Nipype: Neuroimaging analysis pipeline and interfaces in Python.

Problem

- Multiple analysis packages, each with their own pipelining functionality and language
- Each package has a steep learning curve
Ideally

- Mix-and-match components from different packages
- Compare different packages
- Iterate over a parameter set
- Provenance tracking
Solution

- Nipype: A common framework for interfacing multiple analysis packages, and for elegant pipelining.

- http://nipy.sourceforge.net/nipype/
from nipype.interfaces.spm import Realign, Coregister
from nipype.interfaces.fsl import Bet
...
rlgn = NodeWrapper(interface=Realign())
rlgn.inputs.register_to_mean = True

coreg = NodeWrapper(interface=Coregister())

skullstrip = NodeWrapper(interface=Bet())
ds = NodeWrapper(interface=DataSource())
ds.inputs.base_directory = '~/data/exp001'
...
pline = pe.Pipeline()
pline.connect([(ds, rlgn, [('func', 'infile')]),
               (rlgn, coreg, [('mean_image', 'source')]
               ...
               (coreg, skullstrip, ['coreg_files'...])

pline.run()