



# How to add your reactions to generate a Chemical Space

based on BioSolveIT's KNIME nodes

# Introduction to CoLibri™

This tutorial is supposed to show how "normal" drawings of reactions can be easily edited to yield precise reaction definitions that can be handled by BioSolveIT's CoLibri tools.

 In the first section we will show you the step-by-step addition and processing of a reaction using an esterification as very easy example. This part includes as well the formal parts regarding the usage and configuration of the KNIME nodes.



- In the second part four examples are shown which are real parts of BioSolveIT's KnowledgeSpace. These shall show you more cases of the reaction adoption to the tools.
- The 3<sup>rd</sup> part deals with some tips and tricks to facilitate debugging or prettify the results.



# **Drawing of Reactions**

In the very first step we define a reaction for CoLibri in the KNIME system. A simple esterification, where a carboxylic acid and an aromatic alcohol form an ester will be used as showcase:



We recommend to use a recent update of the Marvin Sketch node to draw the reaction.



# Set up Marvin Sketch

By default, Marvin uses its own format, but CoLibri requires the reactions in rxn format:

- Open the node configuration
- Go to the "Output option" tab
- Check "Change structure output"
- Choose "RxnCell" from dropdown

🛆 Dialog - 0:1013 - MarvinSketch (Esterification) —		×
File		
Options       Output options       Flow Variables       Job Manager Selection       Memory Policy         Structure output options <ul> <li>Change structure output</li> <li>Structure name</li> <li>Molecule</li> <li>Structure type</li> <li>Rew RxnCell</li> <li>Outputting multities</li> <li>Sof SdfCell</li> <li>Mol</li> <li>Mol</li> <li>Output as o</li> <li>SwilesCell</li> <li>Output mole</li> <li>CML CMLCell</li> <li>Pos PdbCell</li> <li>Pos PdbCell</li> <li>SMA SmartsCell</li> <li>Marts Smarts SmartsCell</li> <li>Marts Smarts Smarts Smar</li></ul>		
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# **Mapping of Atoms**

CoLibri needs a correspondence between the atoms on the educt side and the related atoms in the product molecule. These "mapping atoms" need to be defined within the Marvin Sketch node:

- Right-click on an atom
- Select "Map" and a number
- Right-click on corresponding atom in the product
- Select "Map" and the same number



	Stereo		>		
	Charge		>		
	Valence		>		
	Radical		>		
	lsotope		>		
	Map		2		Off
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	R-group Attachment Order		2		M3
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[] <sub>n</sub>	Group	Strg+G			
	Add		>		
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N]≡	Label Editor				

 Add mapping numbers only to those atoms that occur on both sides. Atoms without mapping number on the reagent side will be removed (e.g. leaving groups)

#### **Test set for Esterification**

- A test set including matching and non-matching molecules.
- Exact matches on our reaction definition are highlighted in red.



## **Run Reactions with CoLibri**

We start with a minimum workflow including CoLibris "Reaction Product Enumerator" node. This node generates some products and statistics that helps debugging when setting up new reactions.

• Set up a workflow like this:



Configure "Reaction Product Enumerator":

Input React	in fandbieb be	b Manager Selection	Memory Policy				
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⊖ Fas							

# **Start Debugging**

Marvin Sketch

Esterification

# Unfortunately the "Reaction Product Enumerator" fails: **SDF Reader** Check out the stats file:

```
Reaction details:
                                                                                           Test set for Esterification
  Name: esterification
 Number of reagents: 2
    Reagent 1 smarts pattern (1): [$([#8]):5]=[$([#6]):4](-[$([#6]):3]-[$([#6]):2]-[$([#6]):1])-[$([#8])]
    Reagent 2 smarts pattern (1): [\$([#6]):7]=1(-[\$([#6]):8]=[\$([#6]):9]-[\$([#6]):10]=[\$([#6]):11]-[\$([#6]):12]1)-[\$([#8]):6]
  Number of new cores: 0
  Product smarts pattern (1): [0:6](-[c:7]-1=[c:12]-[c:11]=[c:10]-[c:9]=[c:8]1)-[C:4](-[C:3]-[C:2]-[C:1])=[0:5]
Matching details:
  Number of matches for reagent 1: 3
    Molecule: O=C(O)CCC Row1
    Molecule: O=C(O)CCC1CCCC1 Row2
    Molecule: O=C(OCC)CCC Row4
  Number of non matches for reagent 1: 9
  Number of matches for reagent 2: 0
  Number of non matches for reagent 2: 12
Fragments statistic:
  Fragments for reagent 1: 2
  Fragments for reagent 2: 0
```

=> No matches on reagent 2! This seems strange, because we have drawn the matching reagent. But it is a question of the details in the drawing...



Reaction Product Enumerator

Node 1018

# **Define Aromaticity in Educt and Product**

When using the RxnCell format in Marvin Sketch, it processes compounds with alternating bonds exactly like they were sketched. The sd-file reagent input is interpreted to have aromatic bonds. Our reaction definition need to be adjusted:

Right-click on an aromatic bond Single Type Select "Type" => "Aromatic" Double Bold Hashed Triple Aromatic Topology Reacting Center Single Up Stereo Search Single Down Single Up or Down  $\sim$ Arrange Double Cis or Trans Align Double C/T or Unspec С/Т × Delete ÷ Single or Double []n Group... Strg+G Single or Aromatic 1 Double or Aromatic :1 Add 1 Anv Transformation Coordinate Format... Edit Properties...

Don't draw alternating single and double bonds!

#### **Rerun "Reaction Product Enumerator"**

Rerunning the node works! But we get 8 products instead of the expected 1. So have many more matches than anticipated. Let's take a look at the enumerated products:

- ▶ Right-click on the "Reaction Product Enumerator"
- Choose "Enumerated molecules"



Max number of enumerated products: 8



#### Look out for trash molecules



# Define your substructures as precise as possible

From this set of products we can learn the most important thing for the correct definition of reactions: your drawing will be interpreted as a substructure!

• Phenol is the substructure of naphtol and ethoxybenzene



CH3

Note that hydrogens are ignored!

They are just added by the drawing program by default

Be as specific as possible and define the environment of an atom!
 E.g. annotate, if something is supposed to be terminal. Even if the naphtyl could be accepted for this reaction, the ether is definitely not!



# **Define the Environment of atoms**

The classical way to define the environment is using SMARTS. You find them in Marvin Sketch here:

- Click on the "periodic table" (1.)
- Go to "Advanced" (2.)
- Choose SMARTS (3.)
- Type in your definition (4.)
   e.g. [O;D1] to define an alcohol
- Close and click on the atom we want to edit

Dialog - 0:10	13 - MarvinSketch (Esterification) -	$\Box$ ×
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	Description	
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<b>→</b> •	G1 G2 G3 G4 G5 G6 G7 G8 G9 Pol *	F
	G10 G11 G12 G13 G14 G15 G16 G17 G18 Alkyl 🗸	
. J <sub>n</sub>	R-groups	2 P
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	Close	
	OK Apply Cancel 🤇	)

#### Phenol with defined Environment

The code [O;D1:6] defines an oxygen with only one heavy atom as neighbor (D1) and a mapping number of 6. It will look like this:





## **SMARTS vs Labels**

Alternatively to SMARTS you can use "labels", which are simply pre-defined SMARTS-pattern that make the drawing easily human-readable. You find this option again in the advanced editor mode.

The molecule will look like this:



odic Table Advanced			
Description			
Generic query atoms	Atom guery properties		
A Q M X	.H+ .v+ .X+ .R+	.r+ .rb+ .s+ .h+ .D	+ .u
AH QH MH XH	.HvXR-	.rrbshD	a/A
Periodic Table Groups		Special nodes	
G1 G2 G3 G4 G5	G6 G7 G8 G9	Pol *	
G10 G11 G12 G13 G14	G15 G16 G17 G18	Alkyl	$\sim$
R-groups			
R1 R2 R3 R4 R5	R6 R7 R8 R9 R10	R11 R12 R13 R14 R1	5 R 16
R17 R18 R19 R20 R21	R22 R23 R24 R25 R26	R27 R28 R29 R30 R3	1 R32
Custom Property			
Type: R-group Alias	Pseudo SMAR	rs Value	
Value: Alcohol			

#### Where to find pre-defined Labels

#### All pre-defined labels can be found and edited in the Enumerator.

	🛆 Preferences				- 0
	type filter text	CoLibri			<> ▼ <
▲ Dialog - 0:1018 - Reaction Product Enumerator — □ × File	> General > Help > Install/Update	Here you may declare (a) substructure labels for (b) SMARTS-patterns that	r SMARTS-patterns that you can use in rxn reaction def t denote protecting groups which should be removed a	nitions fter clipping	
	> Java	Substructure Labels Pro	otecting Groups		
Options Flow Variables Job Manager Selection Memory Policy	✓ KINIVIE ✓ BioSolvelT	// 1st created by (	Greg Landrum, October 2006		
Input Reactions	CoLibri	<pre>// Last edited by ! // Format (<space></space></pre>	Franca Klingler, January 2020 = one or more spaces): Label <space>Smart.</space>	s <space>Comments</space>	
Reaction column Real Molecule V Name column S name V	> Community Scripting	AcidChloride	C(=0)Cl	Acid Chloride	
Capta ra Calibri	Customization Profiles	CarboxvlicAcid	C(=0)[0:D1]	Carboxvlic acid	
	Databases (legacy)	Alphalminologid	re (C_1C+1e (C_114e1) 1_1N+1H0+1e (N_114e+	1411) • 1¢/N_C= [0 N S1) 1) 1 (=0) / [0 • H	-1) alpha Amino Acid
Input Molecules	> Erlwood	Alphanimoacid	[\$(C-[C;:\$(C-[:#6])]-[N;:N0;:\$(N-[:#6;	:#1]);:\$(n=c=[0,n,5])])](=0)([0;n,	-]) alpha Amino Acid
	Generic KNIME Nodes	SulfonylChloride	[\$(S)](=0)(=0)(C1)	Sulfonyl Chloride	
	> HCS-Tools	Sulfone	[\$([#16X4](=[OX1])=[OX1]),\$([#16X4+2](	[OX1-])[OX1-])] any sulfone	
Enumeration	KNIME Explorer	Amine Amine.Primary Amine.Secondary	[N; !H0; \$ (N-[#6]); !\$ (N-[!#6; !#1]); !\$ (N- [N; D1; !\$ (N-C=[0, N, S])] [N; D2; \$ (N (-[#6]) - [#6]); !\$ (N-C=[ [N: D2; \$ (N (=[46]), [#6]); !\$ (N-C=[	C=[O,N,S])] Amine Primary O,N,S])] Secondary	
<ul> <li>Full enumeration (limited to 1,000,000 products)</li> </ul>	> Marvin	Amine. Terciary	[N;D3;\$(N(-[#0])(-[#0])-[#0]);:	(N-C=[0, N, 5])]	
Random enumeration	Master Key Meta Info Deformance	Nitro	[N; \$ (N (=0) 0) ]		
	PIA - Protein Inference A	BoronicAcid	[\$(B-!@[#6])](O)(O)	Boronic Acid	
Number of random products 100 🚖	Preferred Renderers	Isocyanate	[\$(N-!@[#6])](=!@C=!@O)	Isocyanate	
	> Table Backend	Alcohol	[O;H1;\$(O-!@[#6;!\$(C=!@[O,N,S])])]	Alcohol	
Output Settings	> Vernalis	Aldehyde	[CH;D2;\$(C-[#6])]=0	Aldehyde	
Statistics and non matching reagents	openBIS	Halogen	[F,C1,Br,I]	Halogen	
Create full statistics and open in external editor	> Run/Debug	Azide	[N:H0:\$(N-[#6]):D2]=[N:D2]=[N:D1]	Azide	
O Check unmatched molecules for specified reagents and store in 'non matching reagents' error table	> leam	Amountin		Averatic stor	
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		EWG	[F,Cl,N&\$(N(=0)0),S&\$(S(=0)0),C&\$(C(=0	0)] Electron Withdrawing Groups	
Append input columns		EDG	[N&\$([N;H2]),O&\$([O;H]),C&\$([C;H2])]	Electron Donating Groups	
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OK Apply Cancel 🕐	< >				Restore Defaults App
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#### **Update Esterification Reaction**



The aromatic alcohol is precisely defined but the hydroxyl group of the carboxylic acid is not. The label CarboxylicAcid exists but as we cut off a bond inside this group it is better to use the SMARTS [O;D1]:



#### **Rerun "Reaction Product Enumerator"**

The list of enumerated molecules does not contain trash molecules with senseless valences at the oxygen anymore.

But still other building blocks than phenol match the aromatic ring (e.g. naphtol and cresol). Let's look at the input and decide which building blocks to allow for the individual reagents.



# **Building Block 1**

From a chemists point of view free carboxylic acids could work for reagent 1. Which reagents match/ do not match on our definition?

- Reagent 2 & 3 match
- Reagent 1 & 5 does not match
- Reagent 4 & 6 does not match

A butyric acid is drawn which is a substructure only of reagents 2 & 3. We need to reduce our definition to the minimum substructure, which is acetic acid:





# **Building Block 2**

Decide which of the building blocks should run the reaction. If we go for aromatic alcohol only 2 – 5 are desired but not 1 & 6. Which reagents match/ do not match on our definition?

- Reagent 2, 3 & 5 match
- Reagent 1, 4 & 6 does not match

A phenol ring is drawn which is a substructure of reagents 2, 3 and 5 but doesn't match on 4. Again we need to reduce our definition to the minimum substructure. This can be done by using the SMARTS [c] (aromatic carbon marked as 'a') and the label 'Alcohol': 4;Alcohol

OH

5;(a)



# **Debugged Reaction Definition**



# **Build a Fragment Space**

Now that we have debugged the reaction setup we like to build a fragment space. Therefore, replace the "Reaction Product Enumerator" by the "Reaction Space

Generator". Combine several spaces using the "Concatenate" node followed by a "Chemical Space Merger" node to generate a searchable space.



take a look into our BioSphere workflow

#### Part 2: Example Reaction from KnowledgeSpace

- Example 1: Ringclosing Benzoxazole formation
- Example 2: Multicomponent Scicinski reaction
- Example 3: Substitution hetero aromatic substitution
- Example 4: Coupling Di Mauro reaction

# Example 1 – Ringclosing

As first example we use something similar to a benzoxazole ring closure, where an aminophenol reacts with an aldehyde:



Let's make it suitable for CoLibri and add the mapping atoms:



# Example 1 – R Groups

CoLibri does not understand R groups. Replace it with the atom that should be in this position. Think in substructures! In this example R1 can be carbon or nitrogen\_

- open the Advanced settings
- click on SMARTS (1)
- type [C,N] in the "value" field (2)
- Close and replace R1 on educt side



- Open Adanced settings
- Choose Generic query atom "A" (3)
- Close and replace R1 on product side

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AH QH	MH	XH			.H-	.v-	.X-	.R-	.r-	.rb-	•S-	.h-	.D-	.a/A
Periodic T	able Gro	ups								Specia	l node	s		
G1 G2	G3	G4	G5	G6	G7	G8	G9			Pol	*			
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## Example 1 – Functional Groups

The amine definition need to be more precise. Remember: Hyrogens are ignored! You can either use the SMARTS or a label:



Theses three definitions mean similar things, but the label 'Amine.Primary' contains the most precise definition, i.e. [N;D1;!\$(N-C=[O,N,S])]

The oxygen need to be defined as alcohol (and not the substructure of an ether). Again, the easiest way is to use the label 'Alcohol' leading to:



## Example 1 – Reduce to Essential Minimum

In the last step, we remove any needless atoms to define the reaction. Keeping the substructure to the essential minimum reduces the risk of errors during the subsequent processing.

- The aromatic ring can be reduced to the connecting carbons with an implicit SMARTS definition: [cH0;r6] (which means an aromatic carbon without hydrogens in a sixmembered ring.
- Avoid explicit hydrogens! Therefore, atom 5 should be edited to [CD2] (carbon connected to two heavy atoms only) containing the hydrogen in an implicit definition. Note that [CH] and [CD2] are in principle the same. Definition of heavy atoms is easier applicable to more cases.



#### Example 2 – Multicomponent

In this reaction, an amino acid reacts with an alcohol and an amine to form a heterocycle. Reagents were drawn and atom mappings added to all atoms occurring on both sides of the reaction arrow:



First, we define N3 and N7 as primary amines and the oxygen in reagent 2 as an alcohol:



### Example 2 – Any Atom

Atom 1 should be any heavy atom. The "\*" in a SMARTS covers also a hydrogen and need to be adjusted to [\*;!#1]. We recommend to use the label "Heavy.Atom", which leads to a suitable reaction definition. The same expression is used for atoms 5 and 7:





## **Example 3 – Substitution**

In a hetero aromatic substitution, different numbers of nitrogens can be in the aromatic ring. Thus, only one nitrogen is mandatory and in two more positions optional. For this we use lists be adding the SMARTS [c,n] (aromatic carbon or aromatic nitrogen). On the product side the corresponding positions are defined as "A".

Furthermore an amine (primary or secondary) is needed as second reagent, which can be defined with label "Amine".



# Example 4 – Coupling

This coupling reaction can also be described as a two-stage reaction. The core fragment takes place in a carbon-carbon coupling first, followed by an amidation. The reagents are drawn below and all atoms are already mapped:



Think about how the reaction definition needs to be improved. There are 4 unprecise information.



#### Example 4 – Leaving Groups

First, we add the Amine.Primary label to N1. Note that this lable is not needed for N13. All substitutions are allowed at this position.



Second, we modify the leaving group connected to C9. According to the reaction description, it can be either Br or I which is described by the SMARTS [Br,I]:



#### **Example 4 – Unsubstituted Atoms**

Third, c10 need to unsubstituted. The SMARTS [c;D2] ensures that the aromatic carbon is connected to two heavy atoms only. The same SMARTS was added to c3 as this is demanded by the reaction protocol:



Fourth, the carboxylic acid need to be defined to have a terminal hydroxy group, excluding the substructure of an ester using the SMARTS [O;D1]:



# Part 3: Tips and Tricks

- Reaction names
- Compound ID Generation
- Reagent specifier
- Remove protecting groups

#### **Reaction Name – Marvin Sketch**

We recommend to pass the reaction names as properties. This enables CoLibri to generate a product ID including the reaction name. Choose Name column in the "Reaction Product Enumerator"/"Reaction Space Generator" nodes.



# **Compound ID Generation in CoLibri**

Compounds of combinatorial libraries usually have an ID following this scheme: Reaction-name\_ID-building-block-1\_ID-building-block2

In order to generate this name within KNIME the compound ID need to be set as RowID. This can be done in 2 ways:

- SDF Reader: Enable "Use molecule name as rowID" in the node's configuration dialog.
- RowID: Interconnect the RowID node and define the Molecule name as "New RowID column" in the configuration dialog.



# **Reagent Specifier**

For some reactions it might be useful to specifically select building blocks for reagent 1 and building blocks for reagent 2. In this case the implementation of a Reagent specifier (number (integer)) hands over the information to CoLibri. Simply select the reagent specifier column in the "Reaction Product Enumerator".



## **Remove Protecting Groups**

Functional groups not participated in the reaction are sometimes protected. A list of protection groups can be found in the same way as the list of labels. If the "Remove Protecting Groups" is enabled in CoLibri, listed protecting group will be removed in the product molecule.

A carboxylic acid can be protected by a tert-butyl group. The protected or the deprotected form can be obtained in the product molecules





## **Recommendation summary**

- Think in substructures! Identify the minimum substructure that precisely defines a suitable reagent! Use lists, SMARTS and labels to be as specific as needed!
- An "R" for a side chain is not necessary in fact, it is not allowed!
- Use mapping numbers for all atoms which occur on both sides!
- No atom lists on the product side. Use any atom "A" instead!
- Do not draw localized bonds when you mean aromaticity!
- Do not draw explicit hydrogens. If needed define the number of heavy atom neighbors!

