

Nipype 2012 = MORE

packages
reusable workflows
reproducible research



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Example

```
import nipype.pipeline.engine as pe
from nipype.interfaces import spm
import nipype.workflows.fmri.fsl as fsl_wf

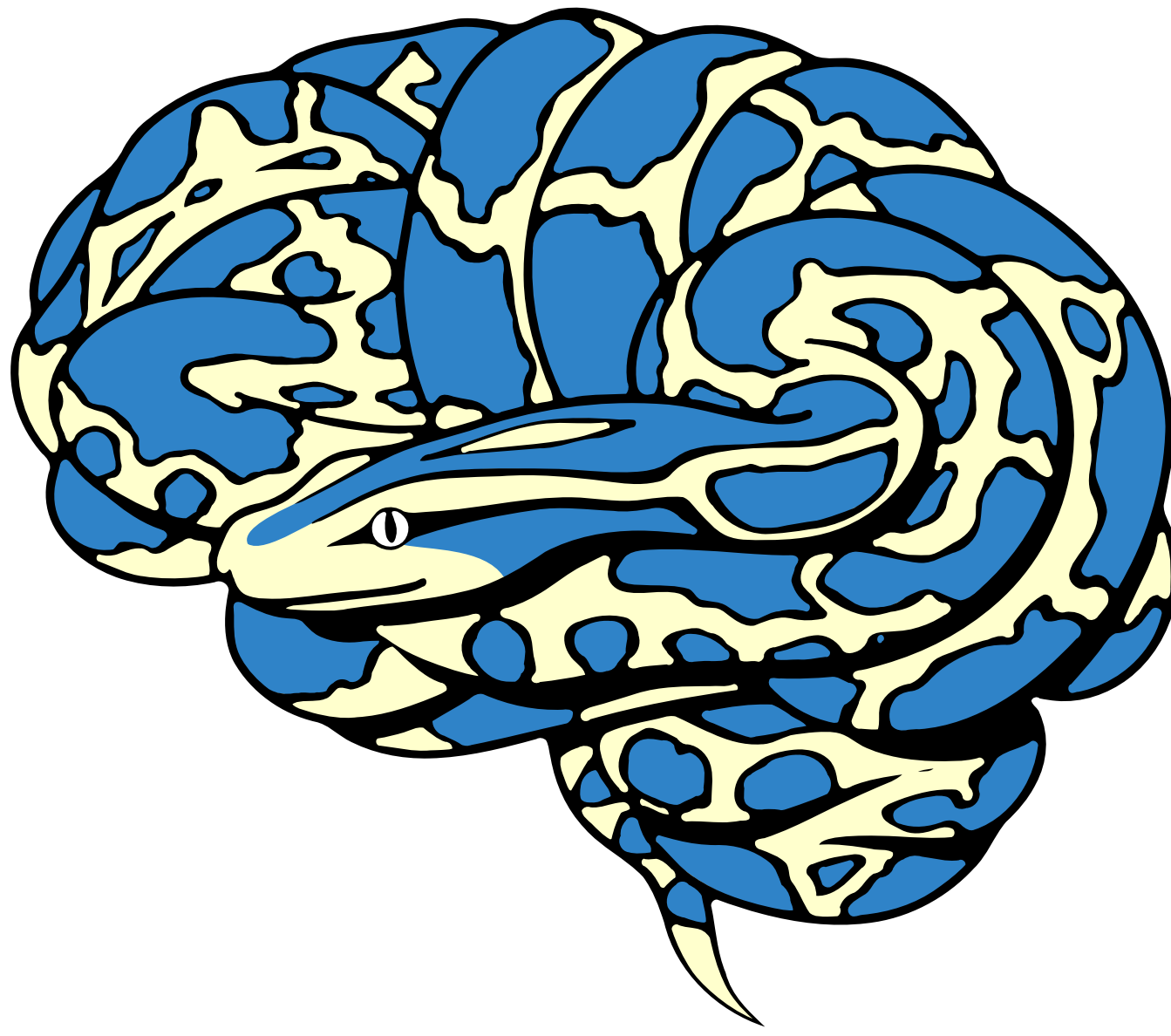
workflow = pe.Workflow(name="preprocessing")

realign = pe.Node(spm.Realign(), name="realign")

smooth = fsl_wf.create_susan_smooth(name="smooth")
smooth.inputs.inputnode.fwhm = 4

workflow.connect(realign, "realigned_files",
                 smooth, "inputnode.in_files")

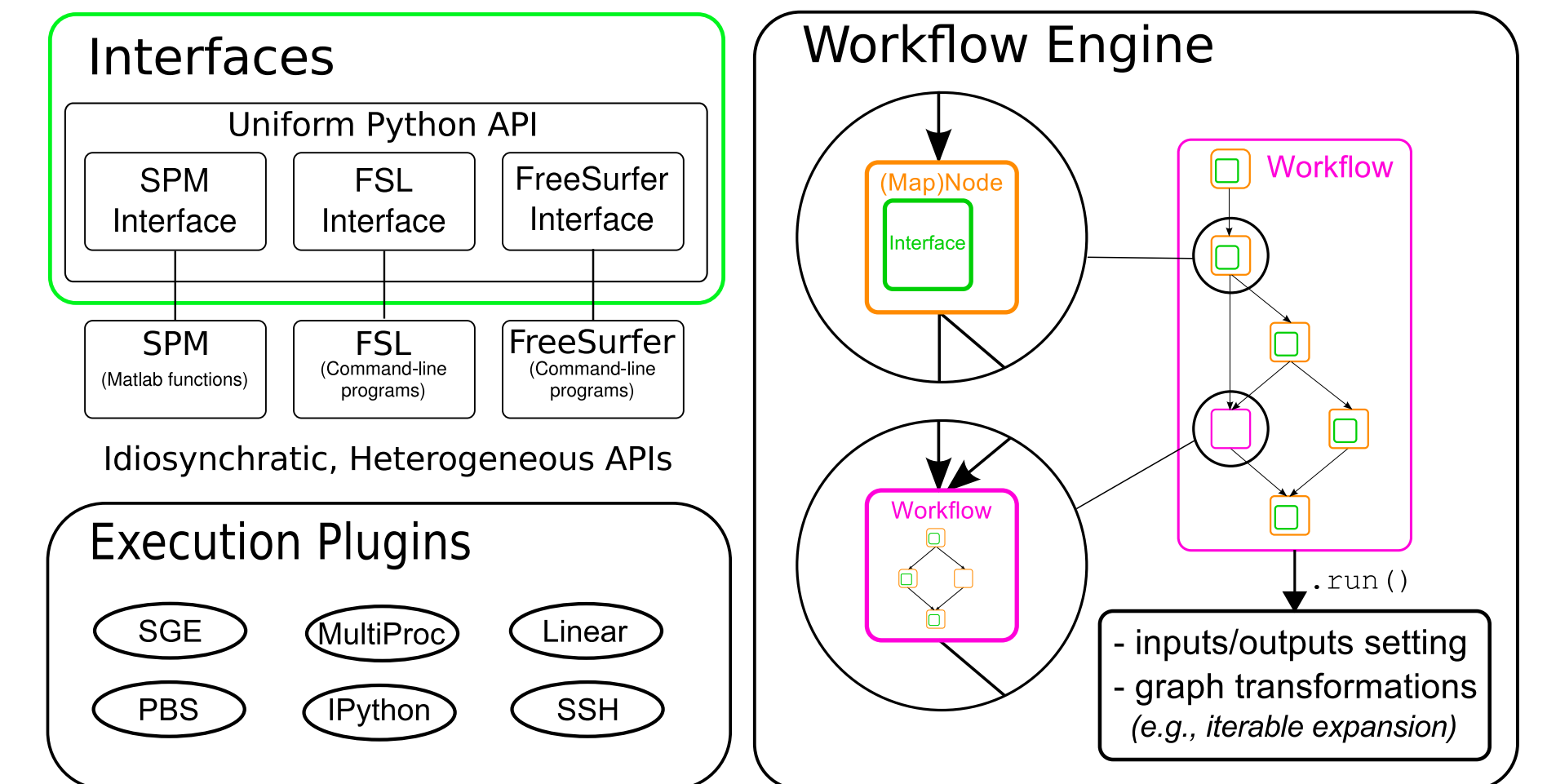
workflow.run()
```



what is nipype?

Nipype is an open-source, community-developed initiative that provides a uniform interface to existing neuroimaging software and facilitates interaction between these packages within a single workflow. It eases the design of workflows within and between packages, and reduces the learning curve necessary to use different packages.

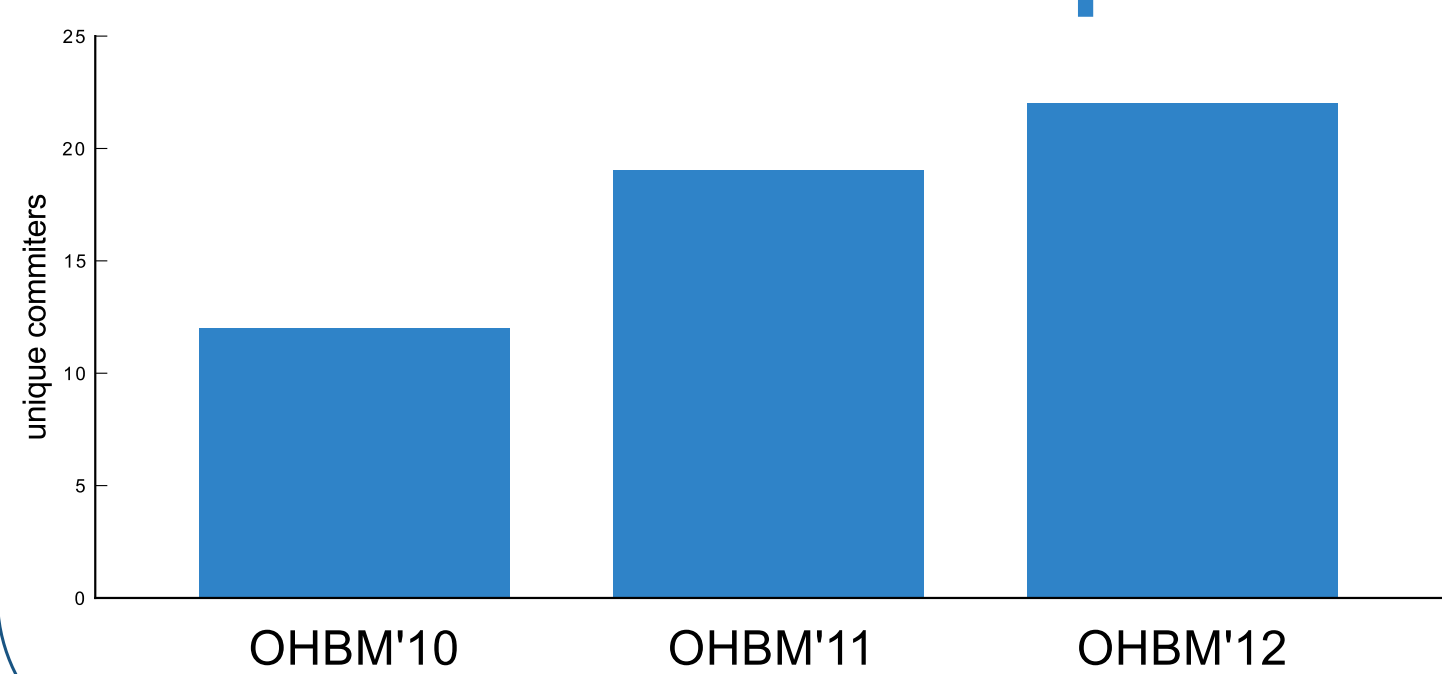
Architecture



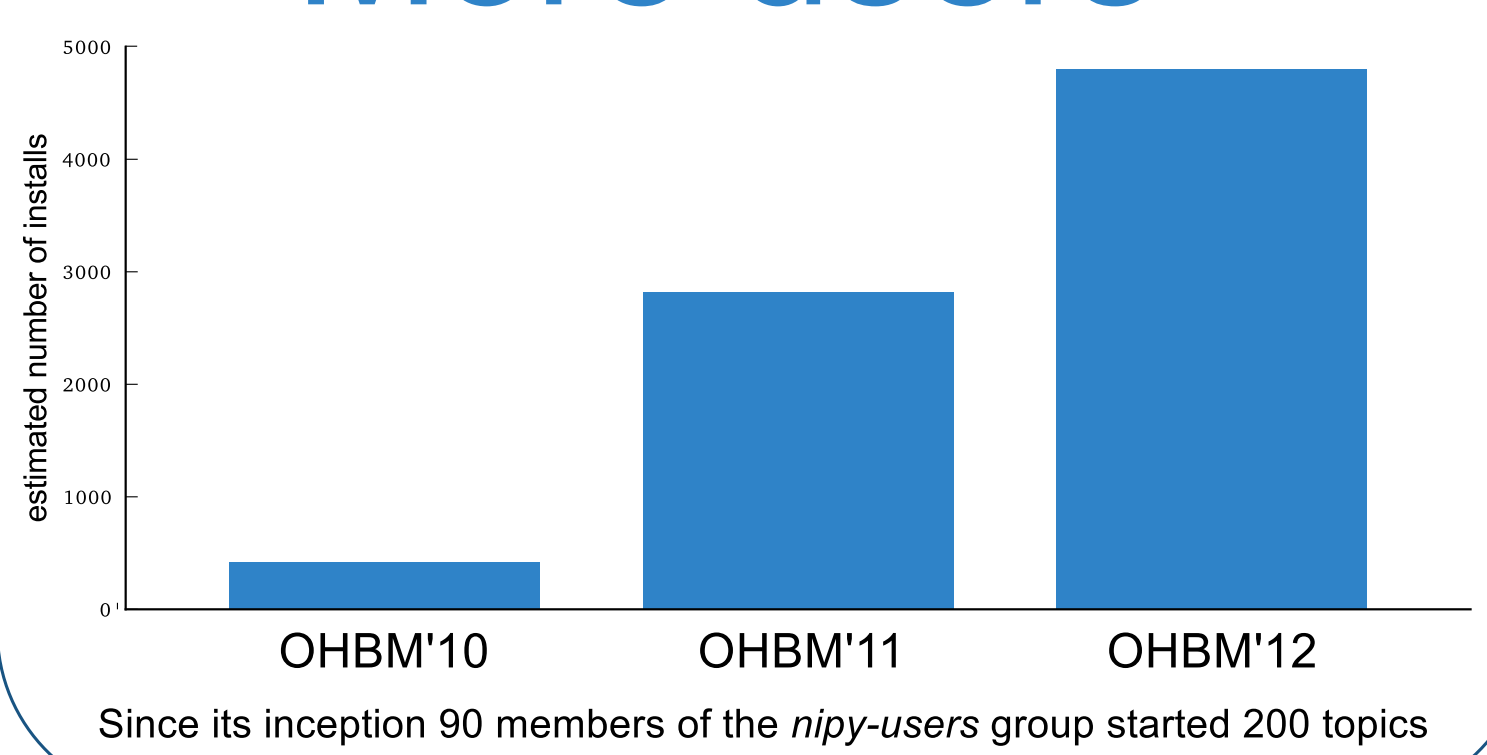
what is new in nipype?

community

More developers



More users



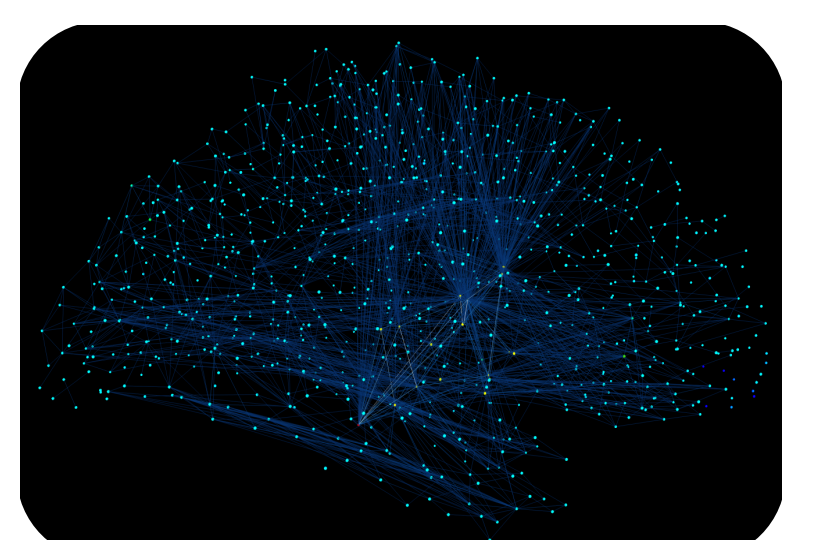
development

New interfaces



New workflows

- connectome estimation
- DTI analysis in FSL, Camino and MRtrix
- VBM preprocessing
- rsfMRI preprocessing



New tutorials
connectome
DARTEL
resting state
beginners guide with over 2400 visitors!

FUTURE

- Automatic and semi-automatic quality control
 - Improved and standardized provenance tracking
 - Flexible and comprehensive reporting system

nipy.org/nipype



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