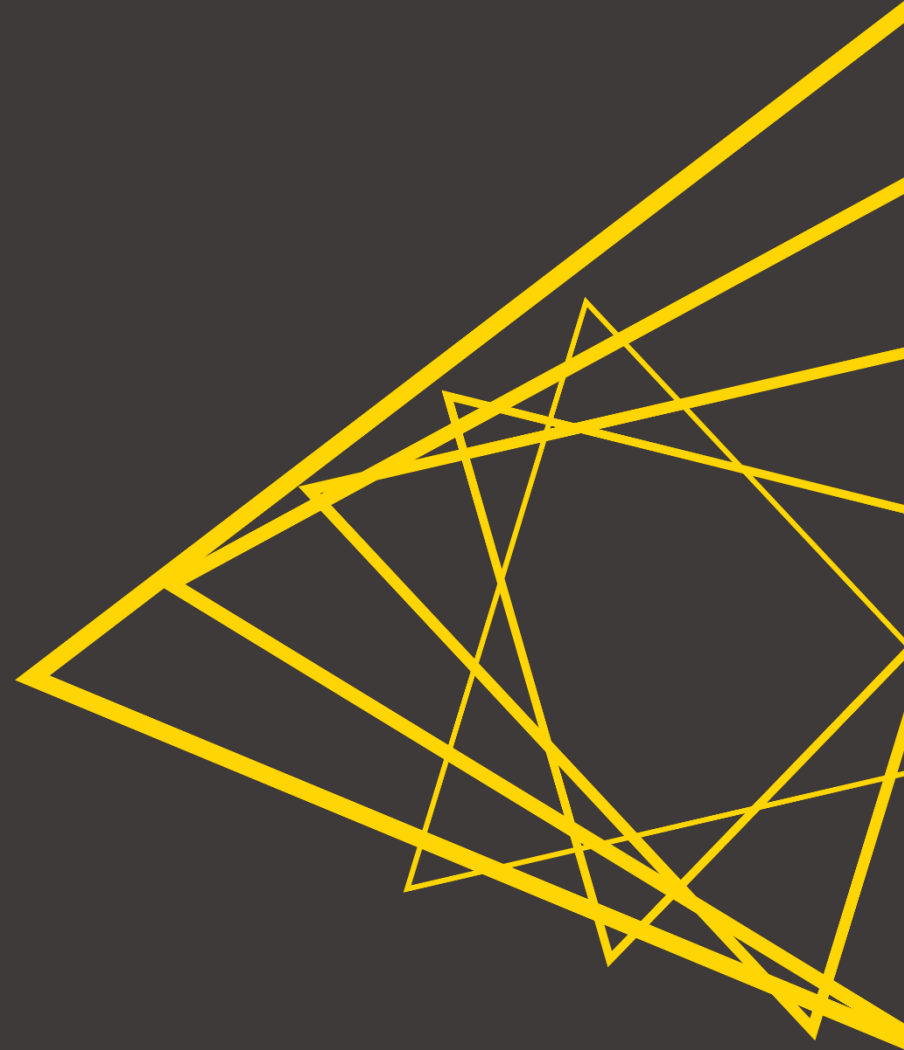


Boston Workshop

Monday, June 12 2023

Dr. Alice Krebs

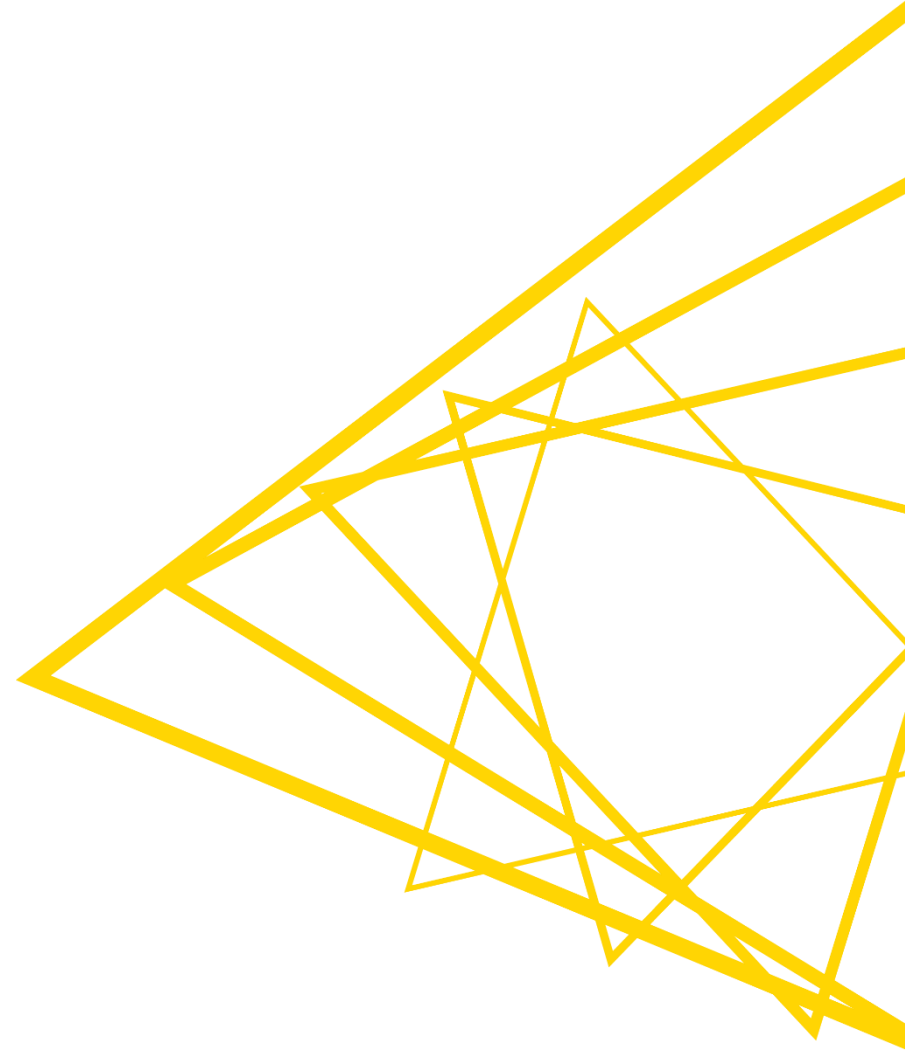


Before we get started...

... some questions for you:

- What tools are you using for data analysis?
- What do you expect/hope to learn today?
- Did you manage to open the “00_Setup” workflow already?

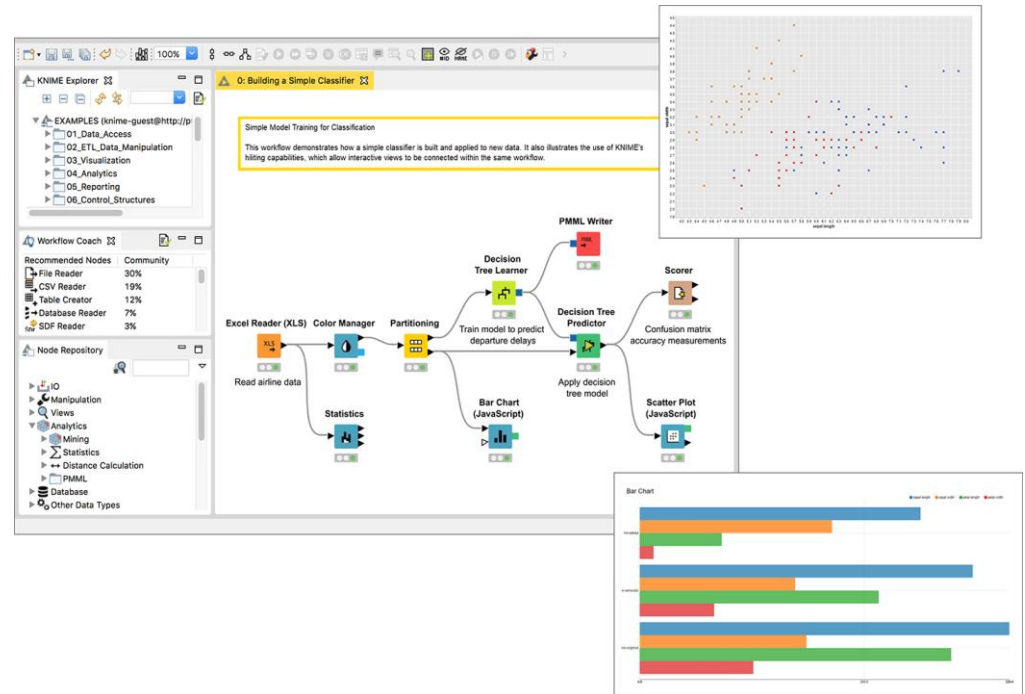
Introduction to KNIME Analytics Platform



What is KNIME Analytics Platform?

- A tool for data analysis, manipulation, visualization, and reporting
- Based on the graphical programming paradigm
- Provides a diverse array of extensions:

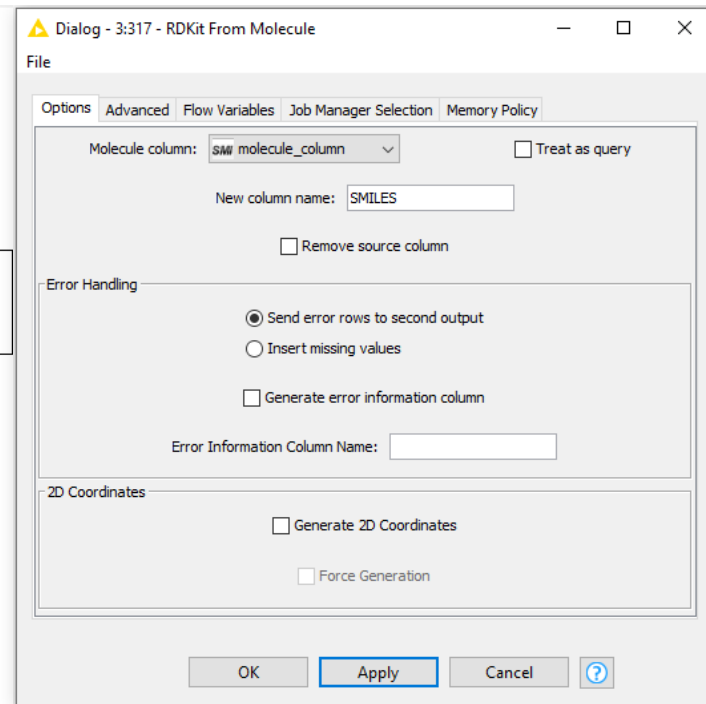
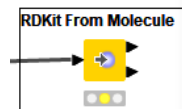
- Text Mining
- Network Mining
- Cheminformatics
- Many integrations, such as Java, R, Python, Weka, Keras, Plotly, H2O, etc.



Graphical programming paradigm?

- Lets users create programs by manipulating program elements graphically rather than by specifying them textually

```
mols = []  
for smi in input_1_pandas[self.molecule_column]:  
    mols.append(Chem.MolFromSmiles(smi))
```



`rdkit.Chem.rdmolfiles.MolFromSmiles((AtomPairsParameters)SMILES, (SmilesParserParams)params) → Mol :`

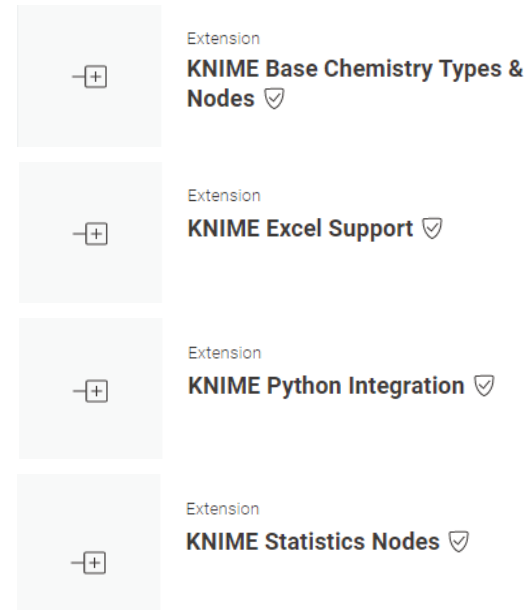
Construct a molecule from a SMILES string.

Extensions?

- KNIME AP comes by default only with basic functionality



- Extensions (and integrations) add specific functionality
- Not default, need to be added



The KNIME Workbench

The screenshot displays the KNIME Analytics Platform interface with the following components:

- KNIME Explorer:** Shows a project tree with folders like '2020_05_NIBR_Chemistry_training_412' and files like '01_Chemistry_basics'.
- Workflow Coach:** Lists recommended nodes: File Reader (28%), CSV Reader (20%), and Table Creator (13%).
- Node Repository:** A categorized list of nodes including IO, Manipulation, Views, Analytics, DB, and Chemistry.
- Main Canvas:** A workflow diagram divided into two steps:
 - Step 1: Read data from different sources** includes a 'File Reader' node, an 'Excel Reader (XLS)' node, and an 'SDF Reader' node, all connected to a 'Concatenate' node.
 - Step 2: Remove duplicates** includes a 'Molecule Type Cast' node, an 'RDKit Canon SMILES' node, and a 'Duplicate Row Filter' node, connected sequentially.
- Description Panel:** Titled '01_Chemistry_basics', it provides a description of the workflow's purpose: demonstrating basic cheminformatics functionality within KNIME.
- Console:** Displays log messages from the KNIME Console, including warnings about column specifications and node creation.

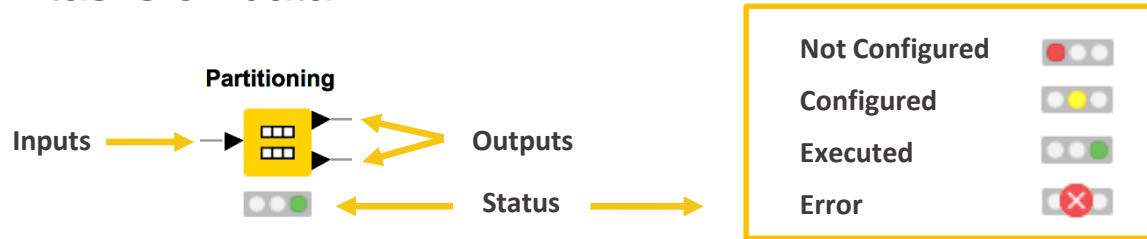
The KNIME Workbench – most important windows

The screenshot displays the KNIME Analytics Platform interface with the following components and callouts:

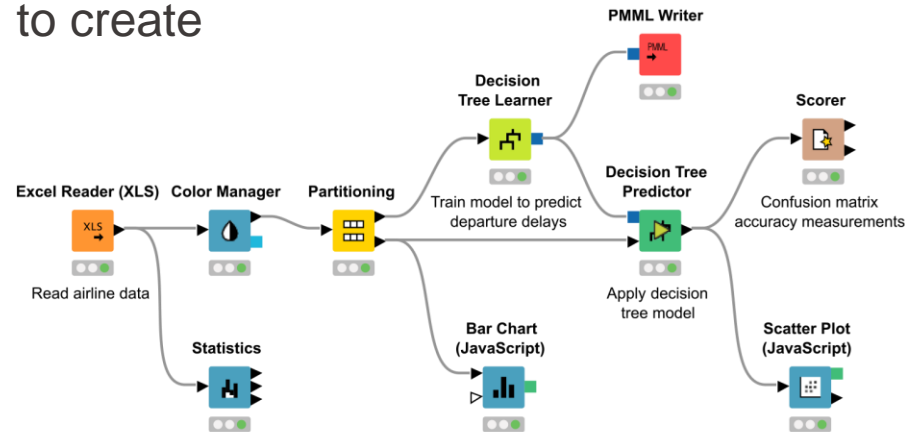
- Workflows:** A callout points to the **KNIME Explorer** window on the left, which shows a project tree with folders like `2020_04_21_RNKit_ChemInformatics` and `2020_05_NIBR_Chemistry_training_412`, and files like `01_Chemistry_basics`, `02_Structure_Rendering`, and `03_Substructure_Search`.
- Nodes:** A callout points to the **Node Repository** window on the left, which lists various node categories such as **IO**, **Manipulation**, **Views**, **Analytics**, **DB**, **Other Data Types**, **Structured Data**, **Scripting**, **Tools & Services**, **Community Nodes**, **KNIME Labs**, **Workflow Control**, **Workflow Abstraction**, **Reporting**, **Chemistry**, and **ChemAxon / Infocom**.
- Workflow editor:** A callout points to the central workspace, which shows a workflow diagram. The workflow consists of **Step 1: Read data from different sources** (containing **File Reader**, **Excel Reader (XLS)**, and **SDF Reader** nodes) and **Step 2: Remove duplicates** (containing **Concatenate**, **Duplicate Row Filter**, and **Row Filter** nodes).
- Node description:** A callout points to the **Description** window on the right, which shows the details for the `01_Chemistry_basics` workflow. The description includes the title, a detailed description of the workflow's purpose (demonstrating basic cheminformatics functionality), and a list of training sets collected from ChEMBL.

Visual KNIME Workflows

NODES perform tasks on data



Nodes are combined to create
WORKFLOWS

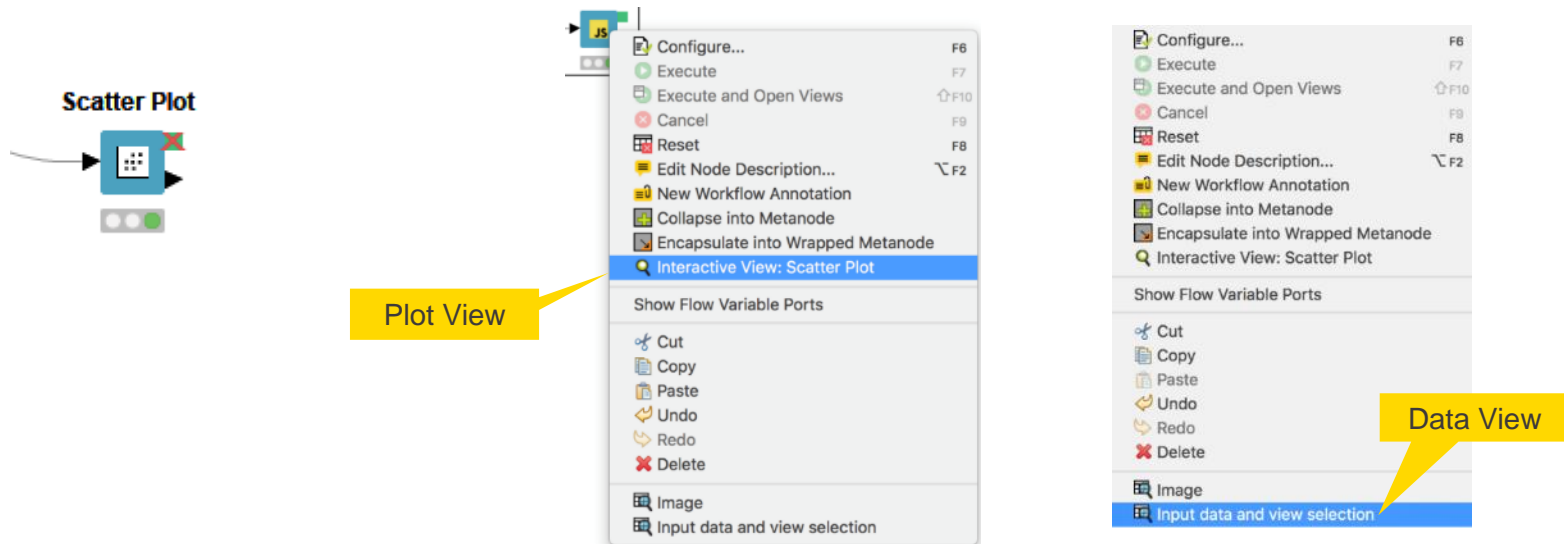


Node Outputs and Views

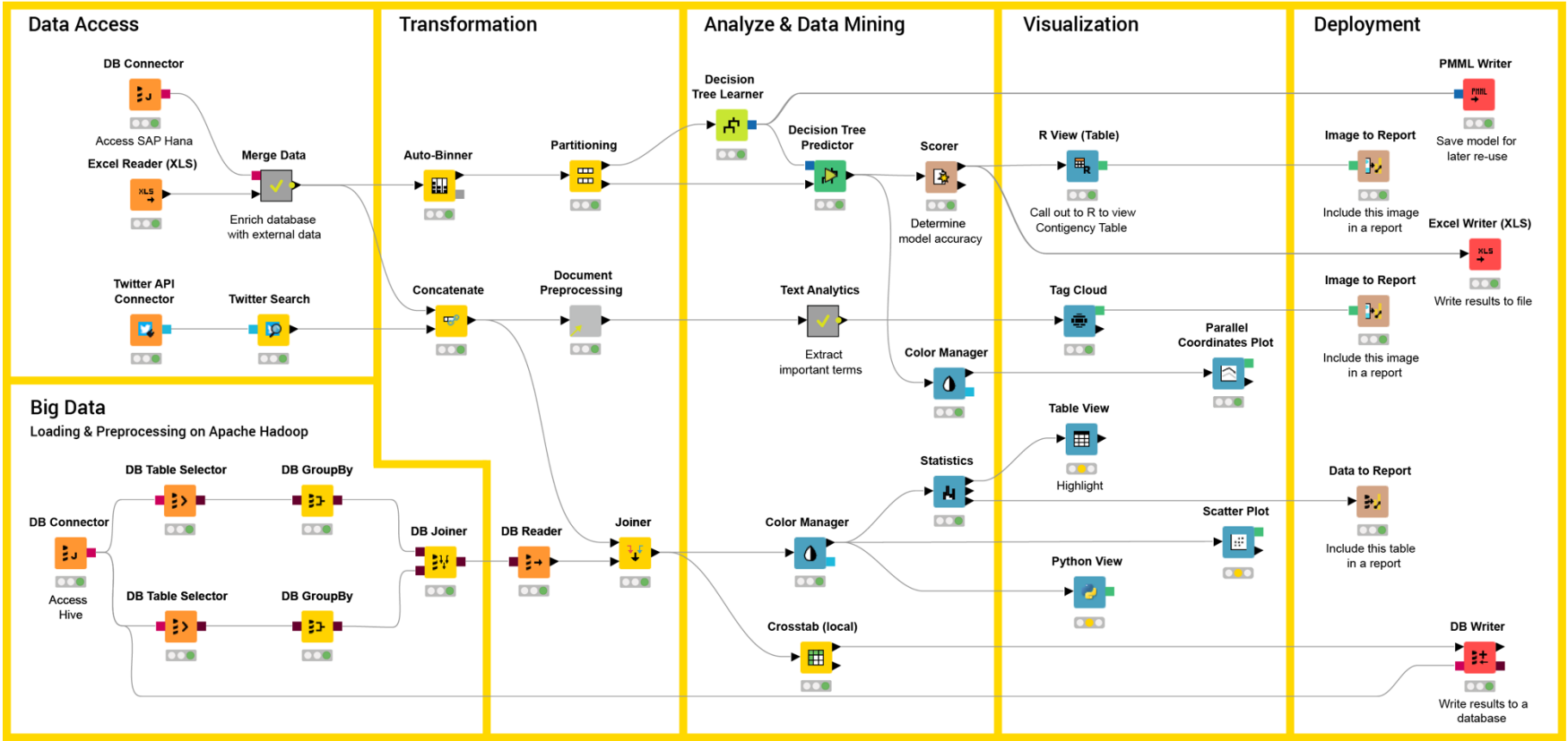
- Right-click executed node
- Select View option in context menu

OR

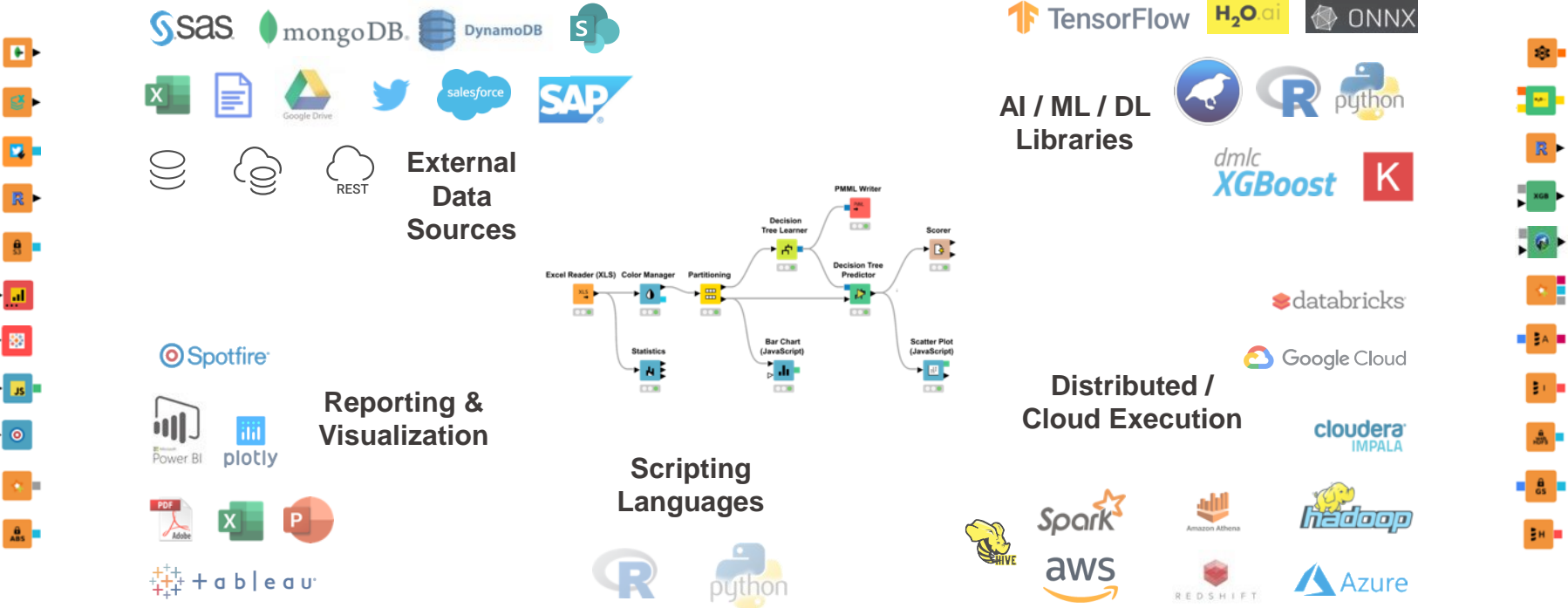
- Select output port (last item) to inspect execution results



4000+ Nodes for all Steps of End-To-End Data Science



Mix & Match Data Sources, Technologies, and Execution



Red indicates large delay



000-7 8



By birded departure time



Red indicates a flight on time, green a delayed flight



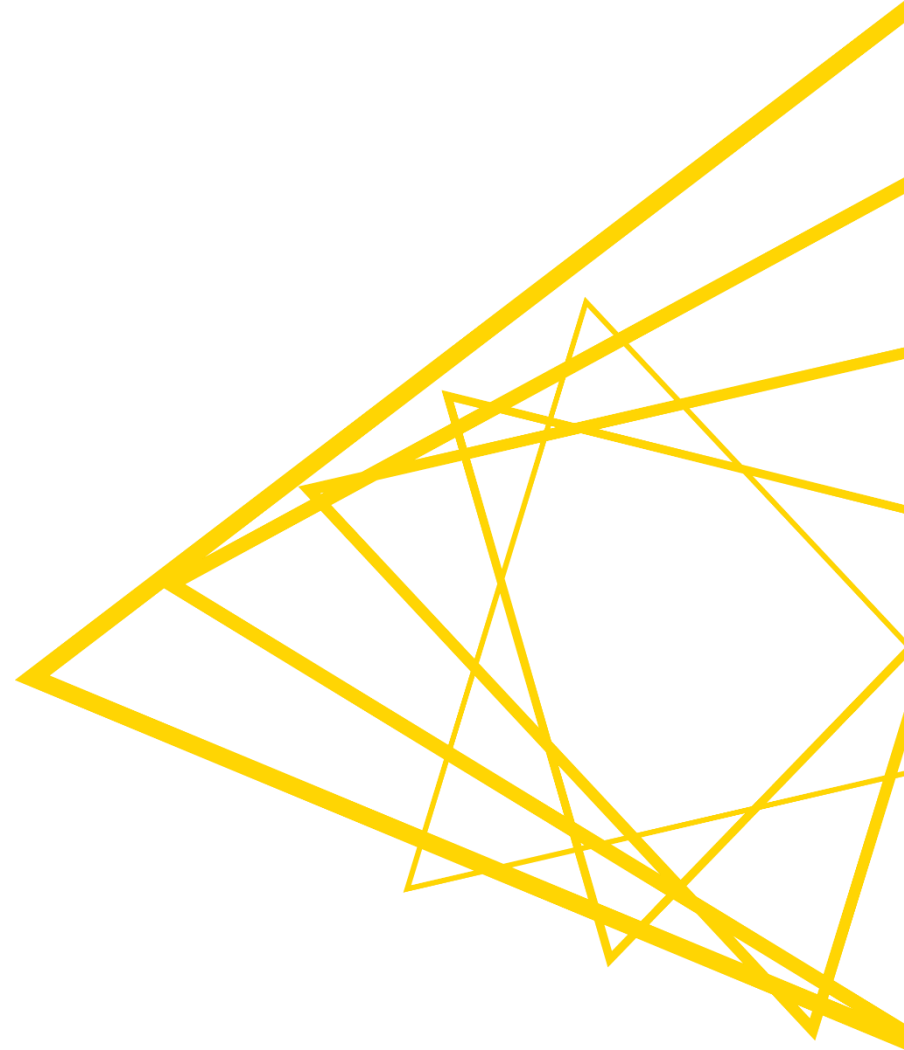
Moving average over the last 20 days



Why KNIME?

- Self-documenting
 - Every workflow is a track of what you did to your data
- Reproducible
 - Once configured, it will run the same way every time and have the same results
- Data is available at every manipulation step
 - Trace and control how the data table is changing throughout the workflow
- Interactive data visualization
- Chemistry capabilities

Setup KNIME AP for today












Set up KNIME Analytics Platform

- Download workflows from the KNIME Community Hub
 - <https://kni.me/s/5Goi-yKrwMLzAU4o>

Public space

Public

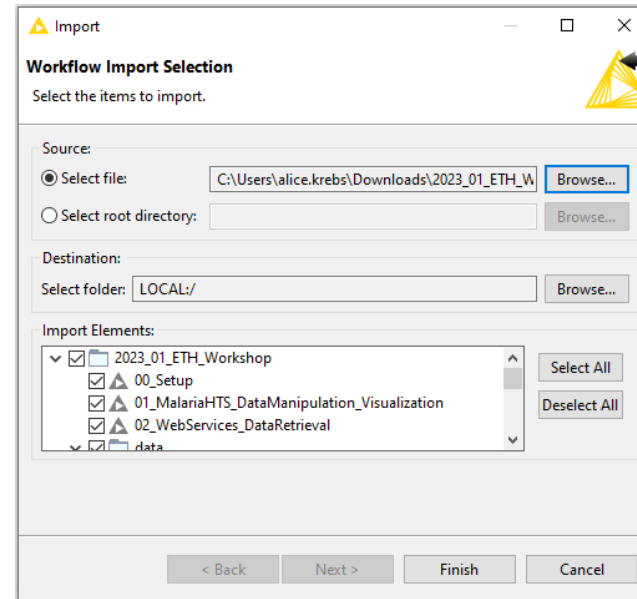
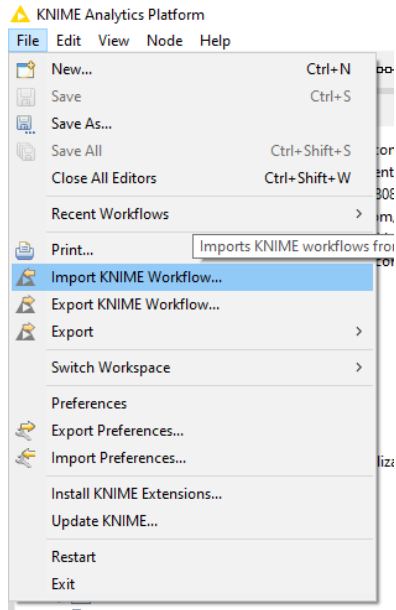
Last edit: Jun 24, 2020

Home	
 2021_11_11	
 2023_01_ETH_Workshop	
 2023_06_Boston_Workshop	
 CNS Multiparameter Optimization	

Import the workflow group

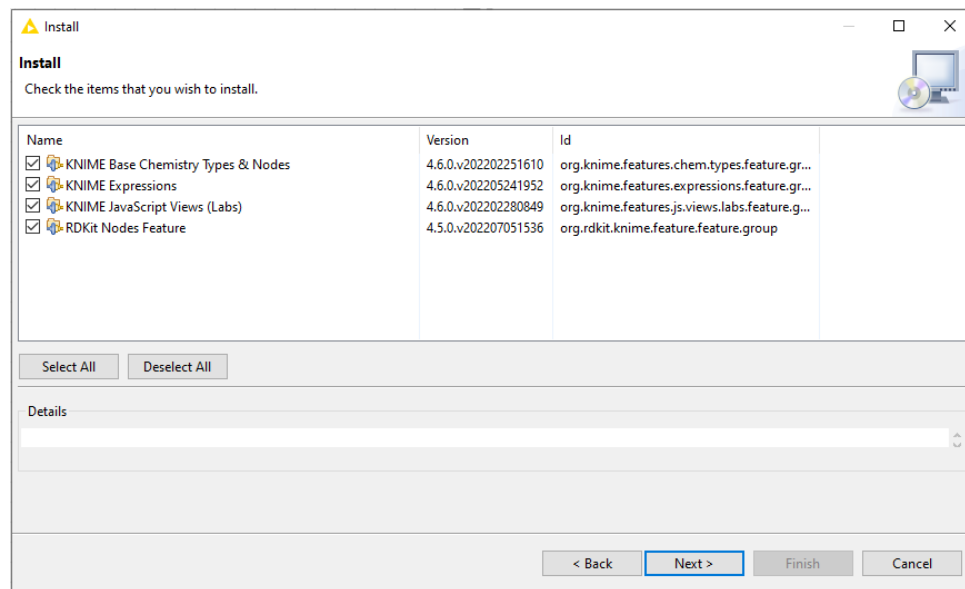
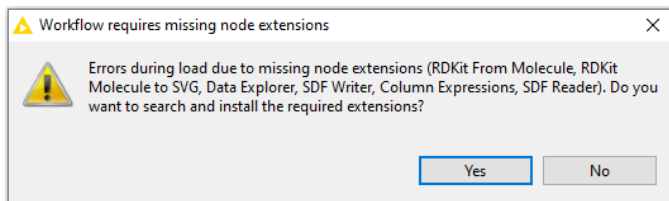
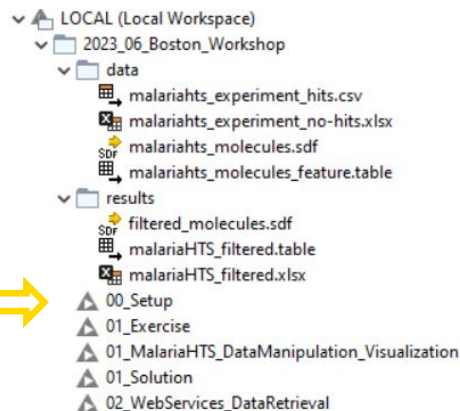
- Navigate to your download folder and choose the “2023_06_Boston_Workshop.knar” file

.knwf → single workflow
.knar → group of workflows



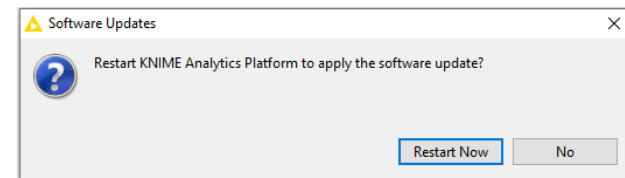
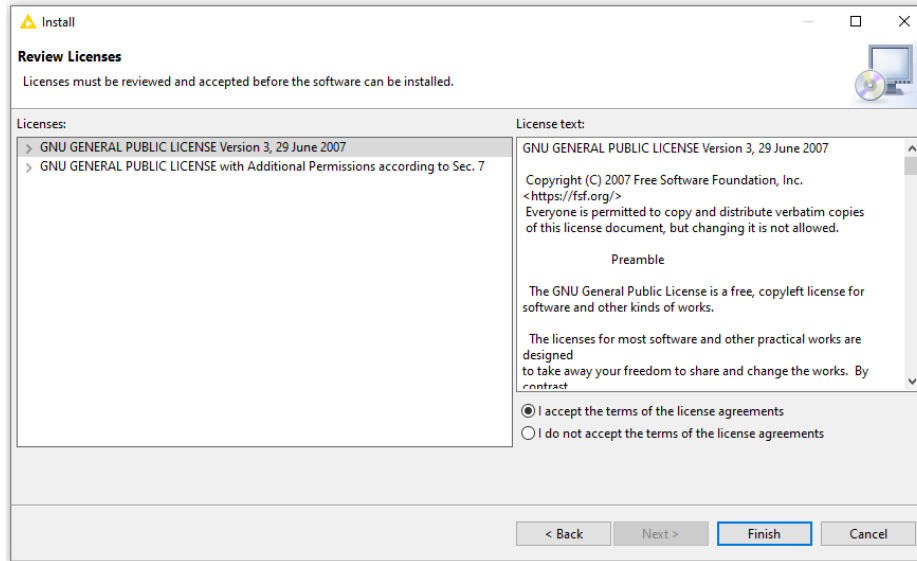
Getting started

- Open the “00_Setup” workflow to install all the extensions you need today

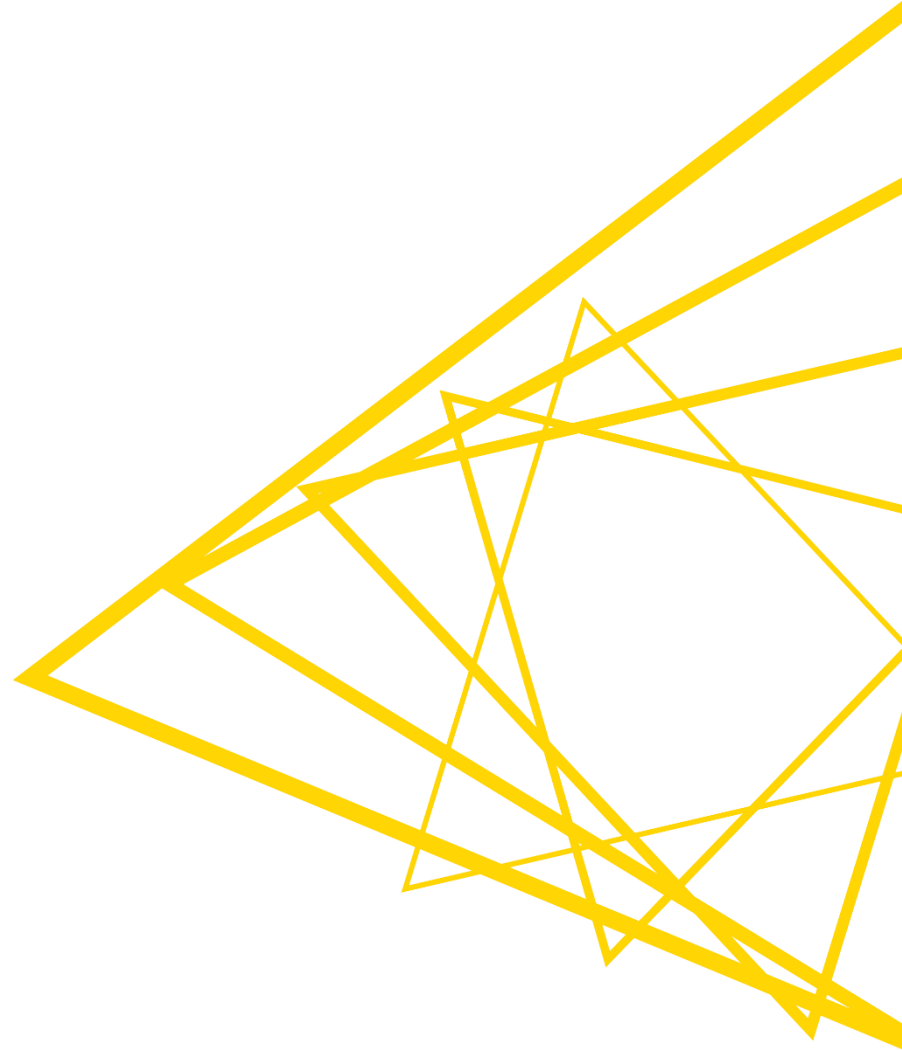


Getting started

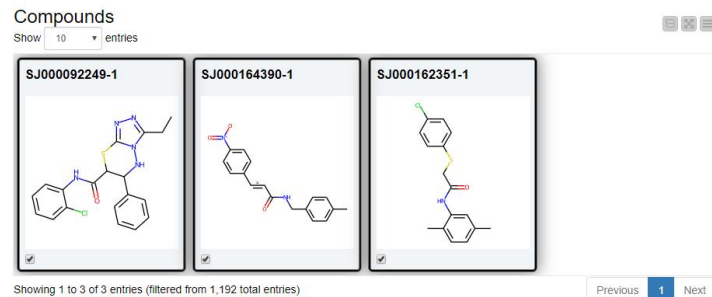
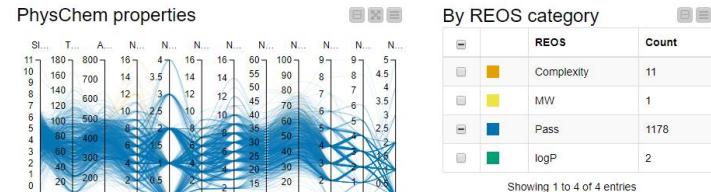
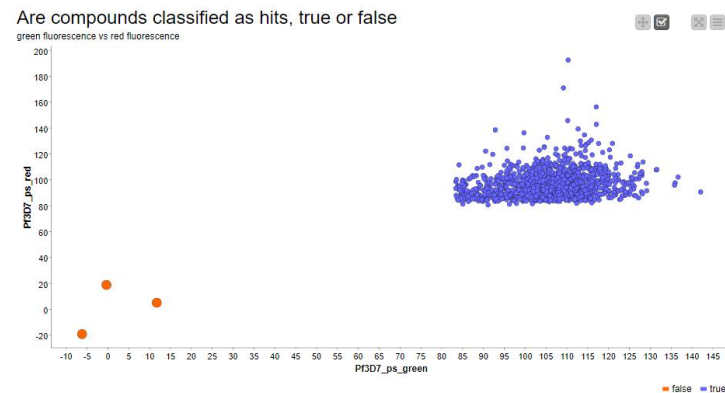
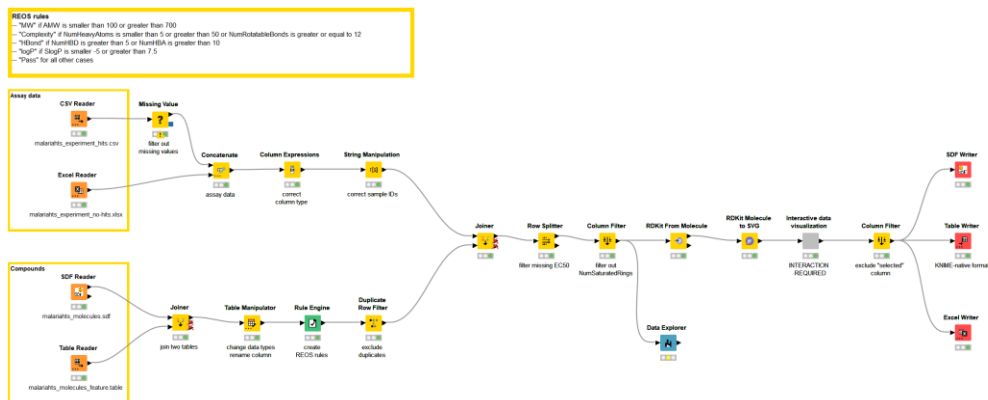
- Open the “00_Setup” workflow to install all the extensions you need today



Ready to go!



- 01_MalariaHTS_DataManipulation_Visualization

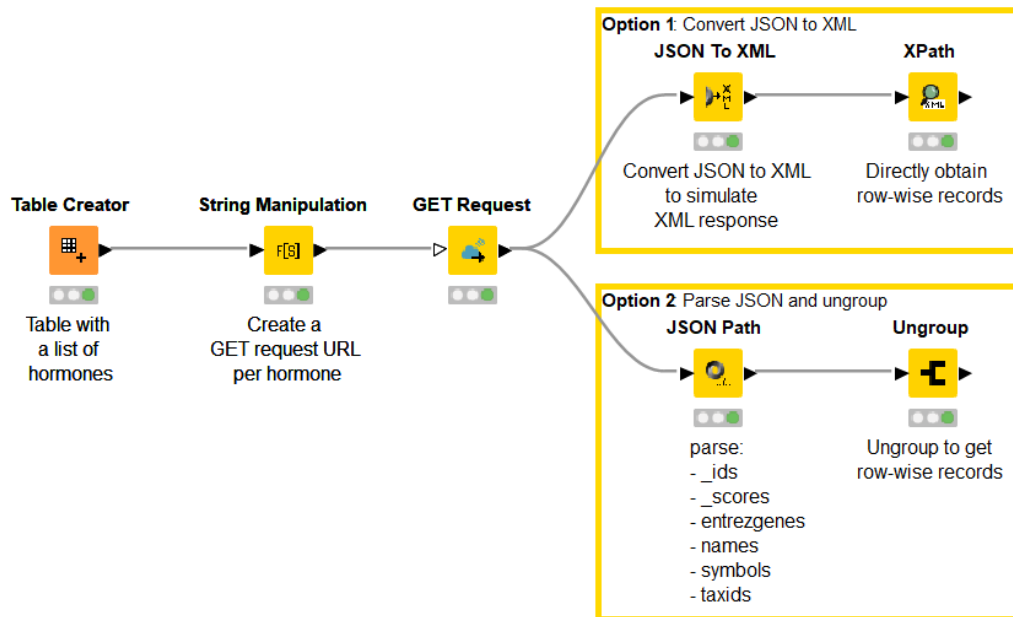


Today's workflows II

02_WebServices_DataRetrieval

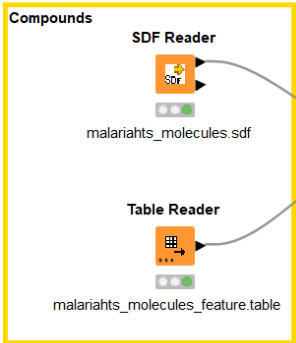
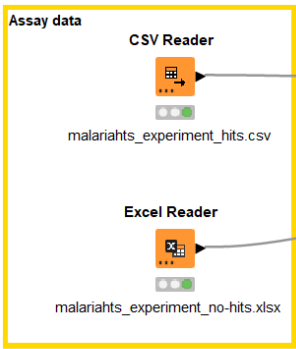
In this workflow snippet, we will use the REST service provided by MyGene.info to obtain a list of human genes related to specific hormones. Then, we parse the JSON response into a table that is easy to read.

Sometimes, responses come in XML format. We have also included a way to parse XML responses by first converting the JSON response directly to XML.



01_MalariaHTS_DataManipulation_Visualization

■ Step 1: import data from 4 different sources



File Table - 4:276 - CSV Reader (malariahts_experiment_hits.csv)

File Edit Hilite Navigation View

Table "default" - Rows: 1528 Spec - Columns: 5 Properties Flow Variables

Row ID	[S] Sample	[D] Pf3D7_ps_green	[D] Pf3D7_ps_red	[S] Pf3D7_ps_hit	[D] Pf3D7_pEC50
Row0	SJ000259230-1	102.523	80.893	true	?
Row1	sj000282539-1	113.112	88.908	true	6.227
Row2	SJ000033142-1	122.304	104.185	true	6.069
Row3	sj000079671-1	105.88	97.726	true	4.824
Row4	sj000179372-1	98.684	84.861	true	6.142
Row5	sj000276817-1	98.44	86.477	true	5.14
Row6	SJ000273047-1	100.665	80.332	true	?
Row7	sj000260256-1	102.336	96.501	true	4.824
Row8	sj000123502-1	113.261	101.839	true	5.433
Row9	SJ000170548-1	107.117	111.154	true	5.416
Row10	SJ000092590-1	105.653	98.151	true	6.121
Row11	SJ000033131-1	116.077	96.145	true	7.284
Row12	sj000257328-1	111.211	122.335	true	?
Row13	sj000117911-1	114.424	84.23	true	6.239
Row14	sj000018305-1	82.184	89.21	true	?
Row15	SJ000217742-1	100.72	94.014	true	5.64
Row16	sj000128935-1	98.061	90.995	true	5.565
Row17	sj000114920-1	114.096	87.336	true	5.272
Row18	sj000225626-1	111.027	93.789	true	5.309

File Table - 4:275 - Excel Reader (malariahts_experiment_no-hits...)

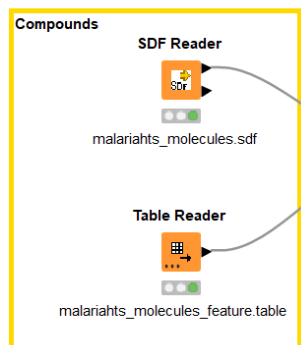
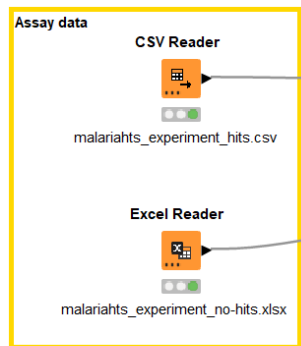
File Edit Hilite Navigation View

Table "default" - Rows: 10000 Spec - Columns: 5 Properties Flow Variables

Row ID	[S] Sample	[D] Pf3D7_ps_green	[D] Pf3D7_ps_red	[S] Pf3D7_ps_hit	[S] Pf3D7_pEC50
Row0	SJ000167487-1	-4.5	1.987	false	?
Row1	SJ000072922-1	-16.842	-0.682	false	?
Row2	SJ000223430-1	1.715	2.431	false	?
Row3	SJ000147674-1	2.178	11.964	false	?
Row4	sj000127323-1	-11.221	0.67	false	?
Row5	SJ000018465-1	5.524	5.319	false	?
Row6	sj000178506-1	-4.619	-6.703	false	?
Row7	SJ000007934-1	8.507	0.532	false	?
Row8	SJ000072074-1	11.421	1.934	false	?
Row9	sj000105546-1	-7.541	-3.692	false	?
Row10	sj000066091-1	10.913	0.62	false	?
Row11	sj000301657-1	15.532	-1.949	false	?
Row12	SJ000248175-1	-7.671	-0.126	false	?
Row13	SJ000183613-1	-4.996	3.268	false	?
Row14	SJ000172736-1	-8.381	-27.308	false	?
Row15	sj000291738-1	-4.754	9.031	false	?
Row16	sj000242990-1	-7.57	-10.372	false	?

01_MalariaHTS_DataManipulation_Visualization

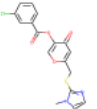


■ Step 1: import data from 4 different sources



Read molecules - 4:267 - SDF Reader (malariahts_molecules.sdf)

File Edit Hilite Navigation View

Table "default" - Rows: 11528 Spec - Columns: 6 Properties Flow Variables

Row ID	sdf Molecule	[S] Sample	[D] SlogP	[D] TPSA	[D] ExactMW	[D] AverageMolecularWeight
SJ000263455-1		SJ000263455-1	3.538	74.33	376.028	376.821
SJ000136517-1		SJ000136517-1	2.78	71.95	307.045	307.4
SJ000244874-1		SJ000244874-1	5.721	71.53	477.118	477.611

Read table - 4:7 - Table Reader (malariahts_molecules_feature.t...)

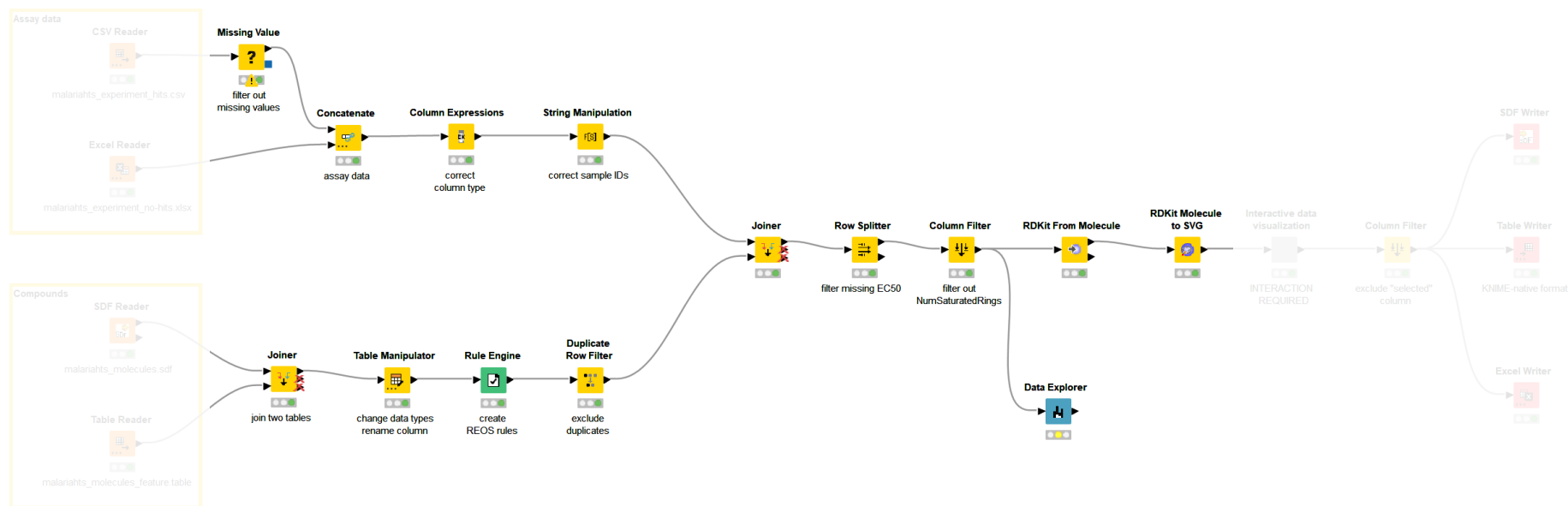
File Edit Hilite Navigation View

Table "default" - Rows: 11628 Spec - Columns: 11 Properties Flow Variables

Row ID	[S] Sample	[S] NumRotatableBonds	[I] NumHBD	[I] NumHBA	[I] NumHeteroAtoms	[S] NumHeavyAtoms	[I] NumAtoms	[I] NumRings	[I] NumAromaticRings	[I] NumSaturatedRings	[I] NumAliphaticRings
Row0	SJ000263455-1	5	0	7	8	25	38	3	3	0	0
Row1	SJ000136517-1	5	1	6	7	20	33	2	2	0	0
Row2	SJ000244874-1	5	1	6	8	33	56	5	4	0	1
Row3	SJ000185650-1	7	0	9	10	27	43	2	1	0	1
Row4	SJ000295142-1	2	0	3	5	21	39	3	1	1	2
Row5	SJ000007375-1	5	1	4	6	28	45	4	4	0	0
Row6	SJ000243289-1	6	2	6	7	24	45	3	3	0	0
Row7	SJ000116582-1	4	1	4	8	30	52	4	3	1	1
Row8	SJ000293545-1	3	2	4	7	27	39	4	4	0	0
Row9	SJ000057137-1	6	1	4	7	25	42	3	3	0	0
Row10	SJ000079475-1	4	1	7	10	28	40	4	4	0	0
Row11	SJ000038023-1	5	2	4	10	27	46	2	1	0	1
Row12	SJ000055177-1	7	0	5	7	34	36	3	2	0	1

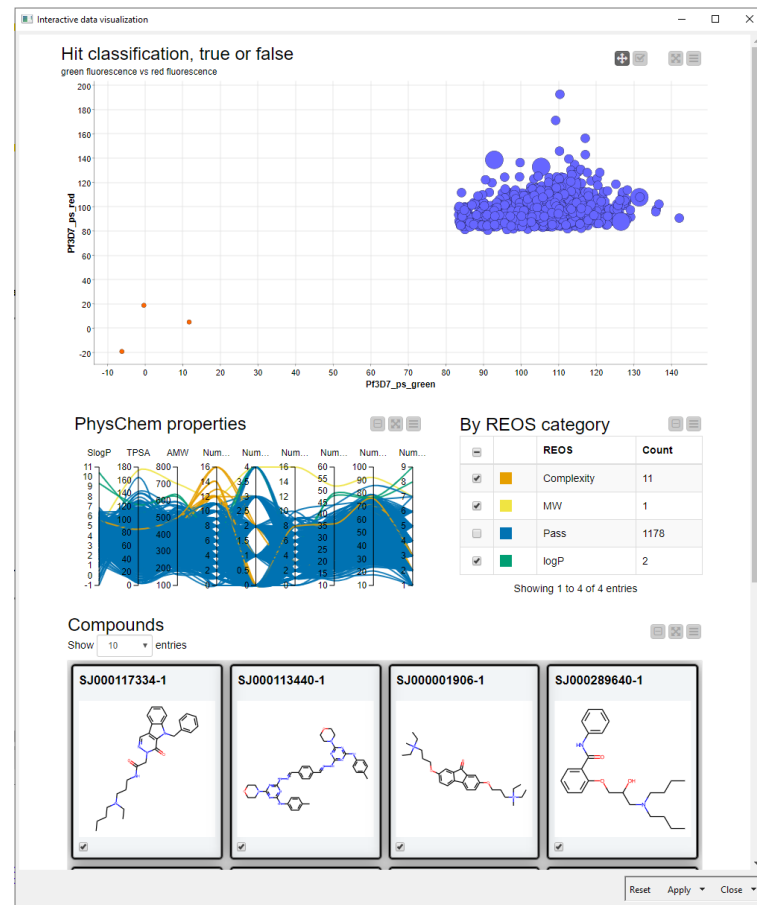
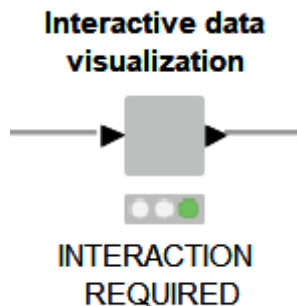
01_MalariaHTS_DataManipulation_Visualization

- **Step 2:** data cleaning, merging datasets, manipulate data, create classification



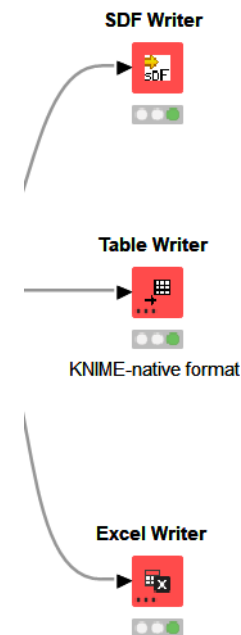
01_MalariaHTS_DataManipulation_Visualization

- **Step 3:** visualize and interactively select data
 - build a component to combine different plots in one view



01_MalariaHTS_DataManipulation_Visualization

- **Step 4: Export the data**
 - SD file
 - KNIME-native table (only re-usable in KNIME)
 - Excel



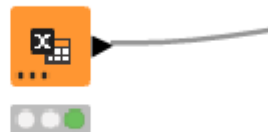
Content, theory, background on...

- Import data
 - Local file system
 - Workflow relative path
- Merging data sets
 - Concatenate
 - Join
- Exclude data
 - Filter
 - Splitter
- Handle missing values and duplicates
- Change data
 - Change assigned data type
 - Capitalize the letters in the sample ID
 - Rename columns
 - Create classification of REOS rules
- Visualize data in components

Import data

- Different Reader nodes for different file formats
- “Table” is a KNIME native format
- Drag and drop the files from the data folder in the KNIME Explorer

Excel Reader



malariahts_experiment_no-hits.xlsx

CSV Reader



malariahts_experiment_hits.csv

SDF Reader



malariahts_molecules.sdf

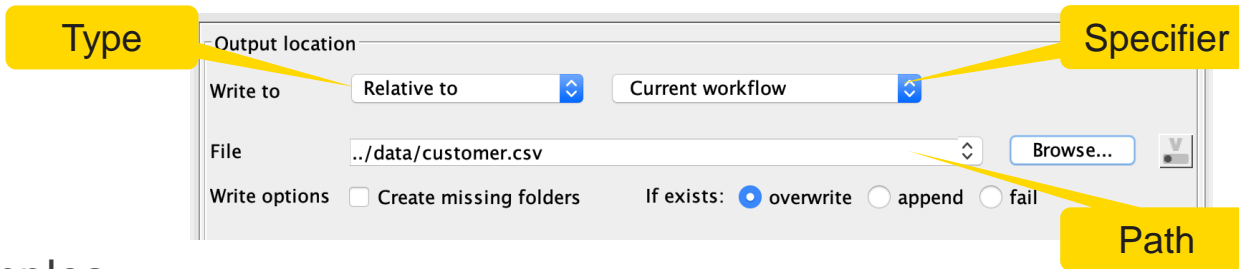
Table Reader



malariahts_molecules_feature.table

Common Settings: File Path

- A path consists of three parts:
 - **Type**: Specifies the file system type e.g. local, relative, mountpoint, custome_url or connected.
 - **Specifier**: Optional string with additional file system specific information e.g. relative to which location (knime.workflow)
 - **Path**: Specifies the location within the file system



- Examples:
 - (LOCAL, , C:\Users\username\Desktop)
 - (RELATIVE, knime.workflow, file1.csv)
 - (MOUNTPOINT, MOUNTPOINT_NAME, /path/to/file1.csv)
 - (CONNECTED, amazon-s3:eu-west-1, /mybucket/file1.csv)

Common Settings: 4 Default File Systems

■ Local File System

Input location

Read from:

Mode: ☒ File ☐ Files in folder

File:

■ Relative to ...

Read from:

- Current mountpoint
- Current workflow data area
- Current workflow

File:

■ Mountpoint

Read from:

File:

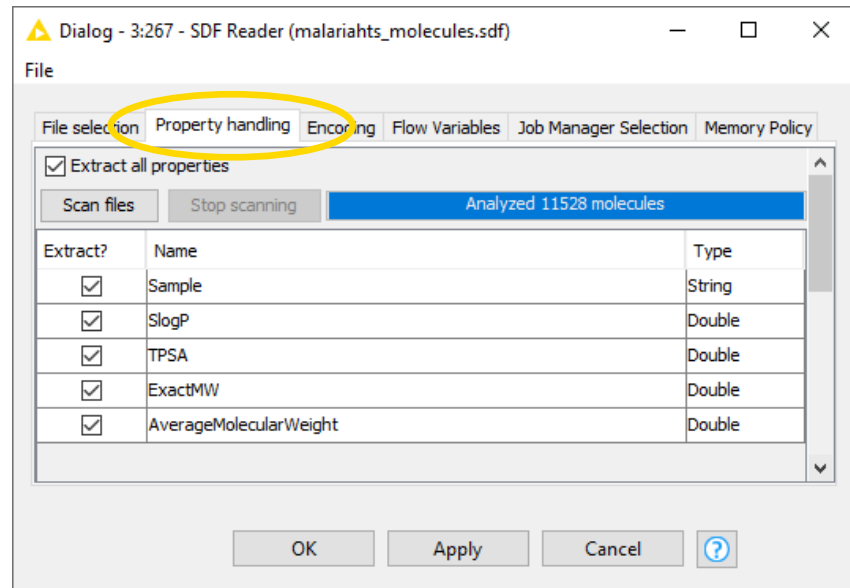
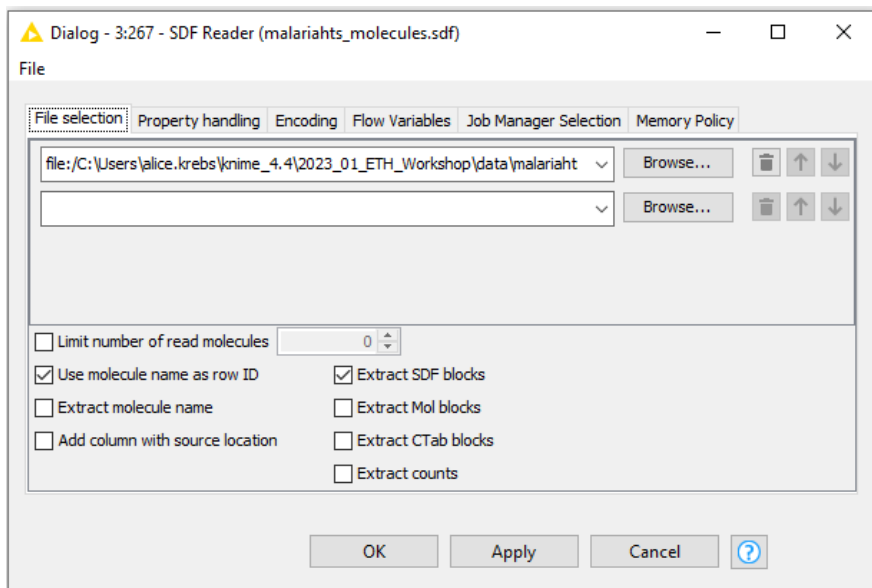
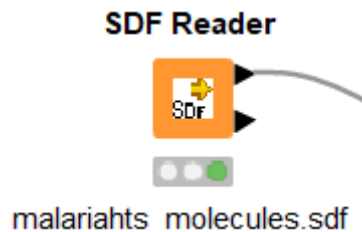
■ Custom URL

Read from:

URL:

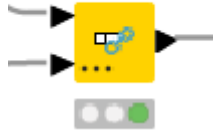
Special case – SDF reader node

- No new file handling
- Extract properties to get all data

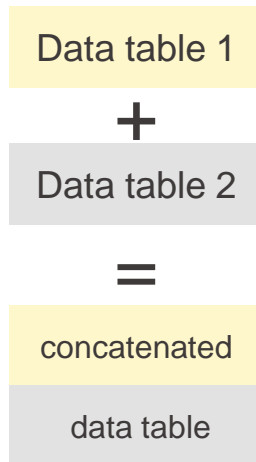


Concatenate vs. Join

Concatenate



- Simply links to tables, appends them underneath each other, like in a chain



Joiner

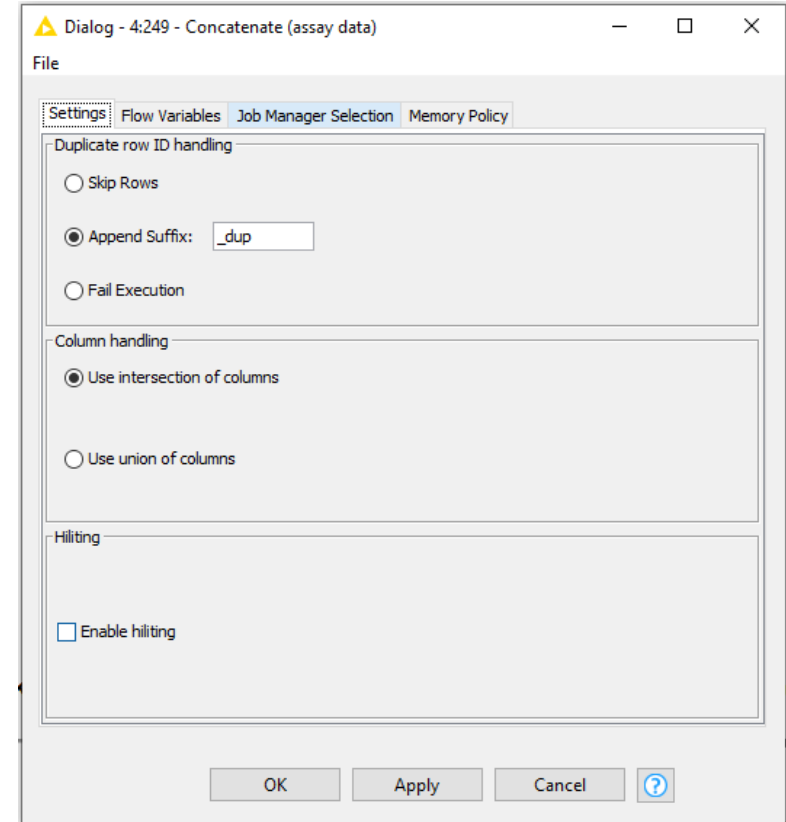
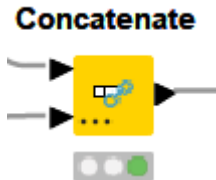


- Combines two tables row wise

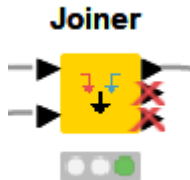


Concatenate node

- Intersection
 - use only the columns that appear in both input tables
- Union
 - use all columns available in the input tables



Joiner node



Dialog - 4:299 - Joiner

File

Joiner Settings | Column Selection | Performance | Flow Variables | Job Manager Selection | Memory Policy

Join columns

Match ☒ all of the following ☐ any of the following

Top Input (left table) Bottom Input (right table)

S Sample S Sample + -

+

Compare values in join columns by ☒ value and type ☐ string representation ☐ making integer types compatible

Include in output

☒ Matching rows

☐ Left unmatched rows

☐ Right unmatched rows

Inner join

Output options

☐ Split join result into multiple tables (top = matching rows, middle = left unmatched rows, bottom = right unmatched rows)

☐ Merge join columns

☐ Hiding enabled

Row Keys

☒ Concatenate original row keys with separator

☐ Assign new row keys sequentially

☐ Keep row keys

OK Apply Cancel ?

Dialog - 4:299 - Joiner

File

Joiner Settings | Column Selection | Performance | Flow Variables | Job Manager Selection | Memory Policy

Top Input (left table)

☒ Manual Selection ☐ Wildcard/Regex Selection ☐ Type Selection

Exclude

Filter

No columns in this list

☒ Enforce exclusion

Include

Filter

S Sample

D PF3D7_ps_green

D PF3D7_ps_red

S PF3D7_ps_hit

D PF3D7_pEC50

☐ Enforce inclusion

Bottom Input (right table)

☒ Manual Selection ☐ Wildcard/Regex Selection ☐ Type Selection

Exclude

Filter

S Sample

☒ Enforce exclusion

Include

Filter

Sample

D SlogP

D TPSA

D AMW

I NumRotatableBonds

I NumHBD

I NumHBA

I NumHeteroAtoms

☐ Enforce inclusion

Duplicate column names

☐ Do not execute

☒ Append custom suffix

OK Apply Cancel ?

Joining Columns of Data – Inner Join

Left Table

molregno	chembl_id	SMILES
22	CHEMBL1794855	CCCN(CCC)
24	CHEMBL278751	CCN(C)
15	CHEMBL103772	CCCN1CC
10	CHEMBL328107	C1CN(CCN1)

Right Table

molregno	Ki_value	Ki_relation	Ki_unit
17	76.0	=	nM
65	6.56	=	nM
35	100	>	nM
15	8	=	nM
10	95.8	=	nM



Inner Join

molregno	chembl_id	SMILES	Ki_value	Ki_relation	Ki_unit
15	CHEMBL103772	CCCN1CC	8	=	nM
10	CHEMBL328107	C1CN(CCN1)	95.8	=	nM

Joining Columns of Data – Left Outer Join

Left Table

molregno	chembl_id	SMILES
22	CHEMBL1794855	CCCN(CCC)
24	CHEMBL278751	CCN(C)
15	CHEMBL103772	CCCN1CC
10	CHEMBL328107	C1CN(CCN1)

Right Table

molregno	Ki_value	Ki_relation	Ki_unit
17	76.0	=	nM
65	6.56	=	nM
35	100	>	nM
15	8	=	nM
10	95.8	=	nM

Left Outer Join

molregno	chembl_id	SMILES	Ki_value	Ki_relation	Ki_unit
22	CHEMBL1794855	CCCN(CCC)	?	?	?
24	CHEMBL278751	CCN(C)	?	?	?
15	CHEMBL103772	CCCN1CC	8	=	nM
10	CHEMBL328107	C1CN(CCN1)	95.8	=	nM

Joining Columns of Data – Right Outer Join

Left Table

molregno	chembl_id	SMILES
22	CHEMBL1794855	CCCN(CCC)
24	CHEMBL278751	CCN(C)
15	CHEMBL103772	CCCN1CC
10	CHEMBL328107	C1CN(CCN1)

Right Table

molregno	Ki_value	Ki_relation	Ki_unit
17	76.0	=	nM
65	6.56	=	nM
35	100	>	nM
15	8	=	nM
10	95.8	=	nM

Right Outer Join

molregno	chembl_id	SMILES	Ki_value	Ki_relation	Ki_unit
17	?	?	76.0	=	nM
65	?	?	6.56	=	nM
35	?	?	100	>	nM
15	CHEMBL103772	CCCN1CC	8	=	nM
10	CHEMBL328107	C1CN(CCN1)	95.8	=	nM

Joining Columns of Data – Full Outer Join

Left Table

molregno	chembl_id	SMILES
22	CHEMBL1794855	CCCN(CCC)
24	CHEMBL278751	CCN(C)
15	CHEMBL103772	CCCN1CC
10	CHEMBL328107	C1CN(CCN1)

Right Table

molregno	Ki_value	Ki_relation	Ki_unit
17	76.0	=	nM
65	6.56	=	nM
35	100	>	nM
15	8	=	nM
10	95.8	=	nM

Values missing in the left table

Full Outer Join

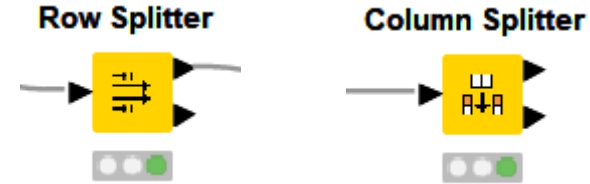
molregno	chembl_id	SMILES	Ki_value	Ki_relation	Ki_unit
17	?	?	76.0	=	nM
65	?	?	6.56	=	nM
35	?	?	100	>	nM
15	CHEMBL103772	CCCN1CC	8	=	nM
10	CHEMBL328107	C1CN(CCN1)	95.8	=	nM
22	CHEMBL1794855	CCCN(CCC)	?	?	?
24	CHEMBL278751	CCN(C)	?	?	?

Values missing in the right table

Filter vs. Splitter



- User-defined criteria
- Only one output port
- Excluded rows or columns are not available for downstream processing

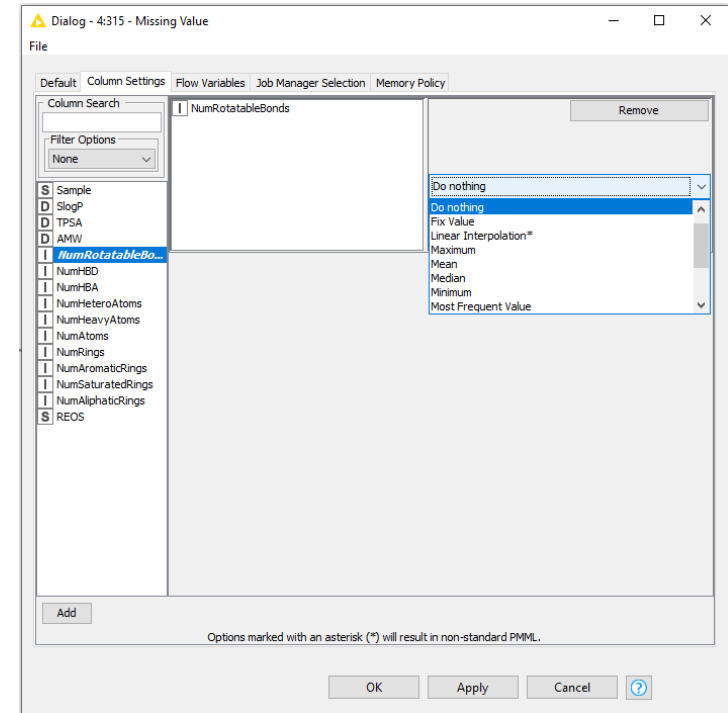
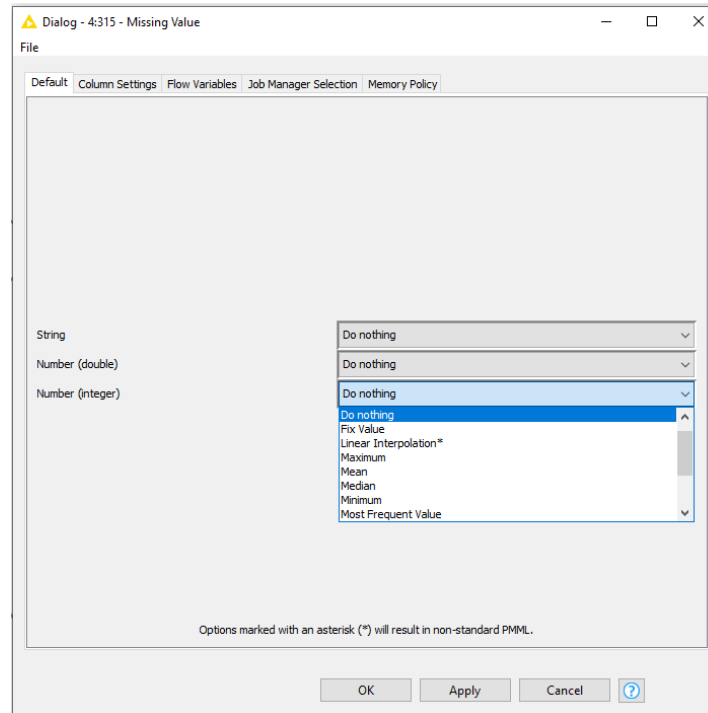


- User-defined criteria
- Two output ports
- Splits a dataset into two
- The 'excluded' data is available at the lower output port for downstream processing

Missing value handling

- First tab: define table-wide action depending on data type
- Second tab: define action for individual columns

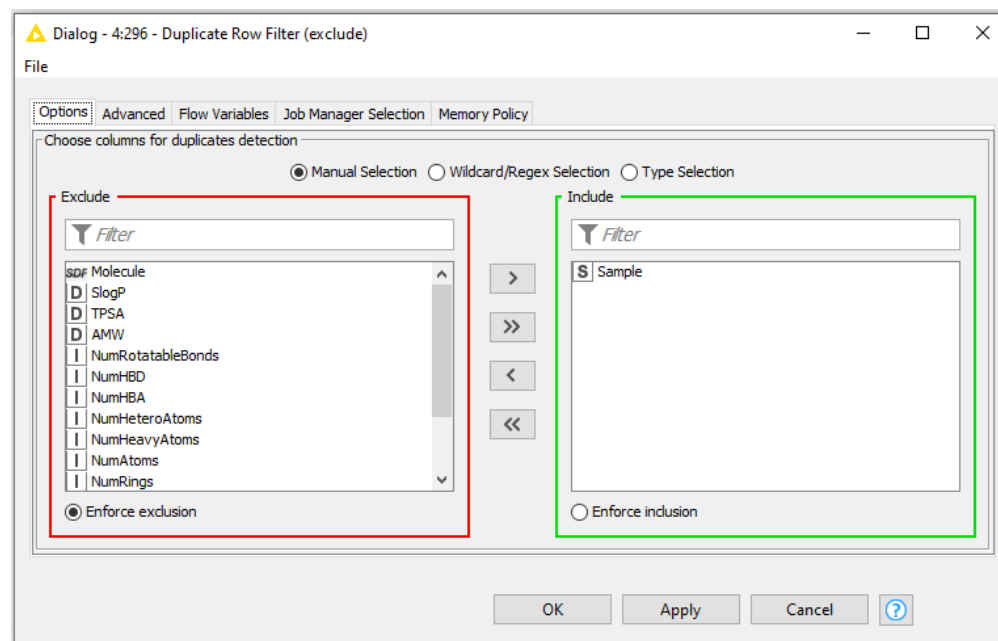
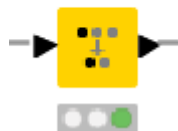
Missing Value



Exclude duplicates

- identifies duplicate rows
- duplicate rows have identical values in certain columns
- user defines the column(s) for duplicate detection

Duplicate Row Filter



Change assigned data type

- modify existing columns using expressions

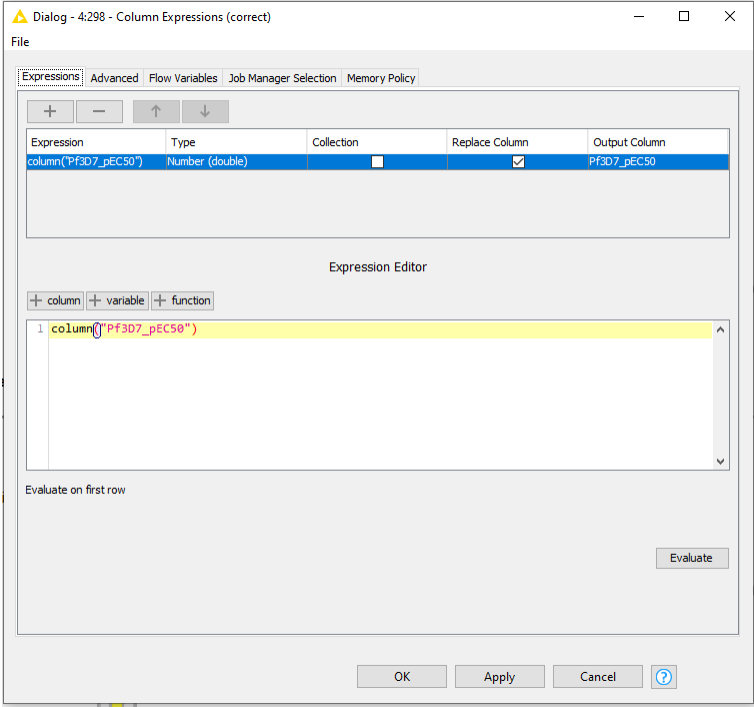


Table "default" - Rows: 11189						Spec - Columns: 5	Properties	Flow Variables
Row ID	[S] Sample	[D] Pf3D7_...	[D] Pf3D7_...	[S] Pf3D7_...	[?] Pf3D7_pEC50			
Row1	sj000282539-1	113.112	88.908	true	6.22650610772...			
Row2	SJ000033142-1	122.304	104.185	true	6.06905096883...			
Row3	sj000079671-1	105.88	97.726	true	4.82390874094...			
Row4	si000179372-1	98.684	84.861	true	6.14158312227...			



Table "default" - Rows: 11189						Spec - Columns: 5	Properties	Flow Variables
Row ID	[S] Sample	[D] Pf3D7_...	[D] Pf3D7_...	[S] Pf3D7_...	[D] Pf3D7_pEC50			
Row1	sj000282539-1	113.112	88.908	true	6.227			
Row2	SJ000033142-1	122.304	104.185	true	6.069			
Row3	sj000079671-1	105.88	97.726	true	4.824			
Row4	si000179372-1	98.684	84.861	true	6.142			

Capitalize the letters in the sample ID

- Manipulates strings
- Many different functions available
- Can also be used for type converting

String Manipulation

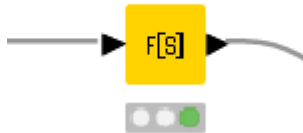
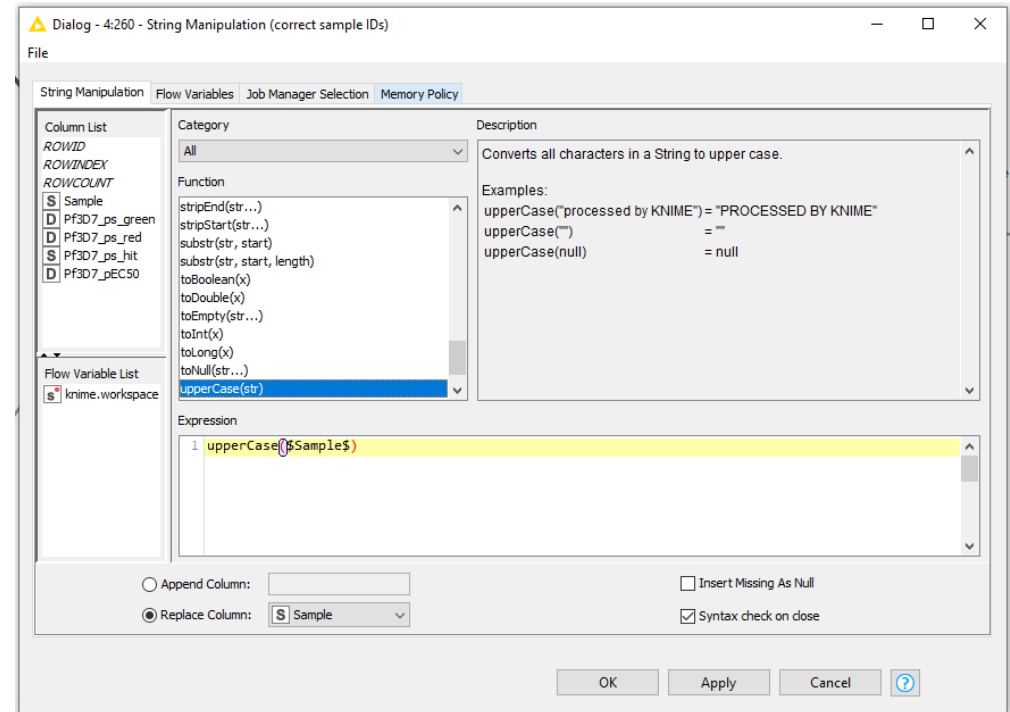


Table "default" - Rows: 1528 Spec -

Row ID	[S] Sample
Row0	SJ000259230-1
Row1	sj000282539-1
Row2	SJ000033142-1
Row3	sj000079671-1
Row4	sj000170377-1



Rename column

- Transformations of input columns
 - Renaming
 - Filtering
 - Re-ordering
 - Type changing
- Check data manipulation in the preview

Table Manipulator



Dialog - 4:278 - Table Manipulator (change data types)

File

Settings | Flow Variables | Job Manager Selection | Memory Policy

Row ID handling
☐ Use existing row ID ☐ Prepend table index to row ID

Transformations
Reset actions ↑ Move up ↓ Move down ☒ Enforce types Take columns from: ☒ Union ☐ Intersection

	Column	New name	Type
<input checked="" type="checkbox"/>	Molecule		sdf SDF
<input checked="" type="checkbox"/>	Sample		S String
<input checked="" type="checkbox"/>	SlogP		D Number (double)
<input checked="" type="checkbox"/>	TPSA		D Number (double)
<input type="checkbox"/>	ExactMW		D Number (double)
<input checked="" type="checkbox"/>	AverageMolecularWeight	AMW	D Number (double)
<input checked="" type="checkbox"/>	NumRotatableBonds		I String → Number (integer)
<input checked="" type="checkbox"/>	NumHBD		I Number (integer)
<input checked="" type="checkbox"/>	NumHBA		I Number (integer)
<input checked="" type="checkbox"/>	NumHeteroAtoms		I Number (integer)
<input checked="" type="checkbox"/>	NumHeavyAtoms		I String → Number (integer)
<input checked="" type="checkbox"/>	NumAtoms		I Number (integer)
<input checked="" type="checkbox"/>	NumRings		I Number (integer)
<input checked="" type="checkbox"/>	NumAromaticRings		I Number (integer)
<input checked="" type="checkbox"/>	NumSaturatedRings		I Number (integer)
<input checked="" type="checkbox"/>	NumAliphaticRings		I Number (integer)

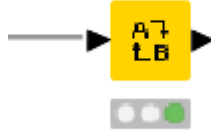
Preview
✔ Data analysis successfully completed.

Row ID	sdf Molecule	S Sample	D SlogP	D TPSA	D AMW	I NumRo...	I NumHBD	I NumHBA	I Num
Row0		S3000263455-1	3.538	74.33	376.821	5	0	7	8
Row1		S3000136517-1	2.78	71.95	307.4	5	1	6	7
Row2		S3000244874-1	5.721	71.53	477.611	5	1	6	8

OK Apply Cancel ?

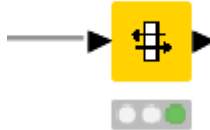
There isn't just one way of doing it...

Column Rename



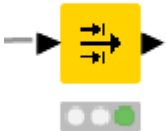
- Rename columns

Column Resorter

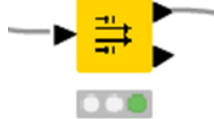


- Change the column order

Row Filter

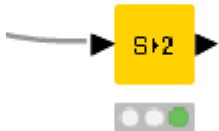


Row Splitter

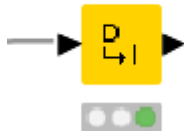


- Exclude missing values

String To Number

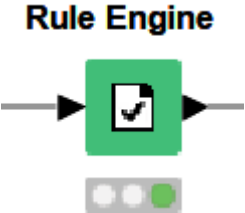


Double To Int



- Convert data types

Create classification REOS rules



Dialog - 4:286 - Rule Engine (create)

File

Rule Editor | Flow Variables | Job Manager Selection | Memory Policy

Column List

- ROWID
- ROWINDEX
- ROWCOUNT
- sdm Molecule
- S Sample
- D SlogP
- D TPSA
- D AMW
- I NumRotatableBonds
- I NumHBD
- I NumHBA
- I NumHeteroAtoms
- I NumHeavyAtoms
- I NumAtoms
- I NumRings
- I NumAromaticRings
- I NumSaturatedRings
- I NumAliphaticRings

Flow Variable List

- knime.workspace

Category

All

Function

- ? < ?
- ? <= ?
- ? = ?
- ? > ?
- ? >= ?
- ? AND ?
- ? IN ?
- ? LIKE ?
- ? MATCHES ?
- ? OR ?
- ? XOR ?
- FALSE
- MISSING ?
- NOT ?
- TRUE

Description

Expression

```
1 // enter ordered set of rules, e.g.:
2 // $double column name$ > 5.0 => "Large"
3 // $string column name$ LIKE "*blue*" => "small and blue"
4 // TRUE => "default outcome"
5 $AMW$<100 OR $AMW$>700 => "M"
6 $NumHeavyAtoms$<5 OR $NumHeavyAtoms$>50 OR $NumRotatableBonds$ >=12 => "Complexity"
7 $NumHBD$>5 OR $NumHBA$>10 => "HBond"
8 $SlogP$<-5 OR $SlogP$>7.5 => "logP"
9 TRUE=>"Pass"
```

Append Column: REOS

Replace Column: NumHeavyAtoms

OK Apply Cancel ?

Define
Condition => Outcome
if condition
is met

If not do this

IF... THEN... ELSE

GroupBy node

- Aggregate rows to summarize data
- Different aggregation methods available

Product ID	REOS	AMW
P001	Pass	462.55
P002	Pass	397.92
P003	Complexity	431.28
P004	Pass	431.28
P005	MW	371.46
P006	logP	389.20




Group	Count*(AMW)
Pass	3
Complexity	1
MW	1
logP	1

GroupBy node

- Aggregate rows to summarize data
- Different aggregation methods available

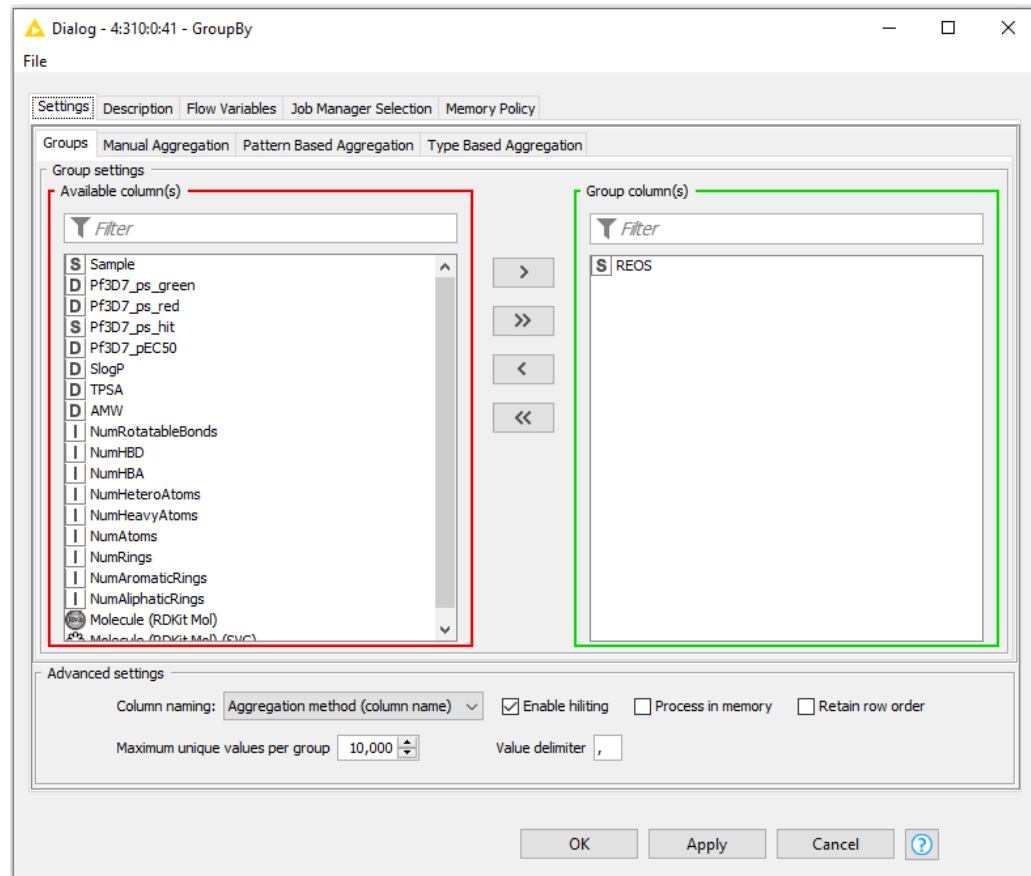
Product ID	REOS	AMW
P001	Pass	462.55
P002	Pass	397.92
P003	Complexity	431.28
P004	Pass	431.28
P005	MW	371.46
P006	logP	389.20



Group	Mean(AMW)
Pass	430.58
Complexity	431.28
MW	371.46
logP	389.20

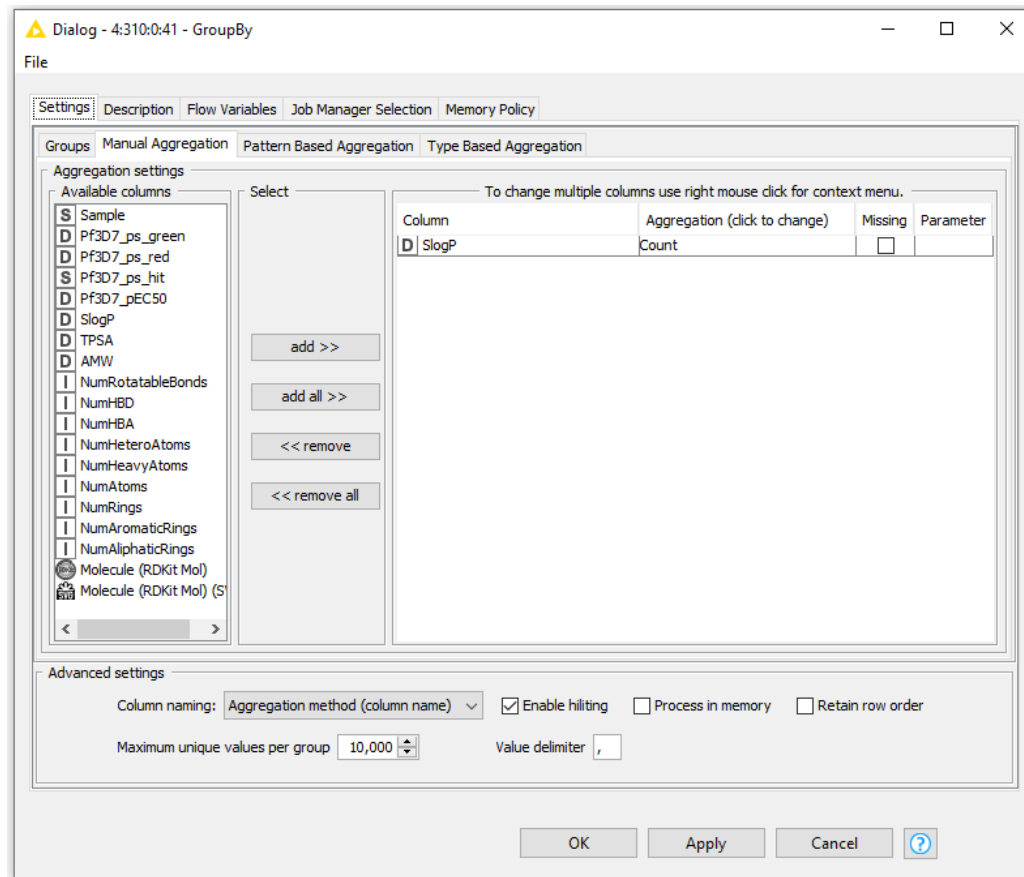
Groupby node configuration

- Define the column to group on in the first tab



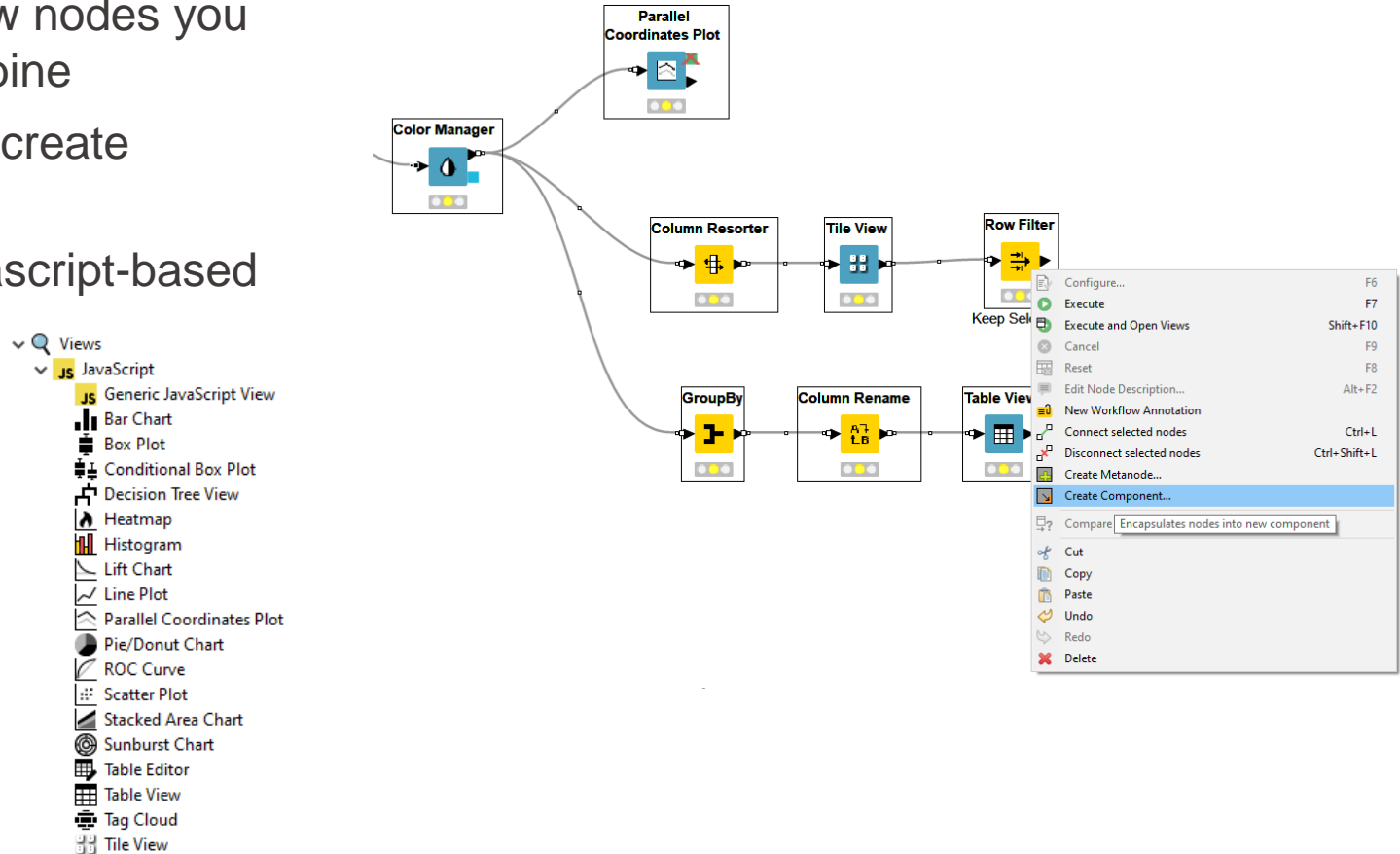
Groupby configuration

- Define the aggregation method in the second tab
- Information about the methods is provided in the Description tab



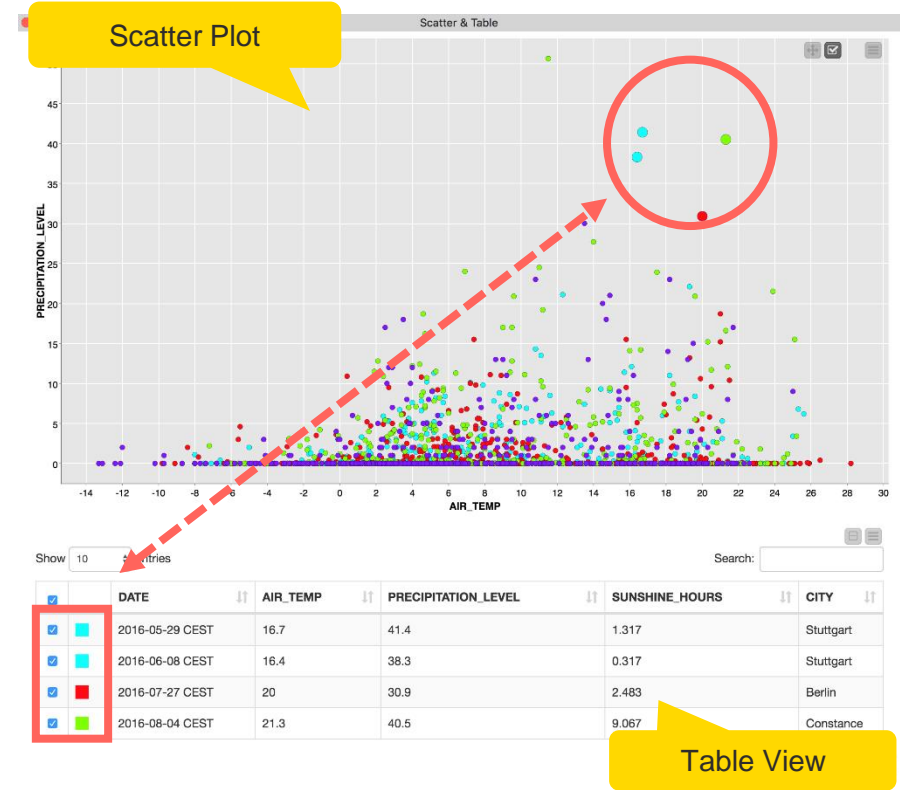
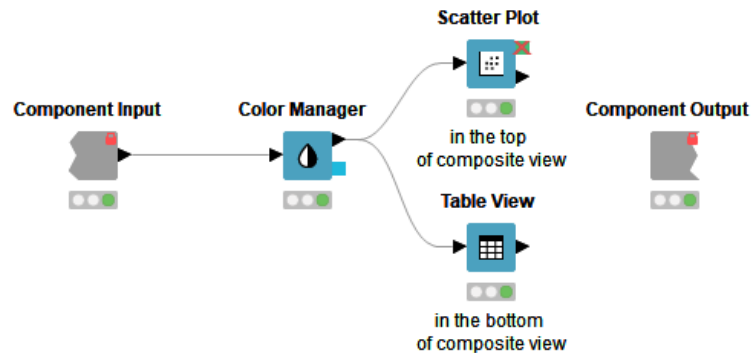
Visualization in components

- Mark the view nodes you want to combine
- Right-click > create component
- Use the Javascript-based nodes

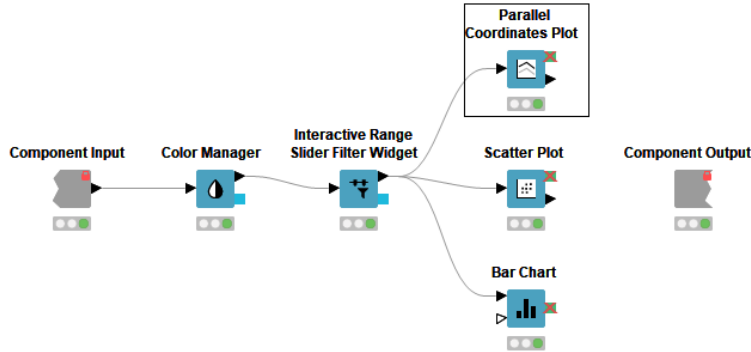


Components – Combined Views

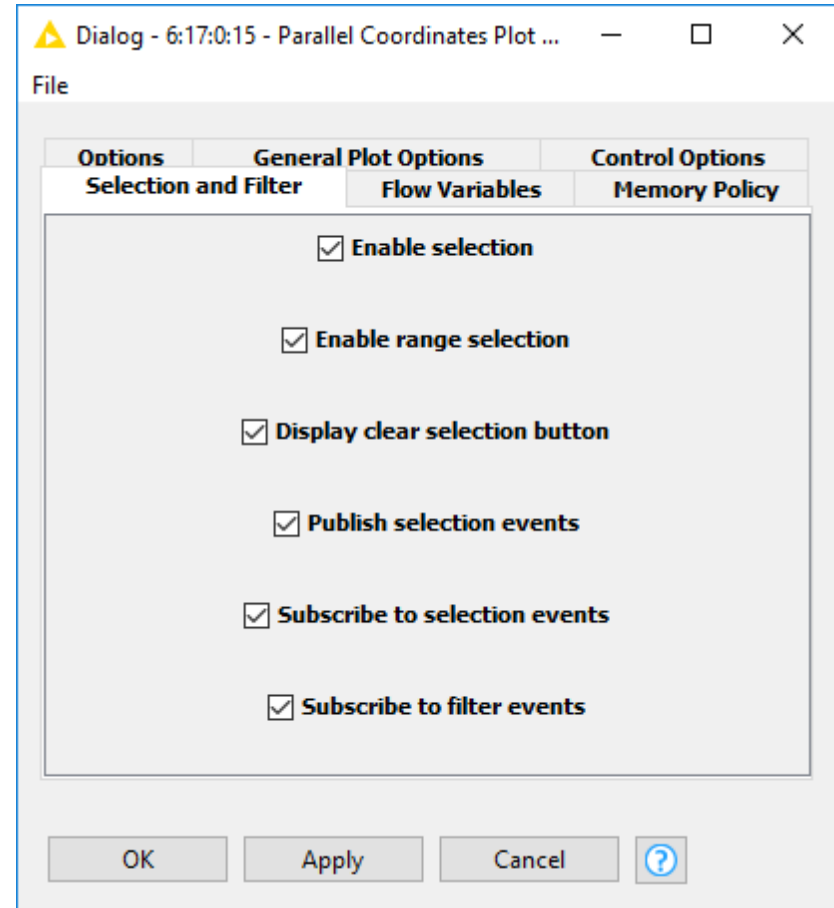
- Multiple JavaScript View nodes can be combined in components
- Selections are transmitted to all other views
- Also for use on the KNIME WebPortal (commercial product)



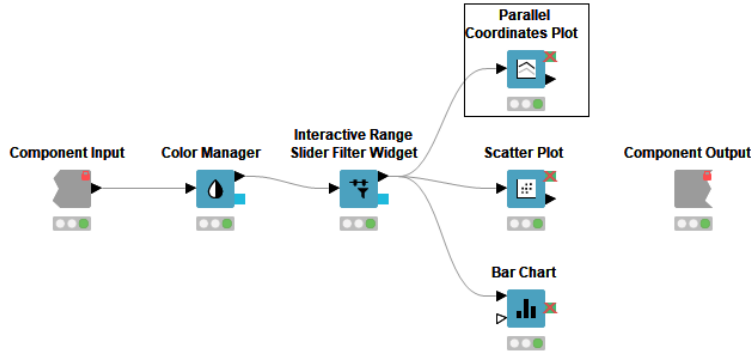
JS-based nodes: Selection and Filter Events



- Selection and Filter tab in many Javascript-based view nodes



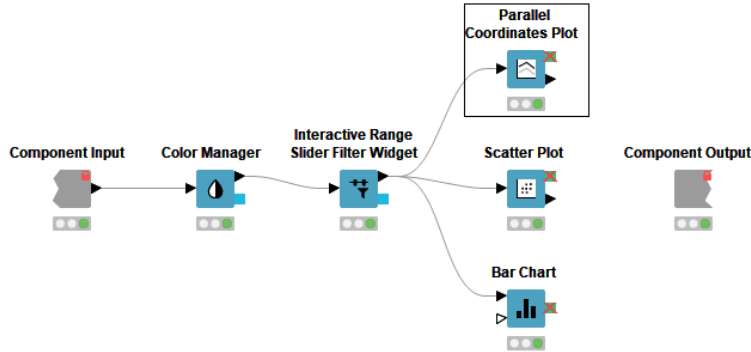
JS-based nodes: Selection and Filter Events



- Listens to the selection made in other view



JS-based nodes: Selection and Filter Events

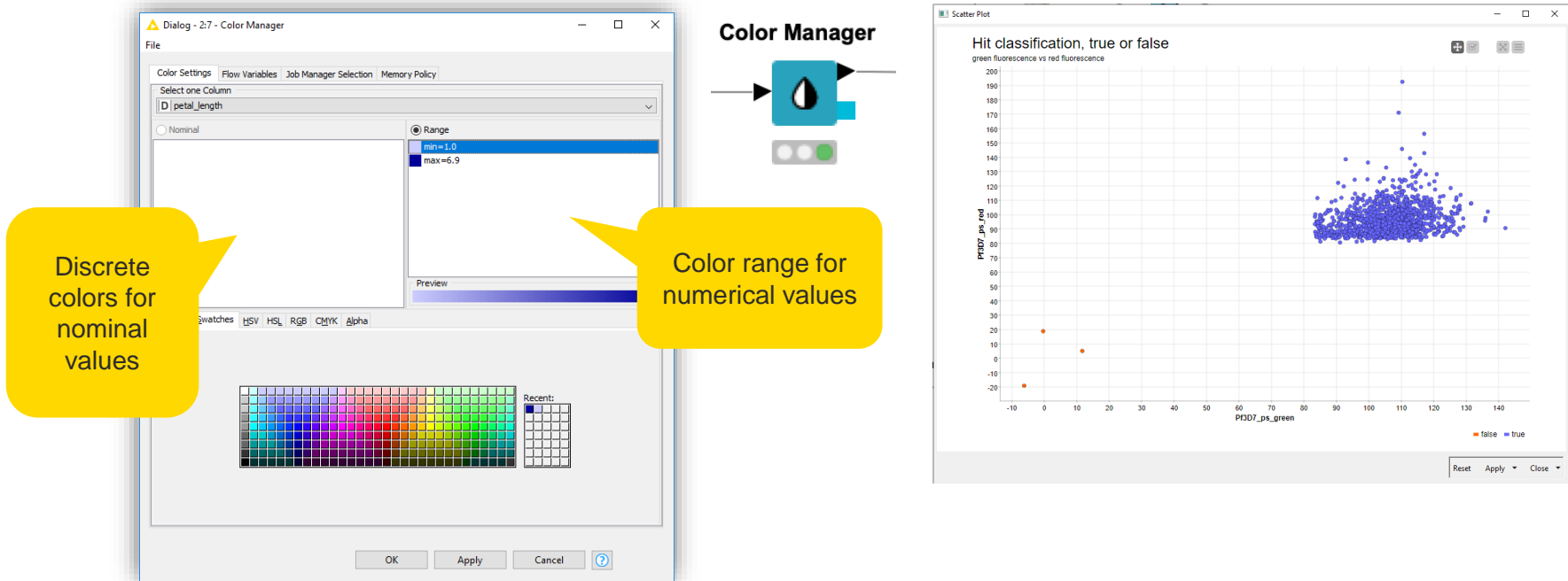


- Makes the other views listen to the selection made in this view



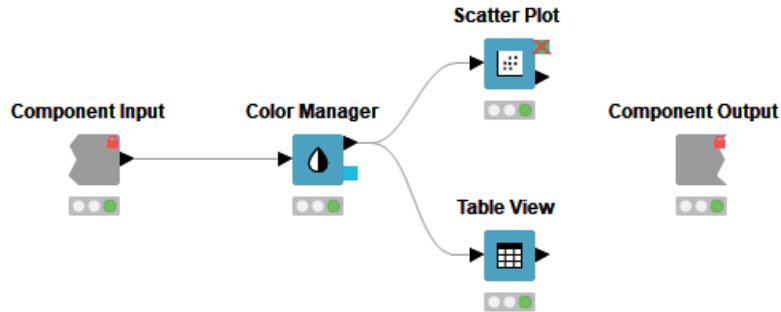
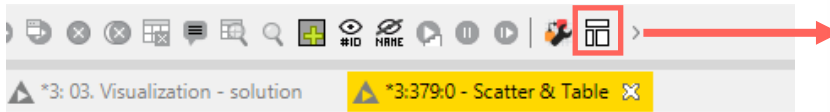
Color Manager

- Colors by nominal or continuous values
- Syncs colors between views using the color model port and Color Appender node

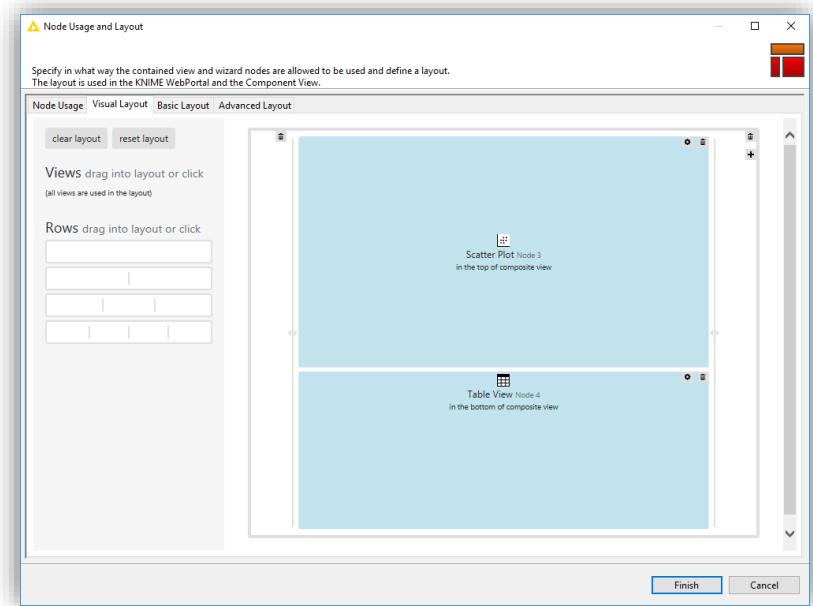


Configure Content and Views Layout

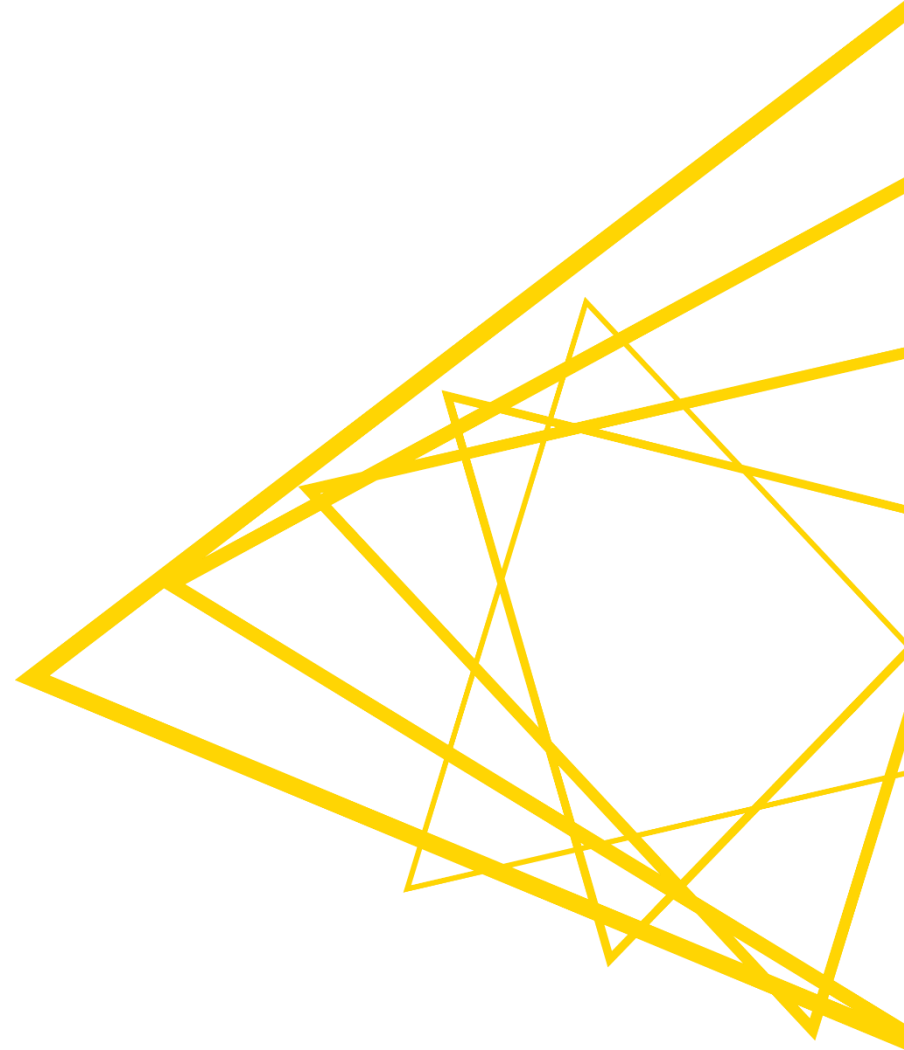
- Click layout button when inside Component to assign views to rows and columns



- Add views and rows via drag&drop
- Add columns using + buttons



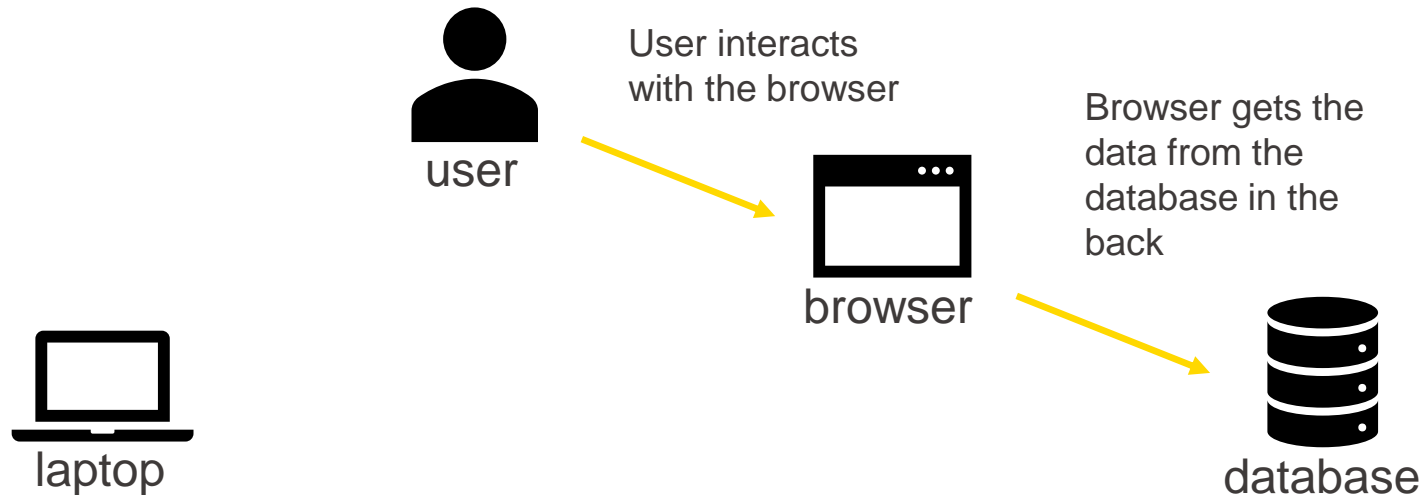
That's it for workflow I...



Workflow II – web service data retrieval

- Instead of retrieving data manually, I can do it in an automated way
- Especially useful for large amounts of data
- Many data sources offer the 'endpoint' to do so (→ REST API, web service)

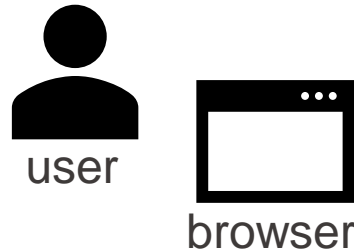
MANUALLY



Workflow II – web service data retrieval

- Instead of retrieving data manually, I can do it in an automated way
- Especially useful for large amounts of data
- Many data sources offer the 'endpoint' to do so (→ REST API, web service)

AUTOMATICALLY



Let the laptop talk to the database directly to retrieve the data



Workflow II – web service data retrieval

- Examples of data sources with an API:
 - <https://docs.mygene.info/en/latest/index.html>
 - <https://chembl.gitbook.io/chembl-interface-documentation/web-services/chembl-data-web-services>
- Construct the according URL to retrieve data for according query

Quick start

MyGene.info provides two simple web services: one for gene queries and the other for gene annotation retrieval. Both return results in JSON format.

Gene query service

URL

```
http://mygene.info/v3/query
```

Examples

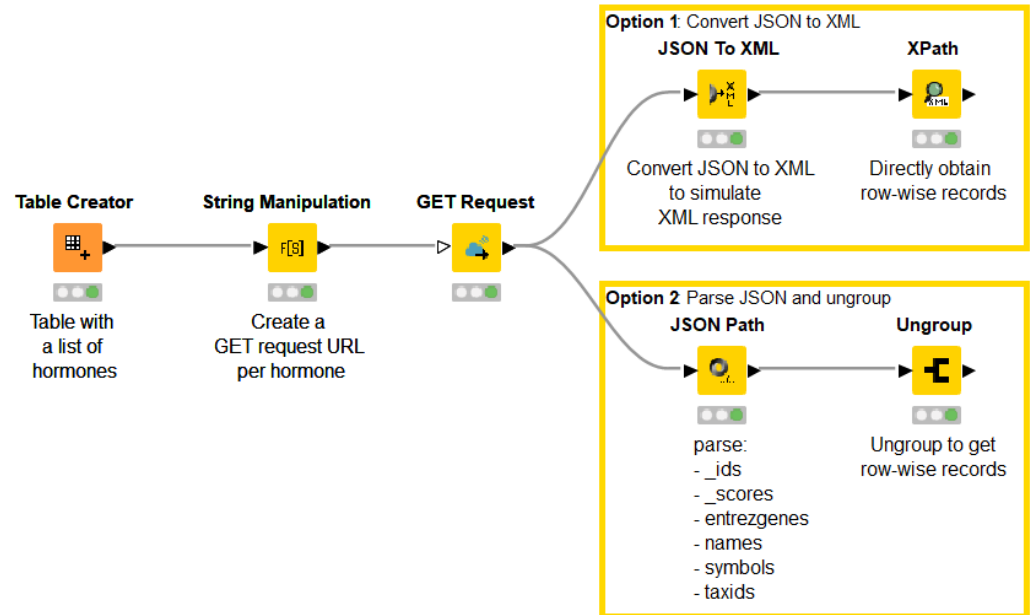
```
http://mygene.info/v3/query?q=cdk2
http://mygene.info/v3/query?q=cdk2&species=human
http://mygene.info/v3/query?q=cdk?
http://mygene.info/v3/query?q=.*
http://mygene.info/v3/query?q=entrezgene:1017
http://mygene.info/v3/query?q=ensemblgene:ENSG00000123374
http://mygene.info/v3/query?q=cdk2&fields=symbol,refseq
```

Steady part

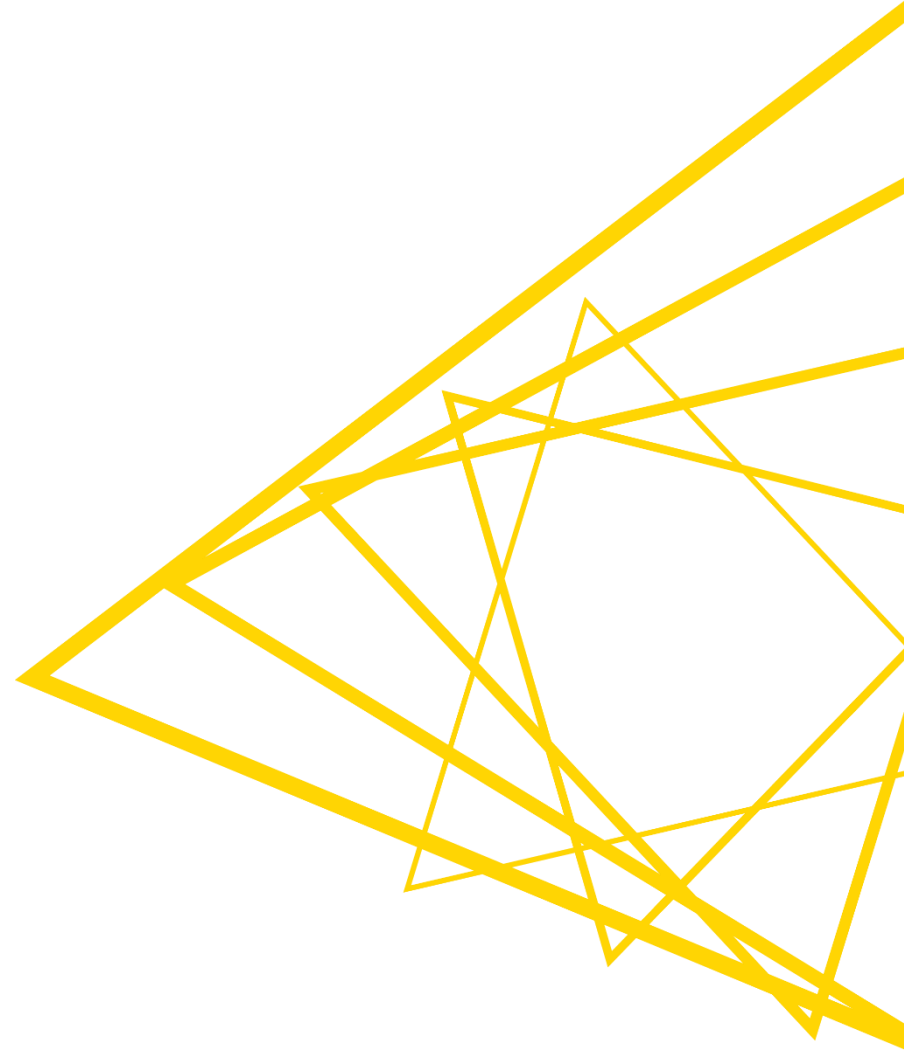


Workflow II – web service data retrieval

- Join the steady part of the URL with your query using the String Manipulation
- The GET Request node ‘talks’ to the DB and retrieves the data
- The result is often not very human-friendly (JSON or XML data format)
- Parse the results to get a neat table



That's it for workflow II...



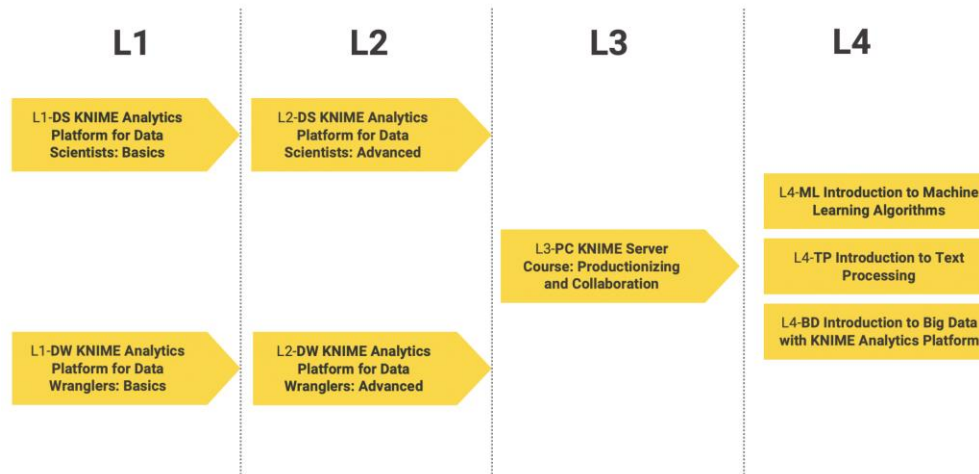
KNIME courses

■ Self-paced courses

- Courses are organized by level L1 (basic) - L4 (specialized)
- lessons with ~5 minutes videos, hands-on exercises, and knowledge-check questions

■ Instructor-lead online courses

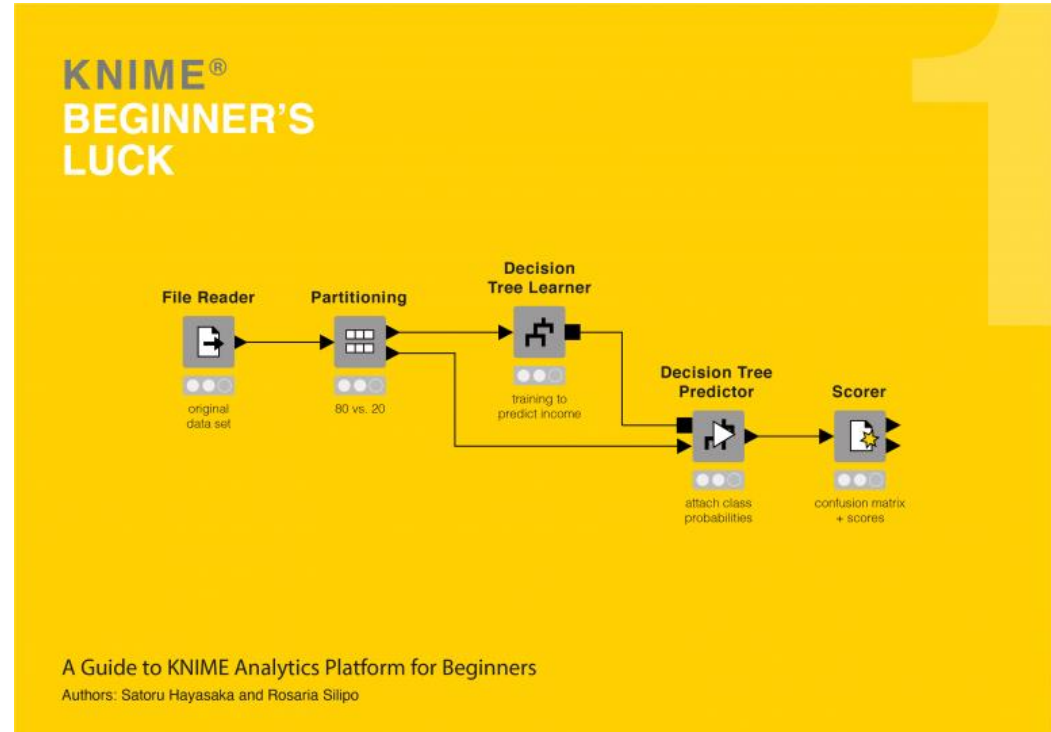
- One week, 1h15 per day
- Possibility to ask questions
- Discount available for academics



<https://www.knime.com/knime-courses>

KNIME book

- KNIME Beginners Luck

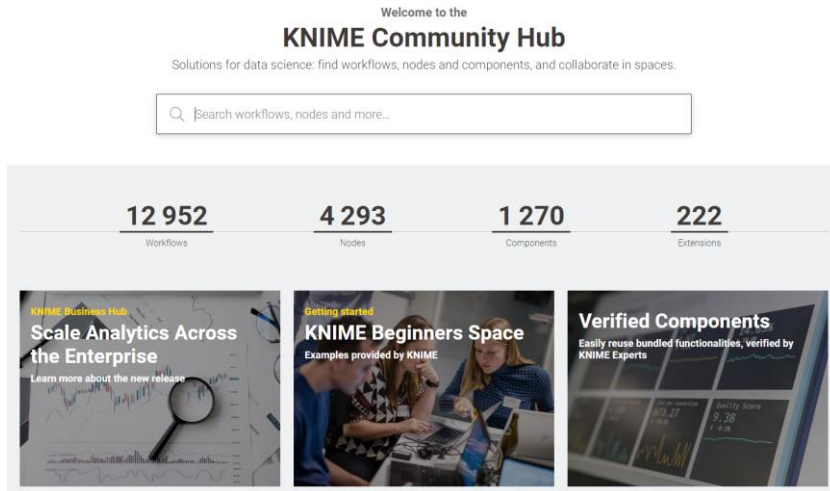


<https://www.knime.com/knimepress/beginners-luck>

More resources

■ KNIME Community Hub

- Find example workflows you can adapt
- Find out e.g. how others use a certain nodes

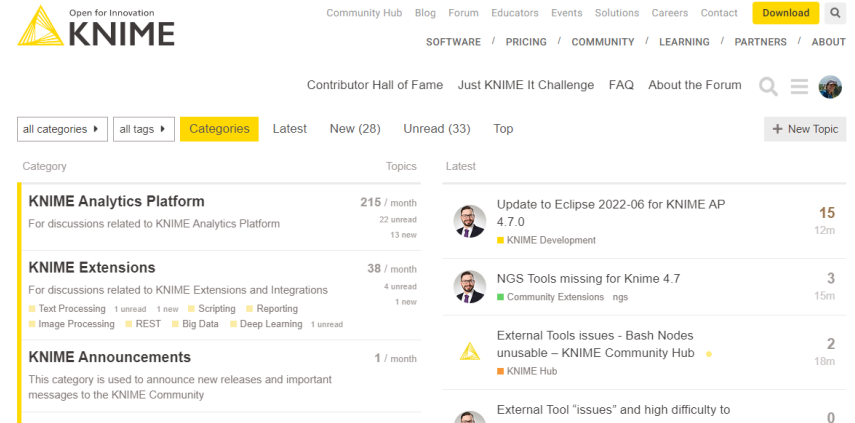


... and Youtube

<https://www.youtube.com/knimetv>

■ KNIME Forum

- Get and find answers to your questions



Cheat Sheets

- Building a KNIME Workflow for Beginners
- Building Components for your Team or the KNIME Community
- Control and Orchestration with KNIME AP
- Data Wrangling with KNIME AP
- Connectors with KNIME AP
- Machine Learning with KNIME AP

Cheat Sheet: Data Wrangling with KNIME Analytics Platform

ACCESS DATA

File Reader
Reads a CSV file from either your local file system or another connected file system. Click the three dots in the lower left corner to add a dynamic connection input port to connect to an external file system. See KNIME AP Access Data Storage.

Database Reader
Reads data from one or more data sources. One connector from each source can be used to read multiple tables from one data source.

Table Reader
Reads data from a table in the database. The table name is entered in the table name field. The table can be specified using a table path, or a path defined in an external file system. A table path is used in the current KNIME installation, or a path defined in an external file system. A table path is used in the current KNIME installation, or a path defined in an external file system.

Table Writer
Writes data from one or more data sources to a table in the database. The table name is entered in the table name field. The table can be specified using a table path, or a path defined in an external file system. A table path is used in the current KNIME installation, or a path defined in an external file system.

Table Reader
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COMBINE DATA

Join
Concatenates the rows of all input tables based on one or more columns. The columns to be joined are specified in the join columns field. The columns to be joined are specified in the join columns field.

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FILTER DATA

Filter
Filters rows in or out of the input table according to a set of rules. The rules are specified in the filter rules field. The rules are specified in the filter rules field.

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WRITE DATA

Table Writer
Writes data from one or more data sources to a table in the database. The table name is entered in the table name field. The table can be specified using a table path, or a path defined in an external file system. A table path is used in the current KNIME installation, or a path defined in an external file system.

Table Writer
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DATE/TIME

Date Reader
Reads data from a date or time column in the input table. The date or time column is specified in the date or time column field. The date or time column is specified in the date or time column field.

Date Reader
Reads data from a date or time column in the input table. The date or time column is specified in the date or time column field. The date or time column is specified in the date or time column field.

Date Reader
Reads data from a date or time column in the input table. The date or time column is specified in the date or time column field. The date or time column is specified in the date or time column field.

Date Reader
Reads data from a date or time column in the input table. The date or time column is specified in the date or time column field. The date or time column is specified in the date or time column field.

Date Reader
Reads data from a date or time column in the input table. The date or time column is specified in the date or time column field. The date or time column is specified in the date or time column field.

RESHAPE AND AGGREGATE DATA

Group By
Groups the rows of a table by the unique values in selected columns and calculates aggregation and statistical measures for the grouped rows. The aggregation and statistical measures are specified in the aggregation and statistical measures field. The aggregation and statistical measures are specified in the aggregation and statistical measures field.

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DATA TYPES & CONVERSIONS

String
Converts the data type of the selected columns from string to integer, double, or boolean.

String
Converts the data type of the selected columns from string to integer, double, or boolean.

String
Converts the data type of the selected columns from string to integer, double, or boolean.

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Converts the data type of the selected columns from string to integer, double, or boolean.

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Converts the data type of the selected columns from string to integer, double, or boolean.

CREATE COLUMNS

Formula
Creates a new column based on a formula. The formula is entered in the formula field. The formula is entered in the formula field.

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Creates a new column based on a formula. The formula is entered in the formula field. The formula is entered in the formula field.

Formula
Creates a new column based on a formula. The formula is entered in the formula field. The formula is entered in the formula field.

Formula
Creates a new column based on a formula. The formula is entered in the formula field. The formula is entered in the formula field.

Formula
Creates a new column based on a formula. The formula is entered in the formula field. The formula is entered in the formula field.

DYNAMIC PORT

Dynamic Port
Adds a dynamic connection input port to the workflow. The dynamic connection input port is added to the workflow by clicking the three dots in the bottom left corner of the node.

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FORMAT EXCEL SHEETS

Format Excel Sheets
Formats the data in the input table to be compatible with Excel. The formatting instructions are specified in the formatting instructions field. The formatting instructions are specified in the formatting instructions field.

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<https://www.knime.com/cheat-sheets>

Thank You!

Questions? Please reach out

`alice.krebs@knime.com`

`zachary.durso@knime.com`

