the results

### Calculate Properties

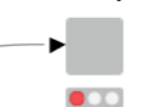


### Process Calculation



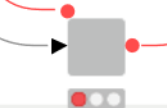
## Output results

### User output



## Helper functionality to handle user selection of the properties for the user output and python environments

### Column Select



# Example workflow: User output in WebPortal

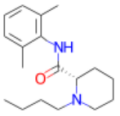
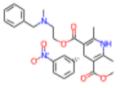
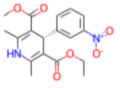
Download

[Download Results \(sdf\)](#)

Results

Show  entries

Search:

<input type="checkbox"/>	Structure	ID	Molecular Weight	Rotbonds
<input type="checkbox"/>		levobupivacaine	288.22	5
<input type="checkbox"/>		(S)-nicardipine	479.21	9
<input type="checkbox"/>		(S)-nitrendipine	360.13	5

## User output: Display of results in WebPortal

If you want to color the cells in the WebPortal, check this cool snippet!

[https://kni.me/w/Q-E\\_6XmNXVqQ\\_WgV](https://kni.me/w/Q-E_6XmNXVqQ_WgV)

## Additionally,

If you are interested in pptx, pdf,... reports, check the BIRT integration in KNIME:

<https://www.knime.com/getting-started-knime-birt>

## Lessons learned

- Always check the output of the nodes! Anything that can go wrong will go wrong.
- In case you need to implement specific, more complex functionality:
  - Check <https://hub.knime.com/>
  - If there is no available KNIME implementation, try to implement it yourself (Python, R or whatever programming language you prefer) and integrate in KNIME environment. There is a good chance that someone already implemented what you are looking for in other programming language.
- If you have any questions or encounter any problems:
  - First check <https://forum.knime.com/>
  - If you still don't find a solution, contact KNIME support
  - This may save you lots of time and energy

# Team

- Vysalini Akshintala
- Andreas Bender
- Chetan Chintha
- Jörg Fanghänel
- **Andreas Göhrig**
- **Nadine Homeyer**
- **Christopher Linn**
- David Machalz
- Franz von Nussbaum
- Gaus Reza
- Holger Steuber
- **Franziska Witte**

Also, we are hiring! Check the positions on  
<https://career.nuvisan.com/>.