### **Tutorial**



### Using CoEd The EGene's Configuration Editor

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### Tutorial: using CoEd

The goal of this tutorial is to explain how to use the graphical tool CoEd to configure and run an EGene pipeline. We will:

 explain how to start CoEd and the various parts of the graphical window;

- configure a pipeline with four steps;
- run the pipeline directly from CoEd;
- produce an EGene Configuration file and run the same pipeline from command line;
- configure a new pipeline using parts of the old one.

### Starting CoEd

- Initially, we need to start CoEd with the command:
   coed.pl
- This is a Perl script that will start the Java application. The graphic window of CoEd will appear:

### Starting CoEd

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### Explaining CoEd: component buttons

• The bottom part of the window contains a bar with buttons representing the components that can be used for the pipeline steps. Here CoEd is configured to show 19 components:

### Explaining CoEd: component buttons

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### Explaining CoEd: the tool bar

 On the top of the canvas we have a tool bar with 10 action icons: new, open, save, close, add pipe, copy, cut, paste, undo, redo, and run pipeline.

### Explaining CoEd: the tool bar



The top part of the window presents 3 pull down menus, offering all the functionality available with the buttons and some extra ones:

- File: new, open, save, save as, import, export, close, exit
- Edit: copy, cut, paste, undo, redo, clear selection, select all
- Add: list all components available for placing on the canvas

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#### Add: list all components available for placing on the canvas

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### Creating a Pipeline

### Now we will configure a pipeline with 4 steps:

- Upload sequences from chromatogram files to the pipeline;
- Trim the low quality regions of the sequences;
- Look for sequences that match a database with ribosomal sequences, eliminating them from the reads being processed (in EGene, invalidating them);
- Generate a graphic report showing the quality of the remaining sequences.

### Creating a Pipeline

First of all: creating a new pipeline

- Click on the New icon.
- ... or on the File New option from the pull down menu.
- Enter a name for the pipeline (i.e. test). This name will appear at the upper left corner tab.
- The bottom status bar will display a message warning that a new pipeline has been created.

### Creating a Pipeline

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### Explaining CoEd: the canvas

• The canvas is the place where icons representing the pipeline steps (nodes) will be placed and manipulated.

### Explaining CoEd: the canvas

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### Configuring the Pipeline: upload traces

- For each step we should select the component from the component button bar or from the pulldown menu.
- After selecting the component, click the left mouse button on the place in the canvas you want the component to be placed.
- A window with the configuration parameters will open up.

### Configuring the Pipeline: upload traces

Upload\_traces only has two mandatory parameters:

Phase name (the text that will show above the icon)
The name of the directory containing the chromatograms to be uploaded

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## Configuring the Pipeline:upload

## After clicking OK, the canvas will display the new component:

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- The next step is to trim the low quality parts of the sequence.
- We use the component trimming.pl.
- You can this time select the component from the pull-down menu.

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## After clicking the left mouse button on the canvas, you get the configuration window:

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Only one argument is mandatory: phase name

There are many optional arguments, all with default values. We will use the default values. For an explanation about the arguments, please see the tutorial on building pipes and the component documentation.

- After the configuration we now have two components on the canvas. We can use the "add pipe" not connect them.
- Click on the arrow (add pipe) icon. Now click first on the component that should process information before (upload), and then on the next one (trimming).

## Configuring the Pipeline: the first two components

#### Now we have a pipeline with two components:

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# Configuring the Pipeline: filtering against ribosomal sequences

- The next step is to filter out ribosomal sequences.
- This will be performed using BLAST.
- We will use the filter-blast.pl component.

## Configuring the Pipeline: filtering against ribosomal sequences

- filter-blast.pl has two mandatory arguments:
   phase name and database to be searched.
- There are also seven optional arguments, all with default values.
- We will accept the default values and assume that the database is located at:
  - ../../databases/ribosome.fasta
- For more details, check the other tutorials or the component's documentation.

## Configuring the Pipeline: filtering against ribosomal sequences

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## Configuring the Pipeline: generating a graphical report

- We now will configure the last component: the simple graphical report
- We repeat the procedure of selecting the component from either the buttons or the pull down menu.
- The configuration window now shows five parameters
  - Three mandatory parameters: phase name, report file name, directory to place the graphics files (for more details check the other tutorials)
  - Two optional parameters: sequence\_valid and primer\_database

## Configuring the Pipeline: generating a graphical report

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# Configuring the Pipeline: generating a graphical report

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## Configuring the Pipeline: connecting the two last components

 We now use the arrow (add pipe) icon to connect the last two components to the pipeline.

- Remember:
  - click the add pipe icon:
  - connect two components, clicking each one with the right button, in the order in which they should be placed in the pipe
- We now have the complete pipe.

## Configuring the Pipeline: connecting the two last components

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## Configuring the Pipeline: setting the first component

- The next step is to define what is the first component to be executed in the pipeline.
- To set a component as the first one, place the mouse over it and use the right button menu, selecting the "first process values" option.
- We can now run the pipe.

## Configuring the Pipeline: setting the first component

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## Running the pipeline: the "run pipeline" icon

• To run the pipeline, click on the "run pipeline" icon:



- CoEd will ask you were should the pipeline be executed (remember that file names can be relative).
- You can click on the mouse right button and navigate to find the directory of the CoEd tutorial.
- Let's assume we are at

/home/tutorials/examples/CoEd/

## Running the pipeline: setting the work directory

andatory fields	
work directory:	
/home/tutorials/examples/CoEd	
standard error file:	
standard error file: bigou.err	
bigou.err	

## Running the pipeline: results

#### CoEd notifies you that the pipe is running:



 Pipelines run in the background, so you should check your directories to see when the pipe has finished.

## Running the pipe: results

 After completing the pipeline, your directory should contain the file report.html and the directory figures\_dir, which contains the graphical reports. Use a browser to look at the report.html file.

## Pipe results: the report file



### Running the pipe: final comments

- Important note: CoEd is a handy tool for configuring the pipe and testing the appropriate parameters.
- However, for massive processing it is best to use bigou.pl once the pipe is configured. That way, pipeline processing can be included into a Unix script.

### Saving your work

Now use the save button to save your work:



CoEd's standard file extension is \*.gen.

• You can also generate an EGene file (\*.cnf) using "save as" from the pull-down menu. EGene files can be used by bigou.pl, but they do not keep information about the position of the icons.

• Save your pipeline in EGene format as test.cnf

## Saving your work in EGene format

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## Saving your work in EGene format

#### Save your work.

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🗋 xml_phrap.	cnf	
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		Save Cancel

Now use the close button.



## Loading an existing file into EGene

To edit an existing pipeline, open its EGene or CoEd description.

Use the open button:



### Loading an existing file into EGene

## Select the format your pipeline file (EGene or CoEd):

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Look <u>i</u> n:	config_files	
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### Loading an existing file into EGene

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### Test.gen is now back to CoEd

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## Editing pipelines: using the editing operations

- You can use the editing buttons to edit your pipeline.
- You can copy 🗎 , cut 👗 , and paste 🕄 all or some of the components of your pipeline.
- Editing can be undone or redone using...
- ...the undo
   and redo
   buttons.







Try them!

## Creating a new pipe

- First, click on the "new" icon in the tool bar.
- You will be asked for the name of the new pipeline.
- Fill the File Name form with new.gen.

K New		
Look <u>i</u> n: 🔲 d	onfig_files	
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### Creating a new pipe

#### • A tab new.gen will be created on the canvas.

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### Creating a new pipe

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## Creating a new pipe from an existing one

 You can create a new pipeline from an existing one by loading a pipe into CoEd, modifying it, and using the "File Save As" option in the pull-down menu.

## Switching pipelines in CoEd

 You can switch among different pipeline by selecting the respective tab.

Select the test.gen pipe by clicking on the respective tab.

## Creating a new pipe from an existing one

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# Copying part of a pipeline into another pipeline

You can copy parts of a pipeline into another pipeline. Select the part of the pipeline you want:

- We will select all components but the first one.
- To do this, click the left button of the mouse on the canvas and drag it to delimit a region including the three last components.
- Alternatively, you can click on each component.
- To deselect all components click on the canvas.

## Copying part of a pipeline into another pipeline

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Copying and pasting the selected steps into the new pipeline

- Click on the "copy" icon in the tool bar.
- Now click on the the new.gen tab.
- Use the "paste" icon to copy the previous components into the new pipeline.
- You should now have the following pipeline:

# New pipeline added of pasted components

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### Finishing the new pipeline

- We will now add a new upload component, this time for uploading Phred files from a phd\_dir directory
- And... we will generate a graphical report with a new name, changing the specification of the last component.

## Adding a new upload component

• We should use the upload\_phd\_dir component.

Upload Phd

This component has only two parameters, both mandatory: PHASE name and phd directory:

Edit the upload_phd_dir component	
Mandatory fields	
PHASE:	
upload_phd_dir	
phd_directory:	
phd_dir	
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• After placing the component, use the arrow button to put it at the beginning of the pipeline.

## Pipeline with the added component



## Editing the pipeline: changing the parameters of a component

 To change the values of a component, place the mouse over it and use the right\_button menu, selecting the "Change values" option.

## Editing the pipeline: changing the parameters of a component

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# Editing the pipeline: changing the parameters of a component

- The configuration window will appear.
- Let's change the html\_report\_name to rep2.html and dir\_name to other\_figs.

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dir_name:	
other_figs	
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### Running the new pipeline

- Choose the upload step as the first process.
- Now, use the "run pipeline" bar to run the new pipeline.



icon in the tool

- Use the browser to compare the results with those of the previous files.
- You can also save the pipe in EGene format and use bigou.pl from the UNIX command line to run it again.



#### We support pipes! For peace.

**THE END!**