

Hands-On Session

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SMT Pipeline

Preprocessing

- tokenizer
- tagging
- lemmatization

Alignment

Phrase extraction

Tuning

Decoding

Postprocessing

- recasing
- detokenizer

Scoring

- BLEU score

Using the Experiment Management System (EMS)



- In brief
 - from raw data to tuned MT system
- Wrapper for everything needed to
 - Train
 - Tuning
 - Decode
 - Evaluate
- Require
 - config file



Using the EMS

ssh guest@odin.inf.ed.ac.uk

Password = Edinburgh123

```
cd workspace/experiment/fr-en/<river>/  
nohup ./run.new.sh config.pb &
```

config file:

steps/1/config.1

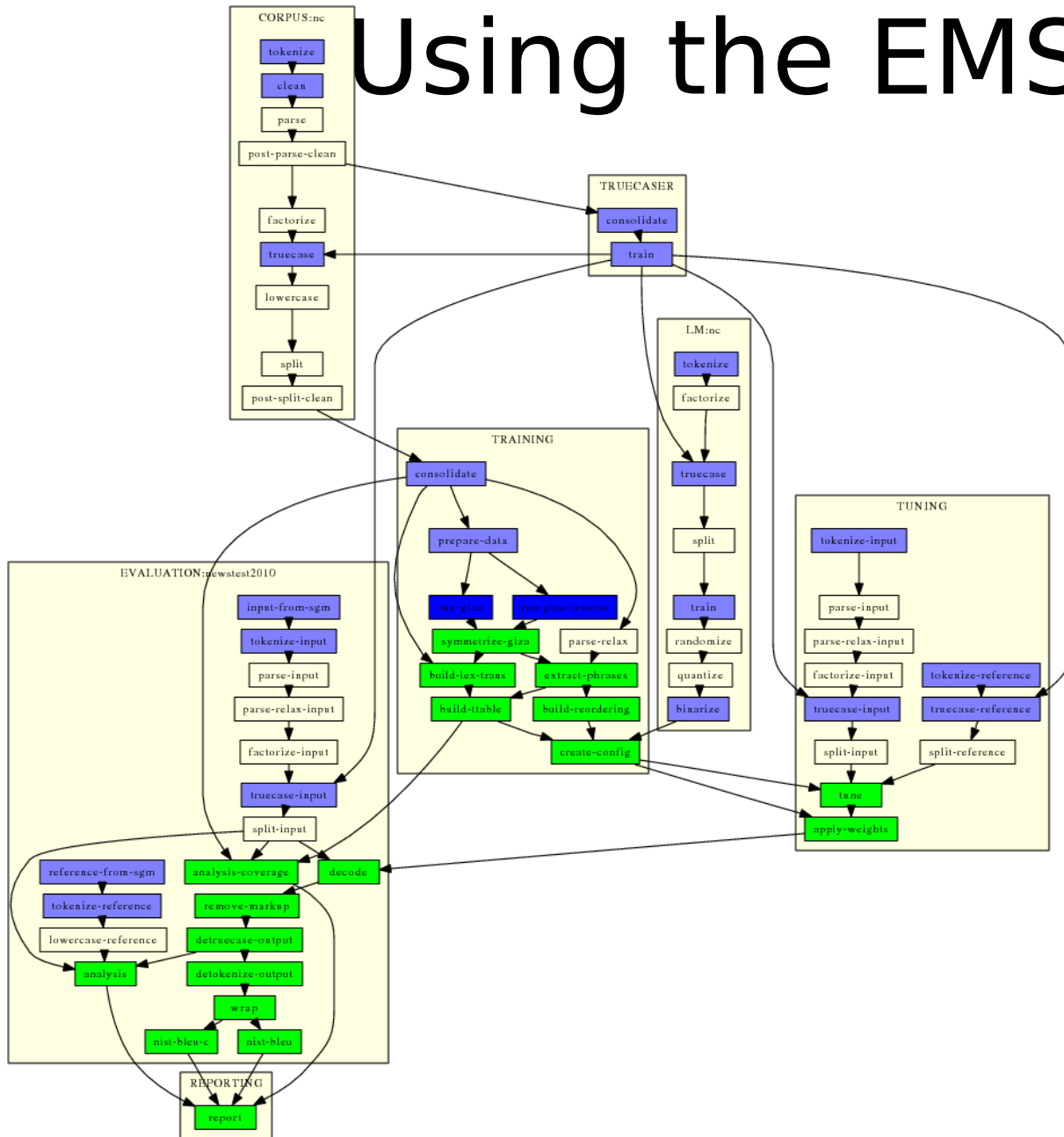
Browse: <http://amta.statmt.org/>

- find your experiment

<input type="checkbox"/> compare	ID	start	end	newstest2010	
<input type="checkbox"/> cfg parling [9-2]	06:33:52	07:12:19	48.63	<input type="checkbox"/> A	<input type="checkbox"/>
		2: 0.0432159	49.20		
<input type="checkbox"/> cfg parling [9-1]	06:33:52	06:54:19	12.75	<input type="checkbox"/> A	<input type="checkbox"/>
		2: 0.0556012	13.40		

Click Here

Using the EMS



Hierarchical/Syntax Models



- Same pipeline
- Different
 - Extraction
 - Decoding
- Reuse common output
 - Data cleaning
 - Tokenization
 - Alignment



Hierarchical/Syntax Models



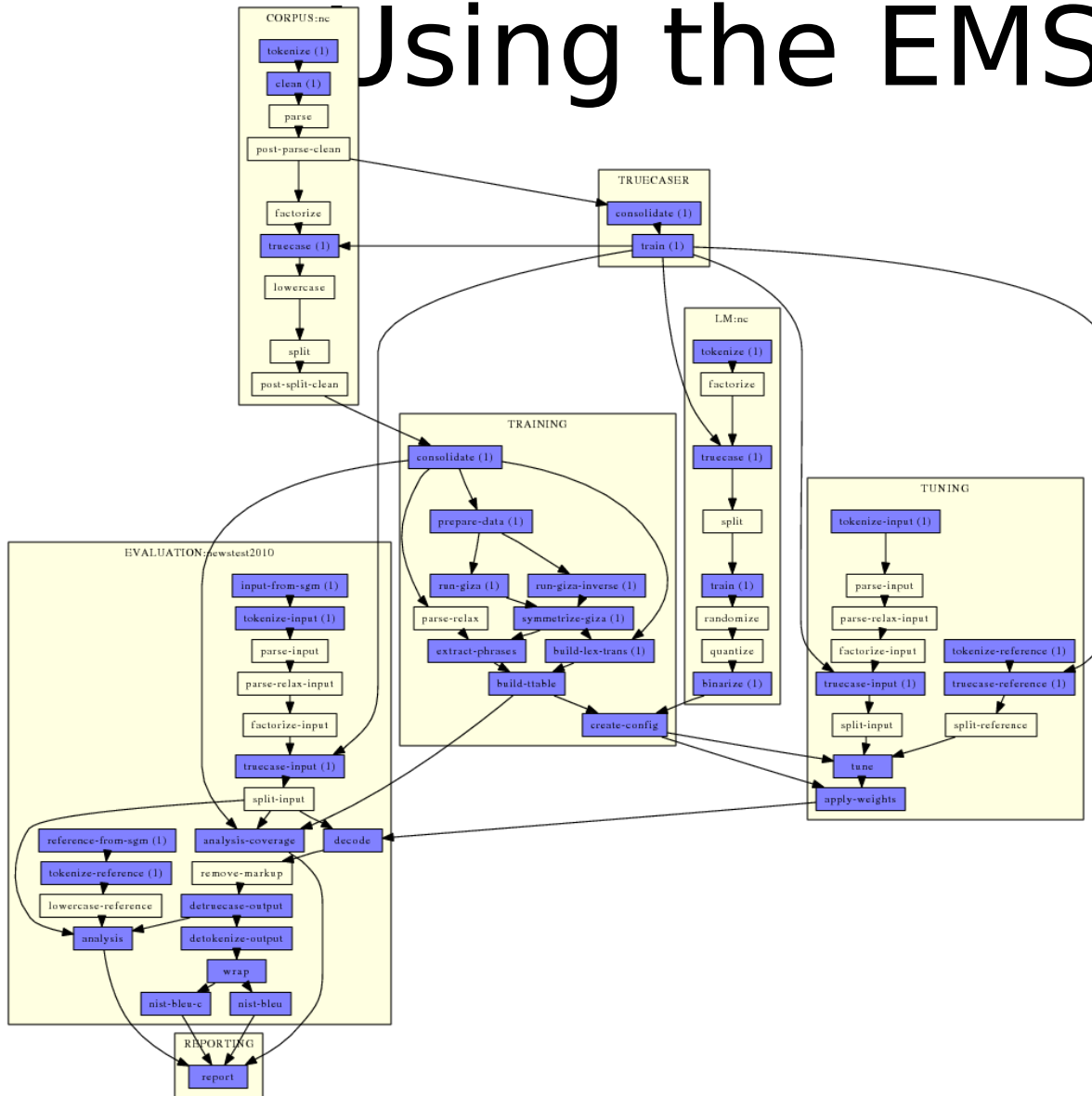
nohup ./run.new config.hiero &

Browse: <http://amta.statmt.org/>
- find your experiment

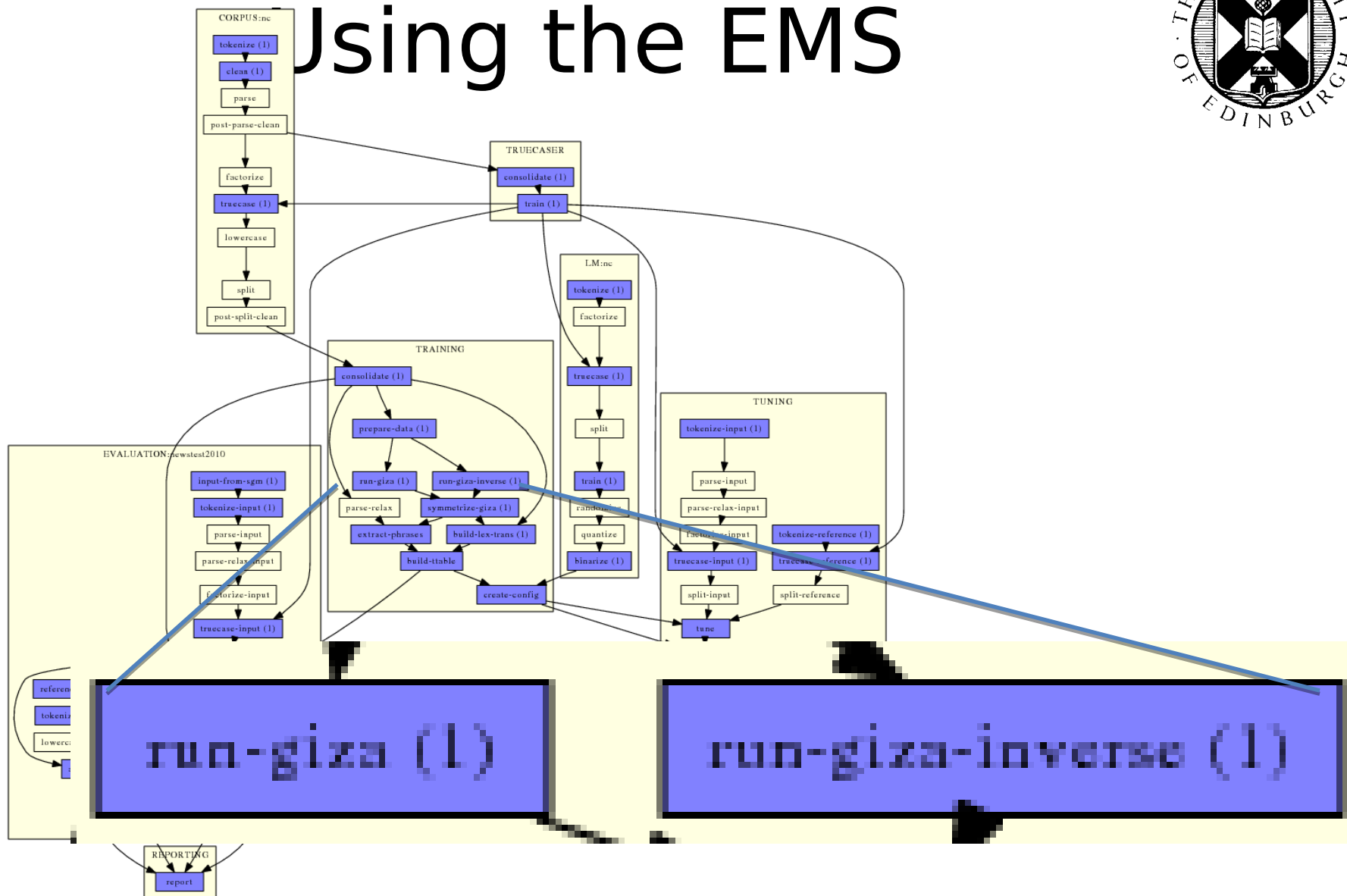
Click Here

compare	ID	start	end	newstest2010	
<input type="checkbox"/> cfg parlimg	[9-2]	06:33:52	07:12:19 2: 0.0432159	48.63 49.20	 <input type="checkbox"/>
<input type="checkbox"/> cfg parlimg	[9-1]	06:33:52	06:54:19 2: 0.0556012	12.75 13.40	 <input type="checkbox"/>

Using the EMS



Using the EMS





Using the EMS

- Standardized directories
 - corpus
 - evaluation
 - lm
 - model
 - steps
 - training
 - recasing
 - Tuning
- Standardized file names for each experiments, eg.
 - nc.lm.1 - nc.lm.2
 - extract.1 - extract.1
 - moses.ini.1 - moses.ini.2



Debugging

- Incorrect file paths
 - Data files
 - Executables
- Bugs in scripts
- Bugs in data

Debugging

- steps /<num>/
 - Working directory of EMS
- config.<num>
 - Parameters for experiment <num>
- Scripts that run moses script
 - eg. TRAINING_run_giza.1
- Error logs produced by every script
 - eg. TRAINING_run_giza.1.STDERR



Summary of EMS

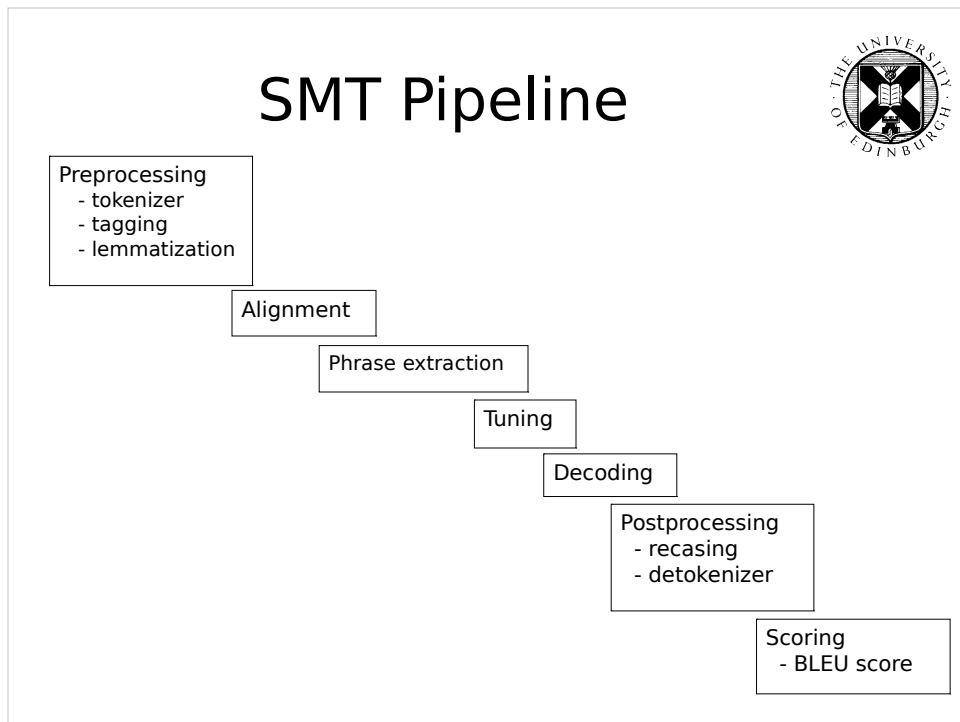
- Create complete MT system from raw data
- Consistent, reproduceable
- Efficient
 - Re-use when it can
- Analysis
- Support parallelization
 - SGI
 - Multi-threading

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MT pipeline

- each part is critical to producing good MT system

Can show you how to do each part

- take a week

Lose the will to live!

However, not necessary to know the mechanics of each & every part to start

Those that don't need to know, or know but just want it to work consistently

- provide a system which wraps up the pipeline

Using the Experiment Management System (EMS)



- In brief
 - from raw data to tuned MT system
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This system is called the EMS

- included with the Moses toolkit
- a script that creates a series of scripts

What does EMS do?

- takes raw data
- turn into a phrase-based system, or hierarchical system

By running the entire pipeline.

All you need to do it give is a config file

Using the EMS



ssh guest@odin.inf.ed.ac.uk
Password = Edinburgh123

cd workspace/experiment/fr-en/<river>/
nohup ./run.new.sh config.pb &

config file:
steps/1/config.1

Browse: <http://amta.statmt.org/>
- find your experiment

compare	ID	start	end	newstest2010
<input type="checkbox"/> cfg par img	[9-2]	06:33:52	07:12:19 2:00:38:139	48.63 49.20
<input type="checkbox"/> cfg par img	[9-1]	06:33:52	06:54:19 2:0:0556012	12.75 13.40

Click Here

We've set up a small experiemtn for you

- so log onto the our server as guest
- password is 'welcome'

And run this script

- it's a standard phrase-based system. Training on just 1000 lines of data
- hopefully it'll finish in 10-15 minutes.

- can look at this script, it's 1 line which runs the EMS, telling it which config file to use, in this case it says the 1st config file.

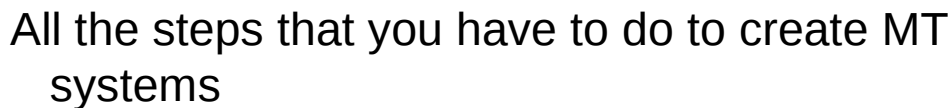
So where's the config file?

- it's in the steps directory, under '1'
- look inside it
- doesn't sayhow things are run, EMS already knows that
- instead, specify where the data and the executables are found
- <PAUSE> for questions

Now it's running, can check on it progress online.

Go to this URL with firefox or whatever

- find your experiment. (Name of fruit)
- 'cfg' is the config file your supplied it with
- par is the parameters the EMS extracted from the config file
- click on the 'image' link
 - shows you progress of your running experiment



Wait for all boxes to turn light-blue. Everything has finished!

Dark blue – Running jobs

If you see RED

R

Hierarchical/Syntax Models



- Same pipeline
- Different
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For hierarchical and syntax models, only the extraction and decoding is different.

Many of the other steps are identical. The EMS understand that

- if a step has identical input and output, and the same arguments
- reuse

Hierarchical/Syntax Models



nohup ./run.new config.hiero &

Browse: <http://amta.statmt.org/>
- find your experiment

Click Here

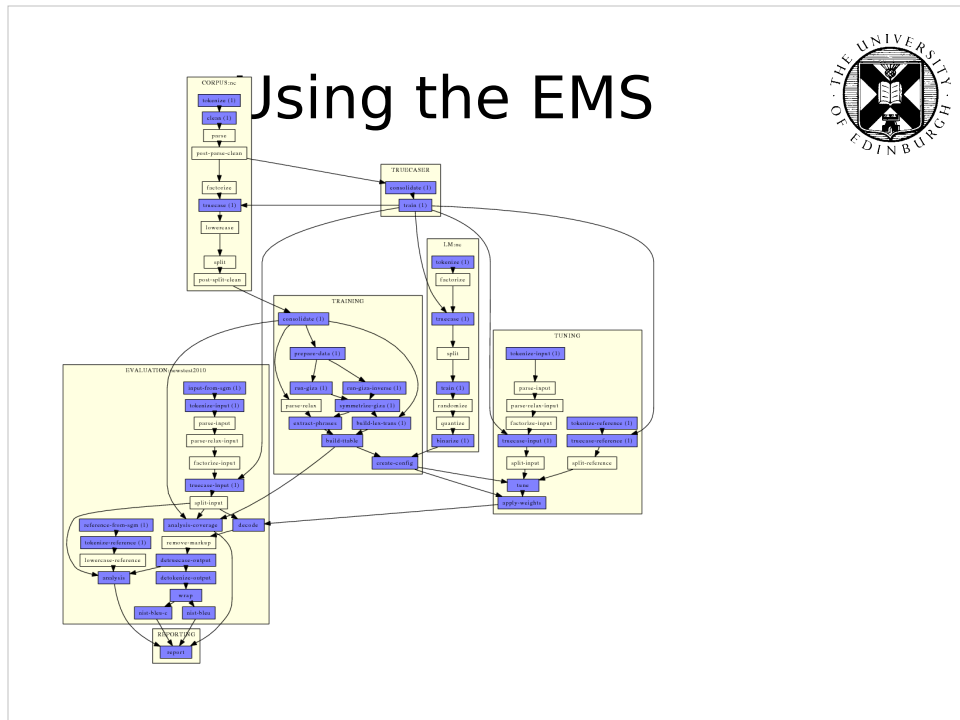
compare	ID	start	end	newstest2010
<input type="checkbox"/> cfglparlm	[9-2]	06:33:52	07:12:19 2: 0.0432159	48.63 49.20 
<input type="checkbox"/> cfglparlm	[9-1]	06:33:52	06:54:19 2: 0.0556012	12.75 13.40 

So do the same thing for another experiment

This uses the same data

- but creates a hierarchical model instead of a phrase-based model

Find your experiment again



Looks exactly like the phrase-based

However, those parts that can be reused from the phrase-based

- aren't green, or blue
- those steps are white
 - meaning the EMS will reuse the output from the phrase-based experiment instead.

- steps like tokenization, cleaning, alignment are all white



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Digging deeper into how the EMS works

Standardized directories

Standardized naming convention for files

- easy to see which exactly which files have been created by which experiment



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