Analysis Preservation and Reinterpretation

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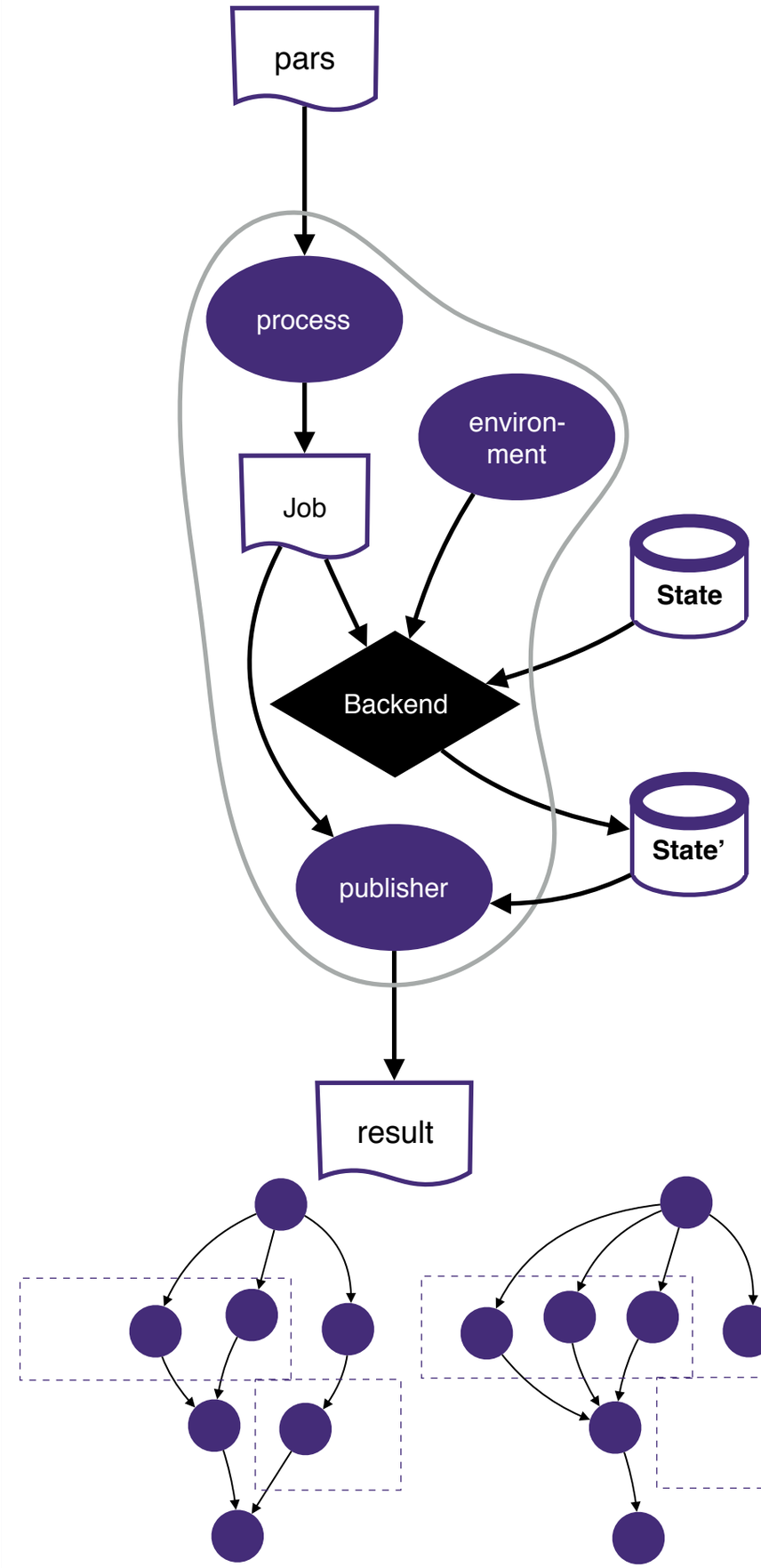
CHEP 2016, San Francisco

NEW YORK UNIVERSITY



Analysis Ingredients:

- ↪ measurement of rates and distribution of *pp collision* observables
- ↪ estimation of expected measurements under model hypotheses
- ↪ statistical evaluation, interval estimation on model parameters

$$\text{result} = f_{\text{analysis}}(\text{data}|\text{model})$$

observable distributions, confidence intervals on model parameters

reconstruction, event selection, stat. evaluation

collision data from LHC detector

model hypothesis (SM, many SUSY models, etc..)

Current Standards / Preservation / Archival efforts:

Efforts like DASPOS and CERN Analysis Preservation try to fill a gap in the preservation efforts.
Data only is not enough.We need software and environment as well.

HepData | **???** | **DPHEP CERN OpenData** | **UFO/SLHA** (HepData?)

$$\text{result} = f_{\text{analysis}}(\text{data}|\text{model})$$

observable distributions, confidence intervals on model parameters

reconstruction, event selection, stat. evaluation

collision data from LHC detector

model hypothesis (SM, many SUSY models, etc..)

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Analysis should be preserve the analysis in a **parametrized form**, not only its concrete application, separately from its application on given dataset.

$$f_{\text{analysis}}(\,\cdot\,), \quad \text{data}, \quad \text{model}$$

Given a **parametrized preservation of an analysis** (even w/ fixed data), we gain ability to extract **new results** using existing resources.

Reinterpretation of Single Analysis under multiple models

Combination of multiple analyses w.r.t. one model
(increased stat. power)

$$\begin{array}{ll} f_{\text{a}}(\text{data}|\text{model}_1) & f_{\text{a}}(\text{data}|\text{model}_2) \\ f_{\text{b}}(\text{data}|\text{model}_1) & f_{\text{b}}(\text{data}|\text{model}_2) \\ f_{\text{c}}(\text{data}|\text{model}_1) & f_{\text{c}}(\text{data}|\text{model}_2) \end{array}$$

How to preserve $f_{\mathrm{analysis}}(\,\cdot\,)$?

Issues:

- preserving software environments
- preserving execution instructions (what programs/scripts to call, etc)
- Analyses consist of many individual steps, possibly complex dependency structure
- mutual incompatibility of environments between steps
- composability / sharing across analyses
- many more…

Strategy:

1. Preserve individual processing steps
2. Preserve workflow / order between steps

How to preserve $f_{\mathrm{analysis}}(\,\cdot\,)$?

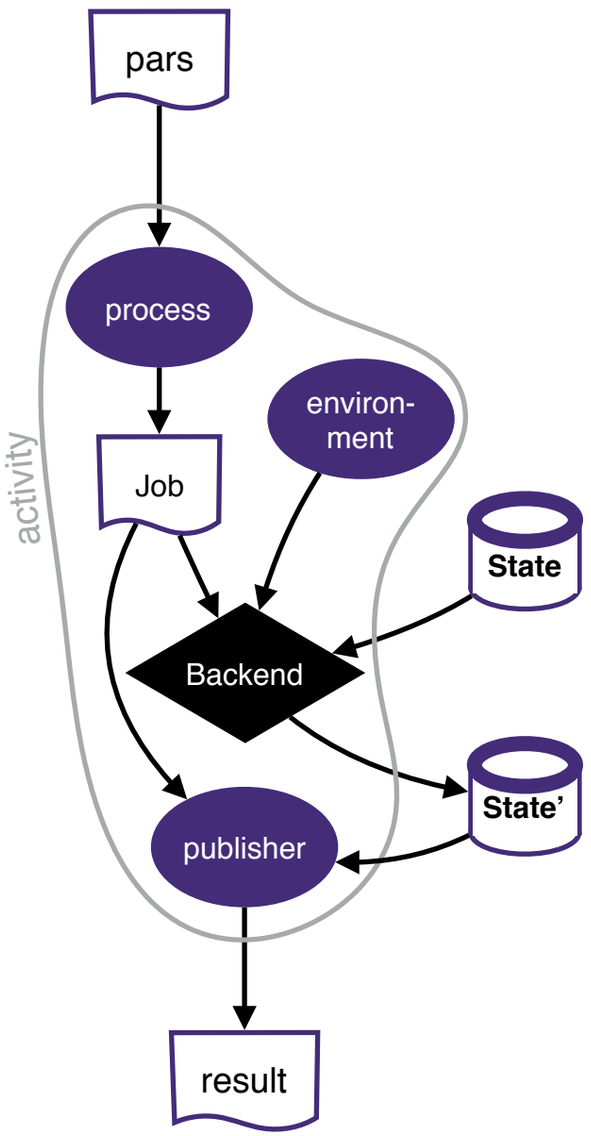
1. Problem: Preserve Individual Processing Steps

(Example: Run Detector Simulation + Reconstruction on MC events)

Steps (“activities”) process data obtained by a global state, and modify state with (eg. writing new files, modify existing files)

$$\mathrm{result\ data},\ \mathrm{state}' = g_{\mathrm{step}}(\mathrm{state}, \mathrm{parameters})$$

It’s useful to have machine readable result data to e.g. identify newly created files.



Three ~orthogonal ingredients that can be described individually:

parametrized process:
template job from which we can produce concrete job
template: “`./DelphesHepMC <input file> <output file>`”
concrete: “`./DelphesHepMC /input/file/path.hepmc /output/file.root`”

environment:
description of computing env in which above job can run. Multiple options, promising: *Linux Containers* (investigating Umbrella, etc)

publisher:
recipe how to extract parsable result data after job completion
e.g. globbing files in a work directory

How to preserve $f_{\mathrm{analysis}}(\,\cdot\,)$?

1. Problem: Preserve Individual Processing Steps

(Example: Run Detector Simulation + Reconstruction on MC events)

Data Format: JSON

- as interchange format for parameters and result data
- as declarative description format for *process/env/publisher*
  - incl. JSON schemas for validation

Essentially, a self-consistent "packaged activity" — a "packtivity"

- JSON API
- archivable, declarative description as JSON
- dependencies captured in environment
  - e.g. Docker Image

$$\text{result data},\ \text{state}' = g_{\mathrm{step}}(\text{state}, \text{parameters})$$

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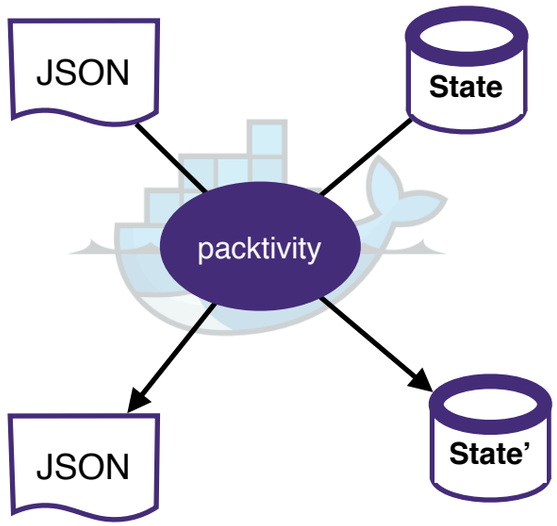

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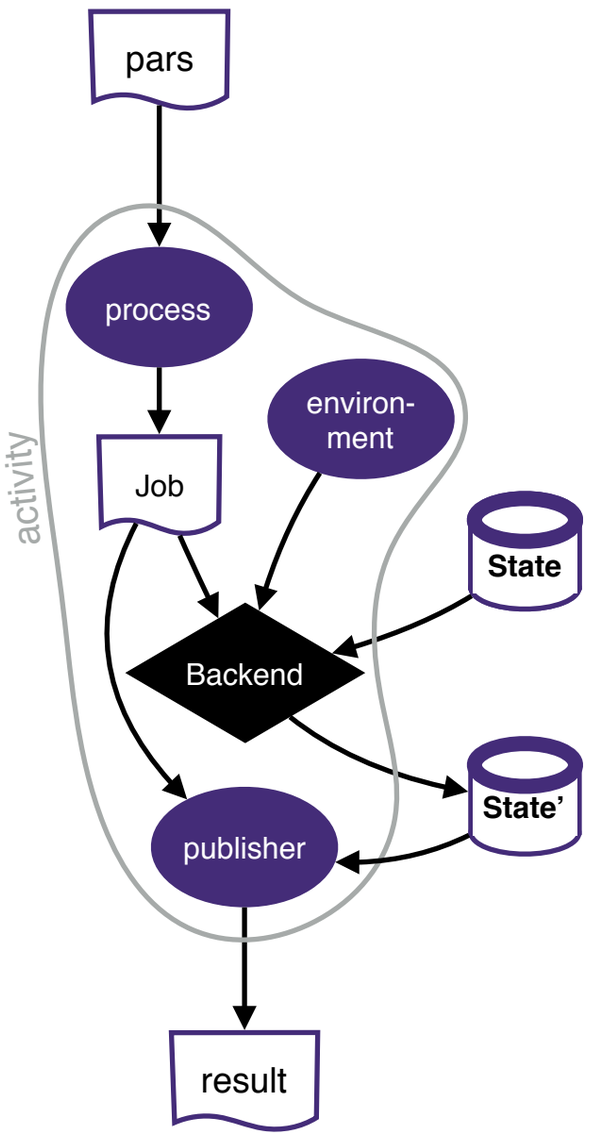


How to preserve $f_{\mathrm{analysis}}(\cdot)$?

1. Problem: Preserve Individual Processing Steps

(Example: Run Detector Simulation + Reconstruction on MC events)

Example:

```
process:
  process_type: 'string-interpolated-cmd'
  cmd: 'DelphesHepMC  {delphes_card} {outputroot} {inputhepmc}'
publisher:
  publisher_type: 'frompar-pub'
  outputmap:
    rootfile: outputroot
environment:
  environment_type: 'docker-encapsulated'
  image: lukasheinrich/root-delphes
```

CLI tool

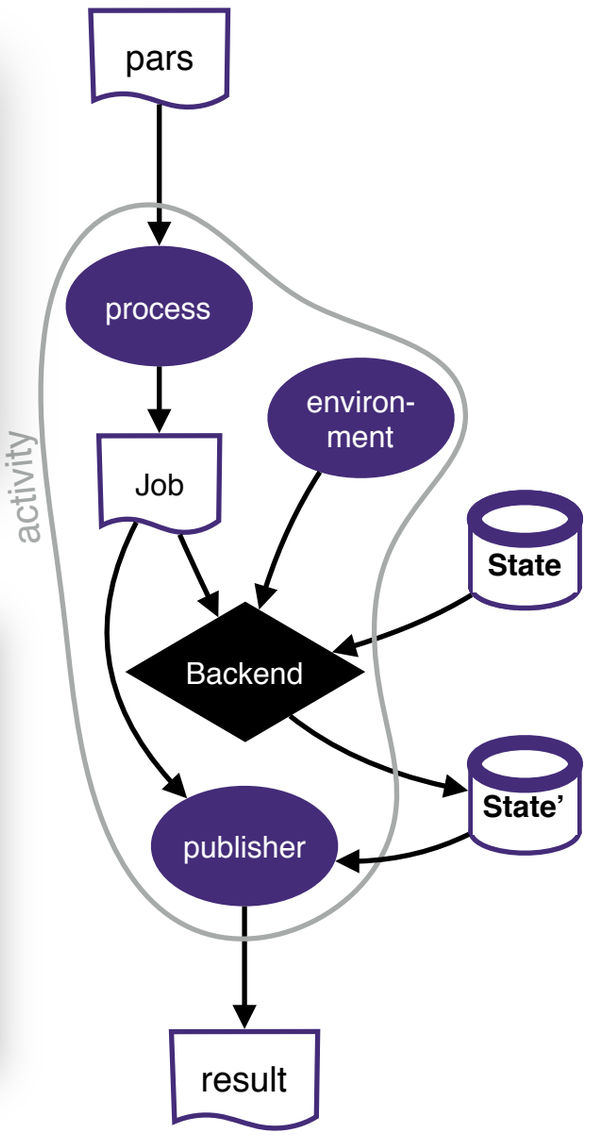
```
172-27-219-223 — -zsh — 64×12
[$>  ls
delphes.yml  input.hepmc  pars.yml
[$>  pygmentize -g pars.yml
delphes_card: 'delphes/cards/delphes_card_ATLAS.tcl'
inputhepmc: '{workdir}/input.hepmc'
outputroot: '{workdir}/out.root'
[$>  packtivity-run delphes.yml pars.yml
{'rootfile': '/Users/lukas/chep2016/out.root'} (prepublished)
$>
```

python bindings

```
pack.py — /Users/lukas/chep2016
pack.py
1   import os
2   import capschemas
3   from packtivity import packtivity
4   from packtivity.statecontexts.poxisfs_context import make_new_context
5   packtivity_description = capschemas.load(
6       'delphes.yml',os.curdir,
7       'packtivity/packtivity-schema')
8   pars = {
9     delphes_card: 'delphes/cards/delphes_card_ATLAS.tcl',
10    inputhepmc: '{workdir}/input.hepmc',
11    outputroot: '{workdir}/out.root'
12  }
13  packtivity(packtivity_description,parameters,make_new_context(os.curdir))
Line 0  File 0  Project 0  ✔ No Issues  pack.py*  15:1  LF  UTF-8  Python  3 updates
```

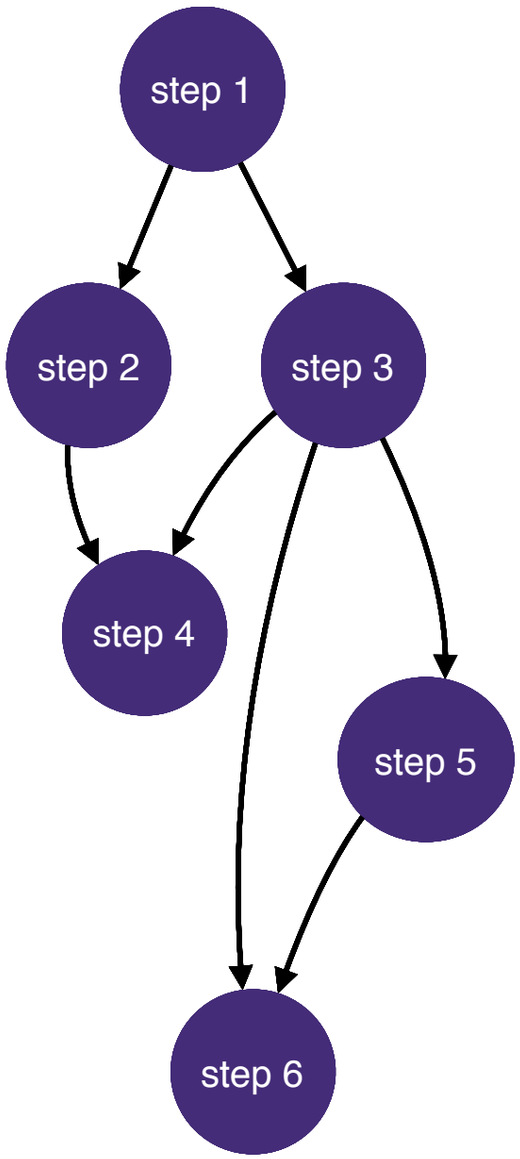
python package: “packtivity”

- executes packtivities according to JSON spec for given parameters
- cli tool and python bindings
- multi-host / remote execution ready via e.g. Docker Swarm



How to preserve $f_{\mathrm{analysis}}(\,\cdot\,)$?

2. Problem: Preserve Parametrized Workflow



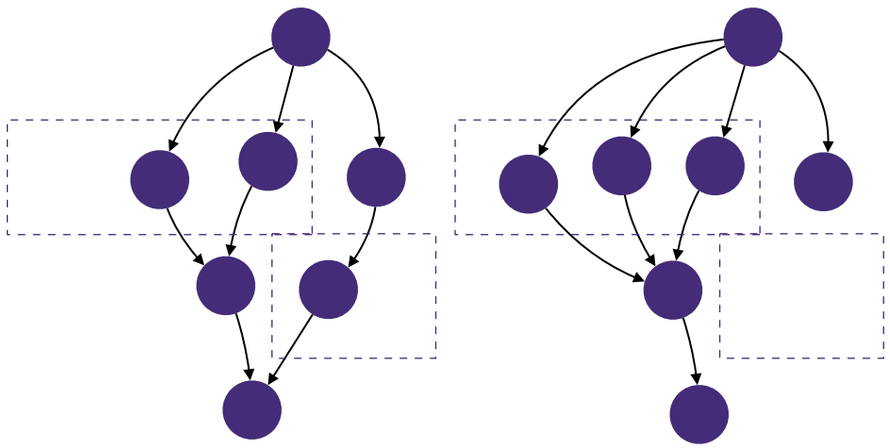
Natural Data Model: *directed acyclic graphs (DAGs)*

- **nodes**: individual steps
- **edges**: dependency relations

Two place where parametrization enter:

1. individual steps parametrized: covered by “packtivities”
   graph topology may *depend on the parameters* of the analysis and only emerge during run-time

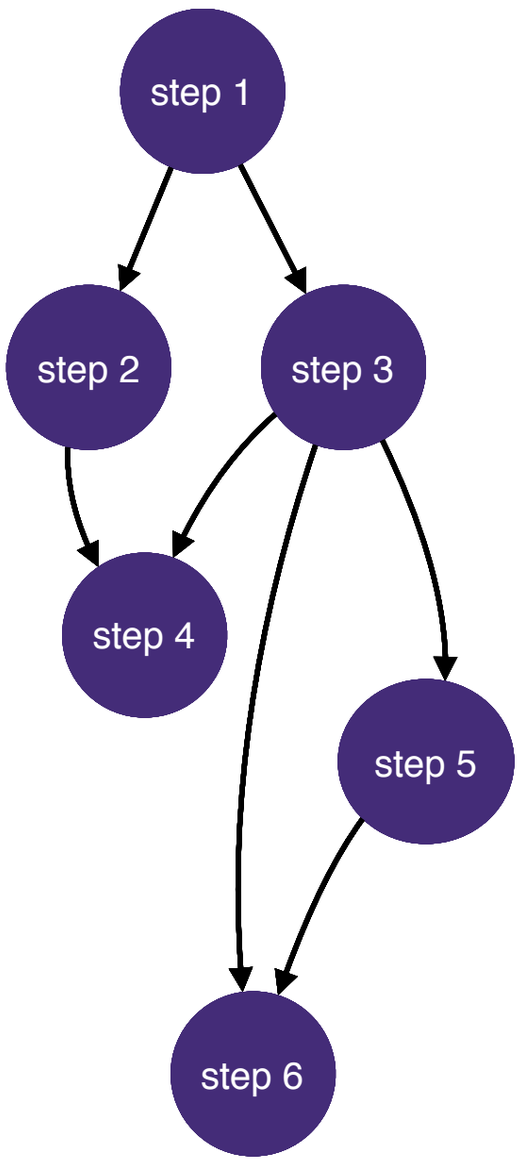
2. Examples:
   - variable number of created files during execution,
   - conditional choices (if/else)/flags do enable/disable steps, e.g. run systematics / not



Par. Set 1 **Par. Set 2**

How to preserve $f_{\text{analysis}}(\cdot)$?

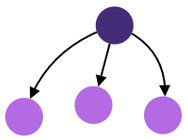
2. Problem: Preserve Parametrized Workflow



Therefore: Sequentially build up graph, as sufficient information becomes available, using a number of stages that add nodes and edges

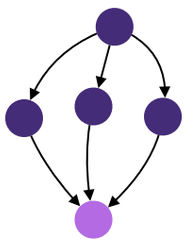
To capture analysis workflow, capture the stages.

Example: Parametrized Map-Reduce

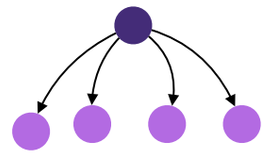


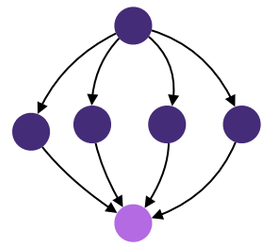
Stage 1:
unknown number of files. e.g. download & unpack archive with a priori unknown # of files

Stage 2:
for each file in the archive, add node to process it
(**only possible after first node done)**



Stage 3:
add a node that merges results of the map nodes
node/edge can be added before execution of map nodes



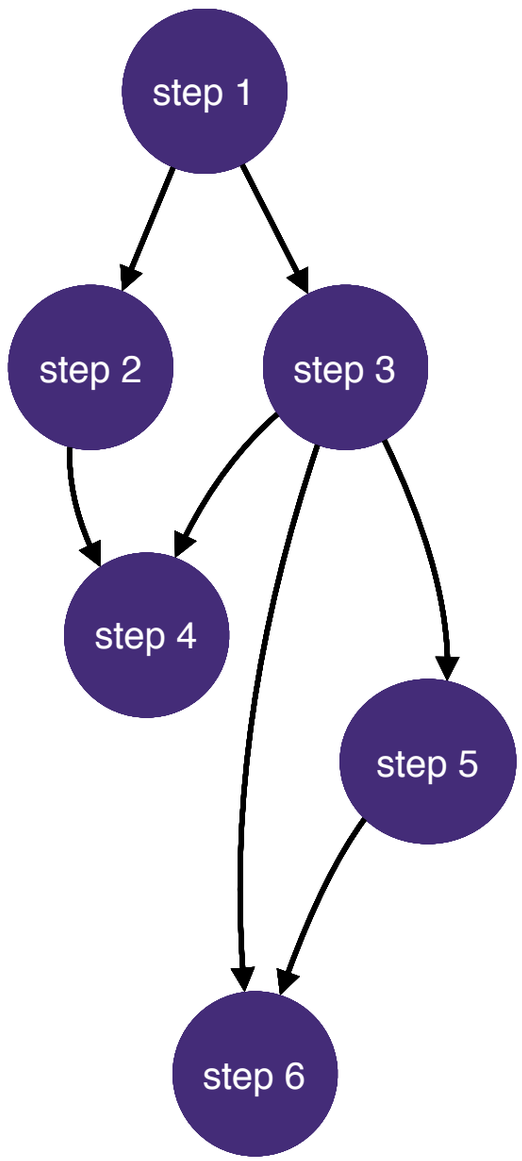


Par. Set 1

Par. Set 2

How to preserve $f_{\text{analysis}}(\cdot)$?

2. Problem: Preserve Parametrized Workflow



Stages captured in JSON (incl. schemas for validation)

- easy to archive in repositories (e.g. GitHub / CERN Analysis Preservation
- easy to parse for clients

```yaml
stages:
  - name: acquisition
    dependencies: ['init']
    scheduler:
      scheduler_type: singlestep-stage
      parameters:
        source: {stages: init, output: sourcefile, unwrap: true}
        localname: '{workdir}/mydata.zip'
      step: {$ref: 'steps.yml#/acquire'}
  - name: map
    dependencies: ['acquisition']
    scheduler:
      scheduler_type: multistep-stage
      parameters:
        inputfile: {stages: 'acquisition', output: 'unzipped', unwrap: true}
        outputfile: '{workdir}/mapout.txt'
      scatter:
        method: zip
        parameters: ['inputfile']
      step: {$ref: 'steps.yml#/mapstep'}
  - name: reduce
    dependencies: ['map']
    scheduler:
      scheduler_type: singlestep-stage
      parameters:
        mapoutputs: {stages: map, output: mapout}
        combinedfile: '{workdir}/out.txt'
      step: {$ref: 'steps.yml#/reducestep'}
```

Stage 1:
unknown number of files. e.g. download & unpack archive with a priori unknown # of files

Stage 2:
for each file in the archive, add node to process it

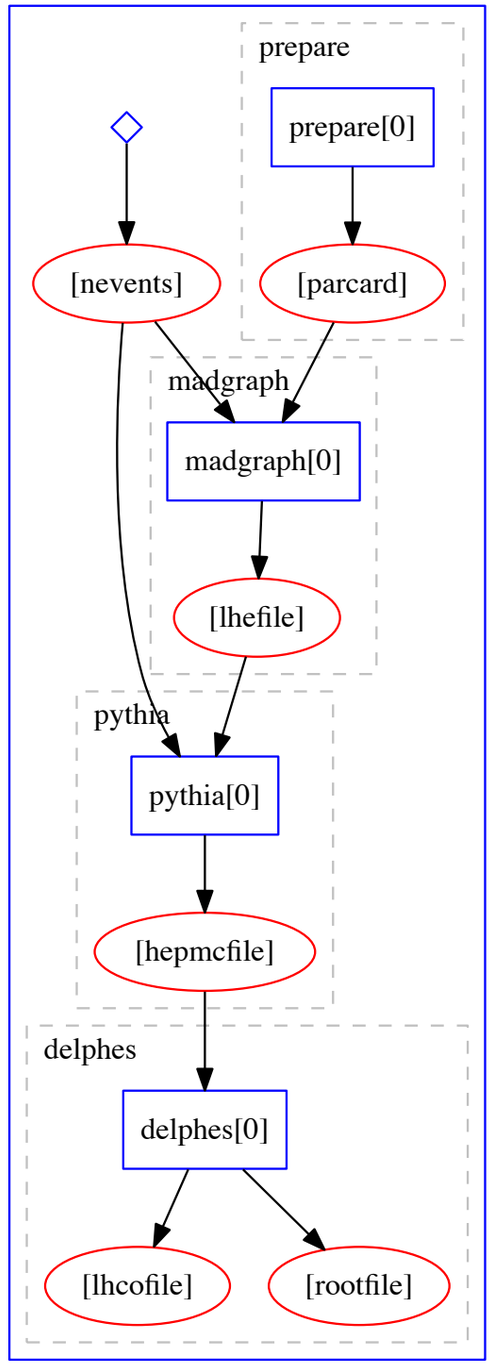
Stage 3:
add a node that merges results of the map nodes (node/edge can be added before execution of map nodes

How to preserve $f_{\mathrm{analysis}}(\,\cdot\,)$?

2. Problem: Preserve Parametrized Workflow

First implementation: **Yadage**

python package.
install from **PyPi** or **…**
… run from from *within docker*
can run complex workflows with vastly different environments on hosts that know nothing about the domain software out of the box just need docker.



172-27-219-223 — -zsh — 99×9

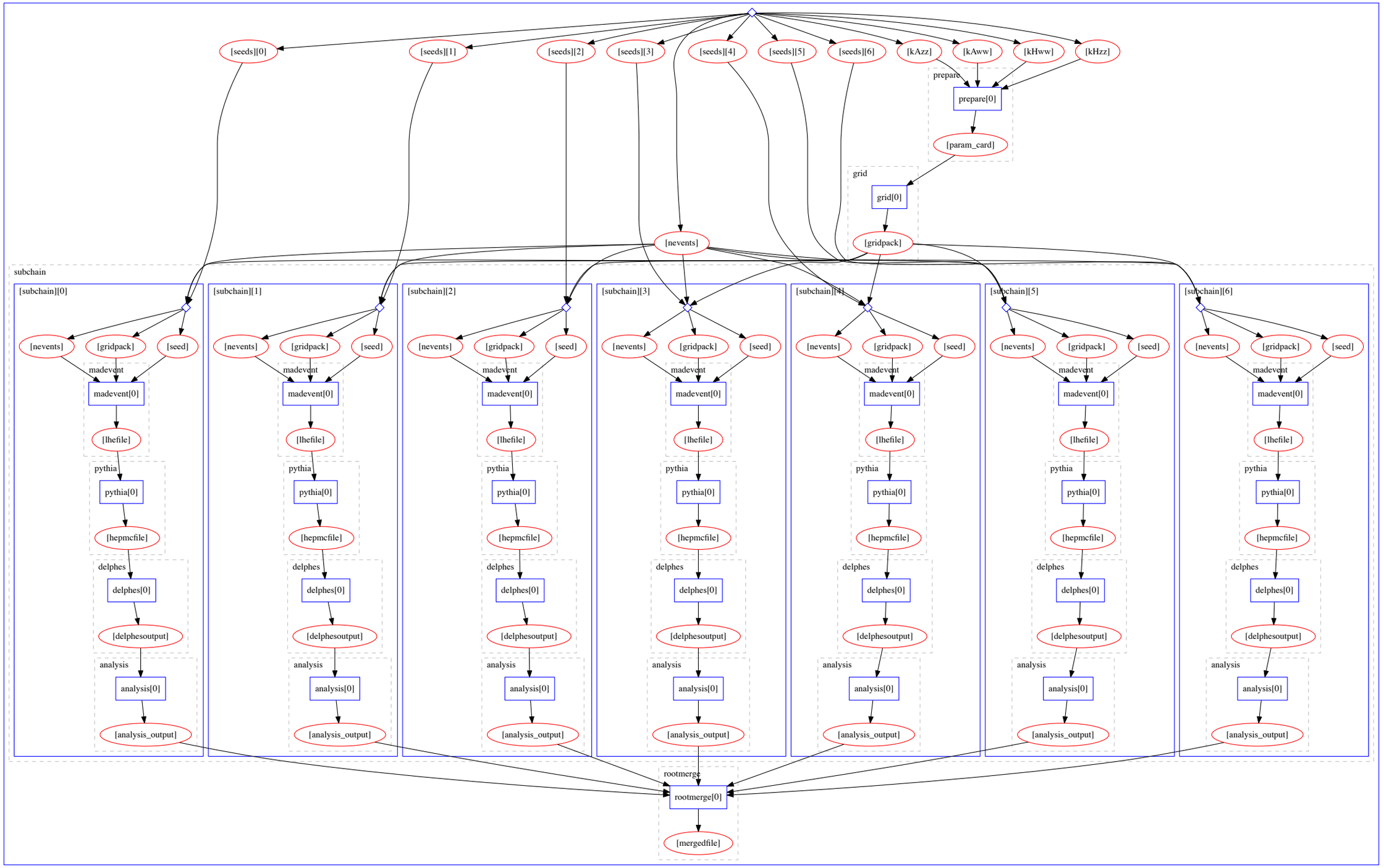
```
[$>  eval "$(curl https://raw.githubusercontent.com/diana-hep/yadage/master/yadagedocker.sh)"
  % Total    % Received % Xferd  Average Speed   Time    Time     Time  Current
                                 Dload  Upload   Total   Spent    Left  Speed
100   182  100   182    0     0   1831      0 --:--:-- --:--:-- --:--:--  1838
[$>  yadage-run -t from-github/phenochain workdir madgraph_delphes.yml -p nevents=100
[$>  ...
[$>  ls workdir/delphes
_packtivity/  output.lhco  output.root
$>
```

172-27-219-223 — -zsh — 99×8

```
[$>  pip install yadage
[$>  ...
[$>  yadage-run -t from-github/phenochain workdir madgraph_delphes.yml -p nevents=100
[$>  ...
[$>  ls workdir/delphes
_packtivity/  output.lhco  output.root
$>
```

Example:

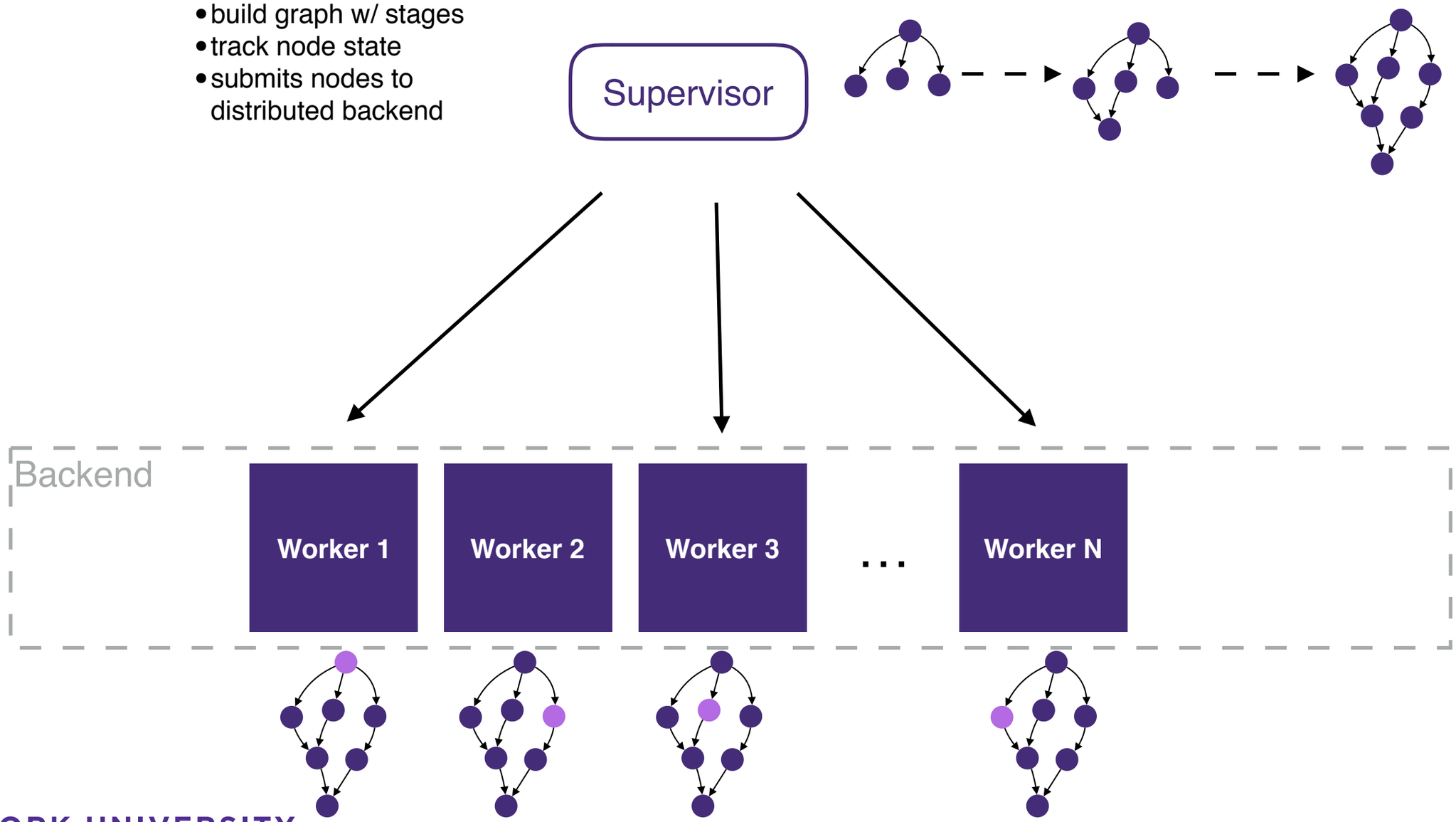
typical analysis using HEP tools (Madgraph, Pythia, Delphes, Custom Analysis Code.



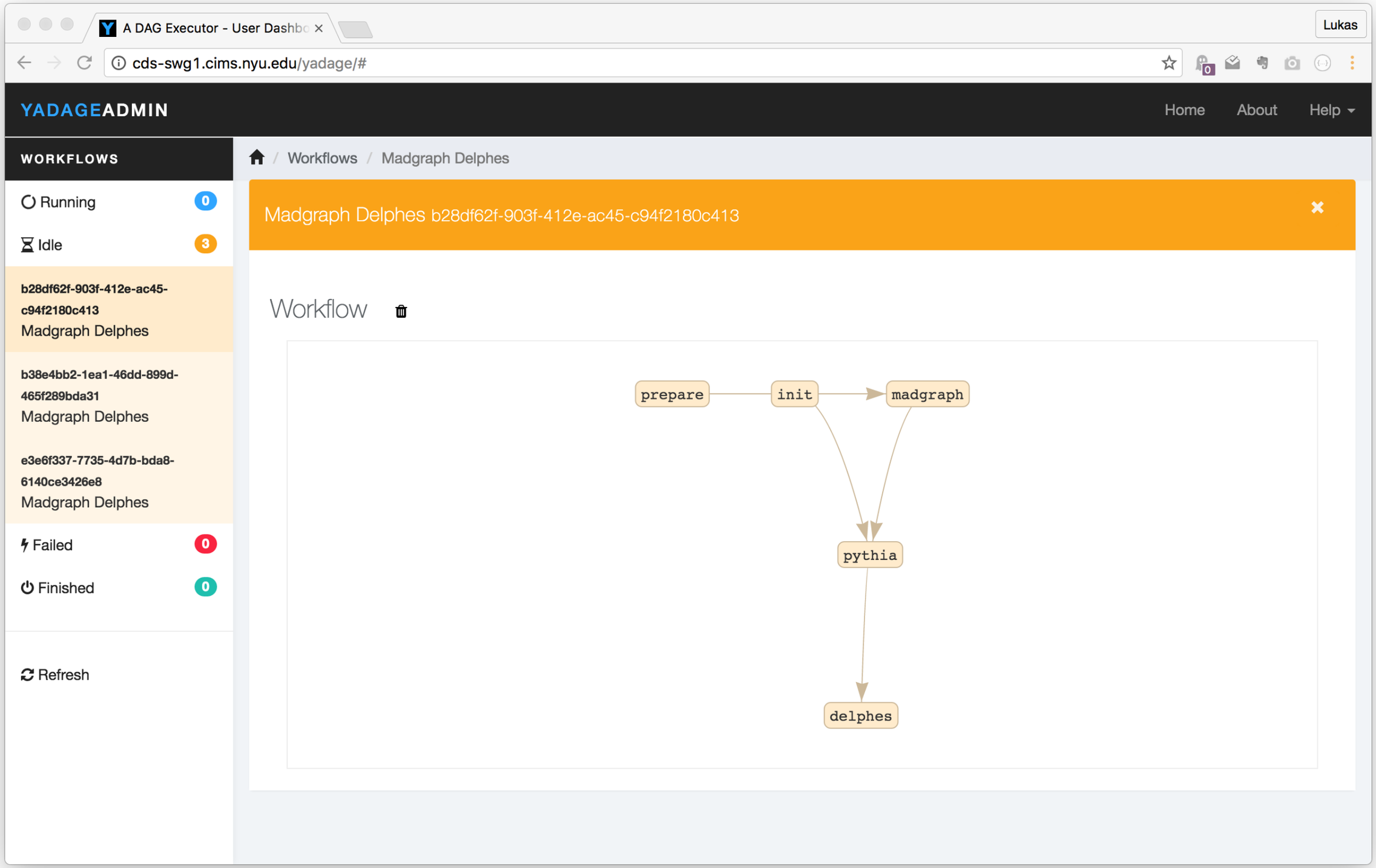
Distributing Workflows across multiple Hosts

easily distributable through packtivity python bindings via Celery

- build graph w/ stages
- track node state
- submits nodes to distributed backend



Web UI in development



Integration with CERN Analysis Preservation Portal (CAP)

JSON schemas integrated with CAP.

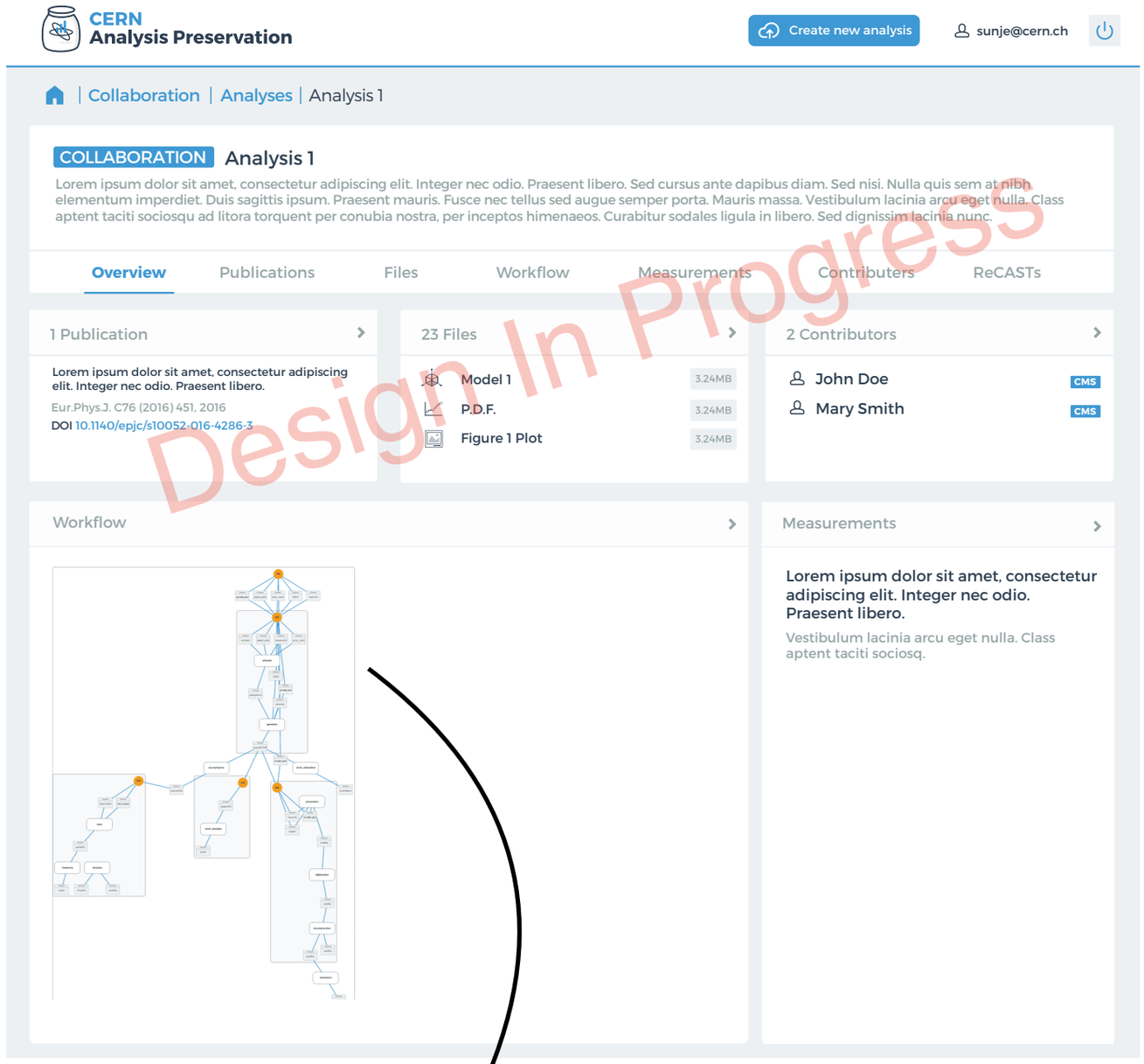
Analyses may store workflow(s) for relevant use cases

- workflows for reinterpretation
- workflows for auxiliaryy measurements
- …

Invenio-based CAP provides REST API for records

→ serve workflow spec via HTTP as JSON

CERN
Analysis Preservation




```
yadage-run -t from-cap/<recordID> <workdir> <workflow name> <parameters>
```

Integration with RECAST prototype

Reinterpretations are specific kind of workflows:

→ original data

→ new model $\quad f_{\text{analysis}}(\text{data}|\ \cdot\ )$

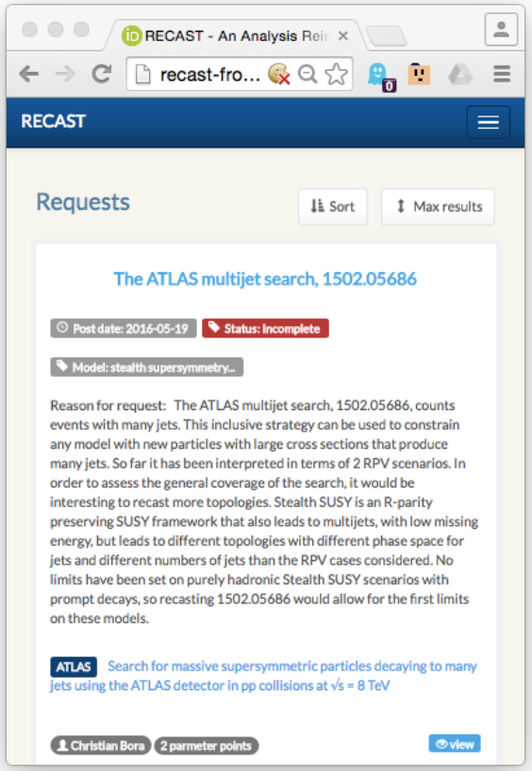
Prototype in development to enable LHC experiments to review requests for reinterpretation from larger HEP community, and if approved honor them.

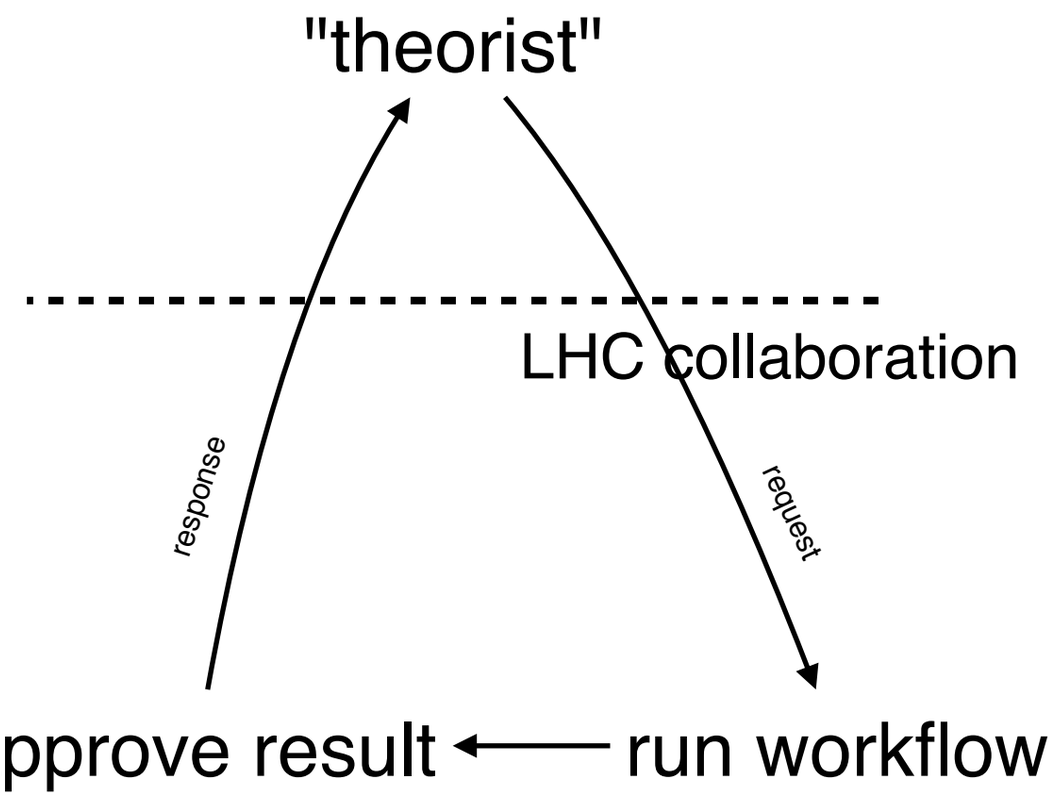
To be efficient / feasible re-usable analysis preservation is crucial

→ workflows where model is parametrized

→ possible interaction with CAP to retrieve workflows

Internal testing (deployed on CERN OpenStack resources) look promising





Yadage/Packtivity tools have been used in ATLAS Reinterpretation Campaigns

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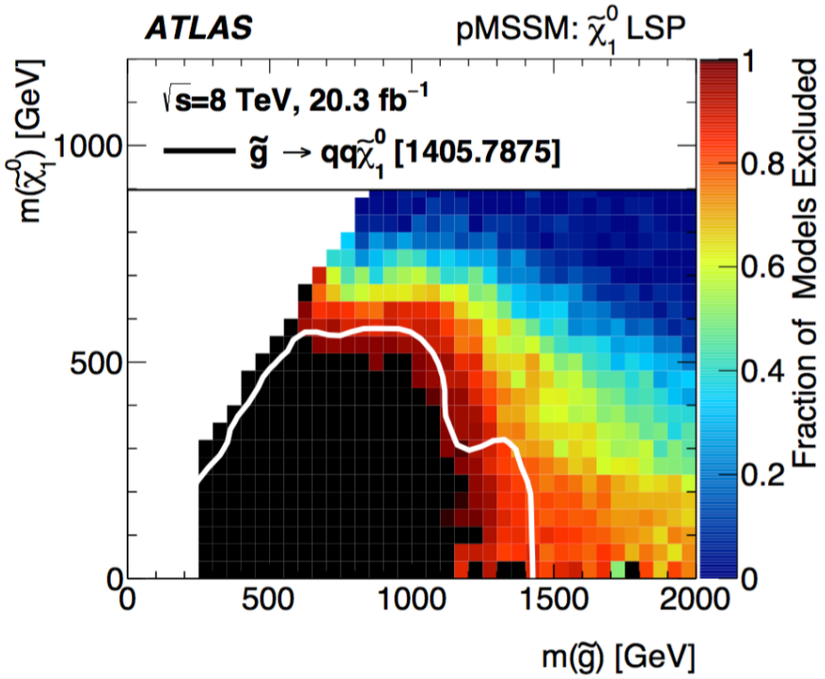
arXiv:1508.06608

19-D(!) pMSSM reinterpretation

Summary of the ATLAS experiment's sensitivity to supersymmetry after LHC Run 1 — interpreted in the phenomenological MSSM



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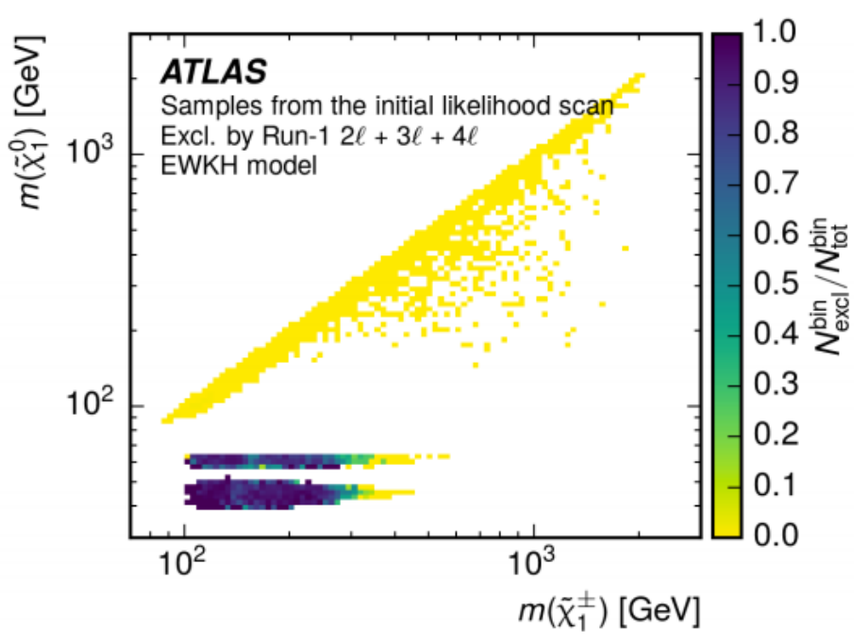
PUBLISHED: *September 30, 2016*

5-D scan of EWKH sector with help from STA

arXiv:1608.00872

Dark matter interpretations of ATLAS searches for the electroweak production of supersymmetric particles in $\sqrt{s} = 8$ TeV proton-proton collisions



A re-interpretation of $\sqrt{s} = 8$ TeV ATLAS results on electroweak supersymmetry production to explore general gauge mediated models

3-D recast for General Gauge Mediated SUSY Models

ATLAS-CONF-2016-033

The ATLAS Collaboration

Conclusions:

- Preserve analyses for Re-execution/Re-use, not just post-facto documentation.
- Source Code not enough, need full environment & notion on how to run software
- Linux Containers / Docker are powerful tools for preservation
- Separate declarative workflow description from concrete backend, aim for long-term preservation
- Dynamic DAGs are important for general solution
- Already producing new results with preserved analyses today with Reinterpretations.

Backup

Templated Scripts, various interpreters…

```yaml
process:
  process_type: 'interpolated-script-cmd'
  script: |
    #!/bin/bash
    echo "Hello"
    source ~/.bashrc
    setupATLAS
    source ./rcSetup.sh
    /recast_auth/getmyproxy.sh
    lsetup fax dq2
    python MultibjetsAnalysis/scripts/Run.py --dataSource 1 --doSyst 1 --doNTUPSyst 1 --doNTUP 0 --doxAOD 0 --doHistFitter 1
    mv {submitdir}/data-output_histfitter/*.root {outputprefix}.{did}.root
publisher:
  publisher_type: 'fromglob-pub'
  globexpression: '*.root'
  outputkey: histfitterfile
environment:
  environment_type: 'docker-encapsulated'
  image: lukasheinrich/multibsel_cvmfs
  resources:
    - CVMFS
    - GRIDProxy
```

```yaml
process:
  process_type: 'interpolated-script-cmd'
  interpreter: python
  script: |
    print 'Hello from Python'
    with open('{infile}') as input:
      with open('{outputfile}','w') as  output:
        output.write(input.read().upper())
publisher:
  publisher_type: 'frompar-pub'
  outputmap:
    outputfile: outputfile
environment:
  environment_type: 'docker-encapsulated'
  image: python
  imagetag: '2.7'
```

Nested Workflows

```yaml
stages:
  - name: prepare
    dependencies: ['init']
    scheduler:
      scheduler_type: singlestep-stage
      step: {$ref: 'steps.yml#/prepare'}
      parameters:
        kHzz: {stages: init, output: kHzz}
        kAzz: {stages: init, output: kAzz}
        kHww: {stages: init, output: kHww}
        kAww: {stages: init, output: kAww}
        param_card: '{workdir}/param.dat'

  - name: grid
    dependencies: ['prepare']
    scheduler:
      scheduler_type: singlestep-stage
      step: {$ref: 'steps.yml#/grid'}
      parameters:
        param_card: {stages: prepare, output: param_card}
        gridpack: '{workdir}/grid.tar.gz'

  - name: subchain
    dependencies: ['grid']
    scheduler:
      scheduler_type: multistep-stage
      workflow: {$ref: 'subchain.yml'}
      parameters:
        gridpack: {stages: grid, output: gridpack, unwrap: true}
        nevents: {stages: init, output: nevents, unwrap: true}
        seed: {stages: init, output: seeds, flatten: true}
      scatter:
        method: zip
        parameters: ['seed']

  - name: rootmerge
    dependencies: ['subchain']
    scheduler:
      scheduler_type: singlestep-stage
      step: {$ref: 'steps.yml#/rootmerge'}
      parameters:
        mergedfile: '{workdir}/anamerged.root'
        inputfiles: {stages: 'subchain.[*].analysis', output: analysis_output}
```

```yaml
stages:
  - name: madevent
    dependencies: ['init']
    scheduler:
      scheduler_type: singlestep-stage
      step: {$ref: 'steps.yml#/madgraph'}
      parameters:
        gridpack: {stages: init, output: gridpack}
        nevents: {stages: init, output: nevents}
        seed: {stages: init, output: seed}
        lhefile: '{workdir}/lhefile.lhe'

  - name: pythia
    dependencies: ['madevent']
    scheduler:
      scheduler_type: singlestep-stage
      step: {$ref: 'steps.yml#/pythia'}
      parameters:
        settings_file: /analysis/mainPythiaMLM.cmnd
        hepmcfile: '{workdir}/outputfile.hepmc'
        lhefile: {stages: madevent, output: lhefile}

  - name: delphes
    dependencies: ['pythia']
    scheduler:
      scheduler_type: singlestep-stage
      step: {$ref: 'steps.yml#/delphes'}
      parameters:
        detector_card: /analysis/template_cards/modified_delphes_card_ATLAS.tcl
        outputfile: '{workdir}/outputfile.root'
        inputfile: {stages: pythia, output: hepmcfile}

  - name: analysis
    dependencies: ['delphes']
    scheduler:
      scheduler_type: singlestep-stage
      step: {$ref: 'steps.yml#/analysis'}
      parameters:
        fromdelphes: {stages: delphes, output: delphesoutput}
        analysis_output: '{workdir}/anaout.root'
```