Scalable Drug Discovery with Apache Beam



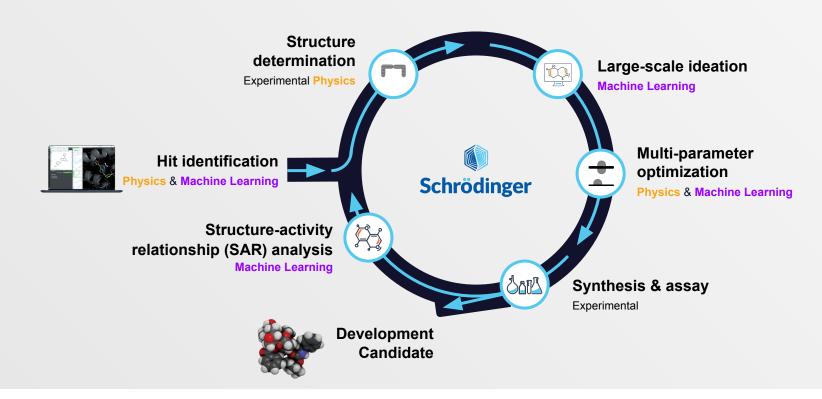


Q Agenda



- Schrodinger
 - The Drug Discovery Platform
 - A Brief History of Schrodinger Workflow Engines
- Schrodinger Beam → Seam
 - SeamRunner
 - Seam Transform Catalog
- Applications
 - AutoDesigner: R-Group Enumeration
 - Crystal Structure Prediction
- Future Direction

The Schrödinger Drug Discovery Platform







Large-scale ideation

Machine Learning







Structure-activity relationship (SAR) analysis

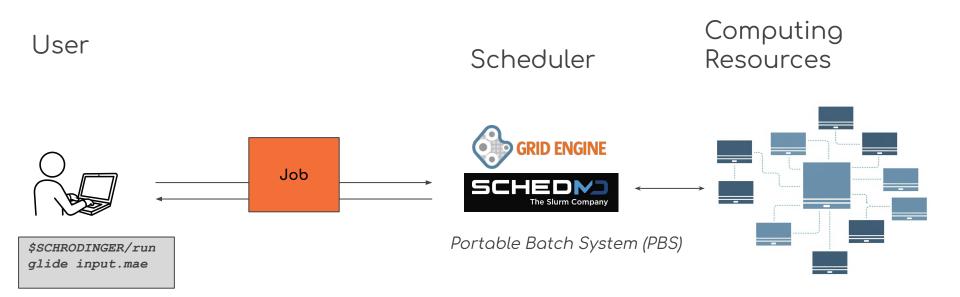
Machine Learning



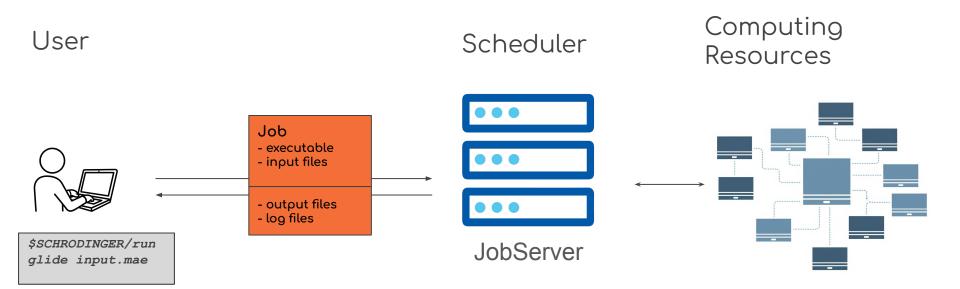
Multi-parameter optimization

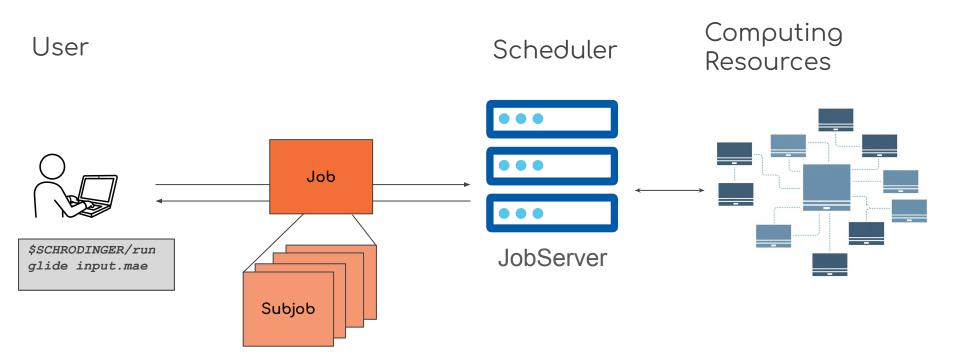
Physics & Machine Learning

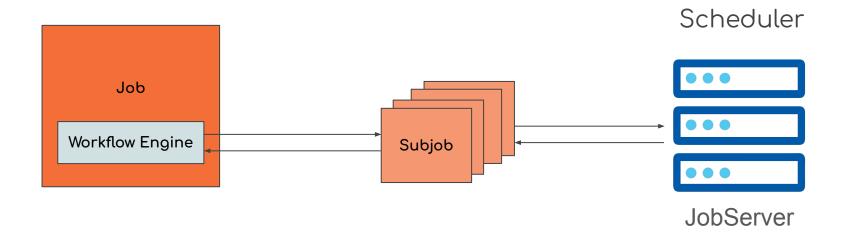


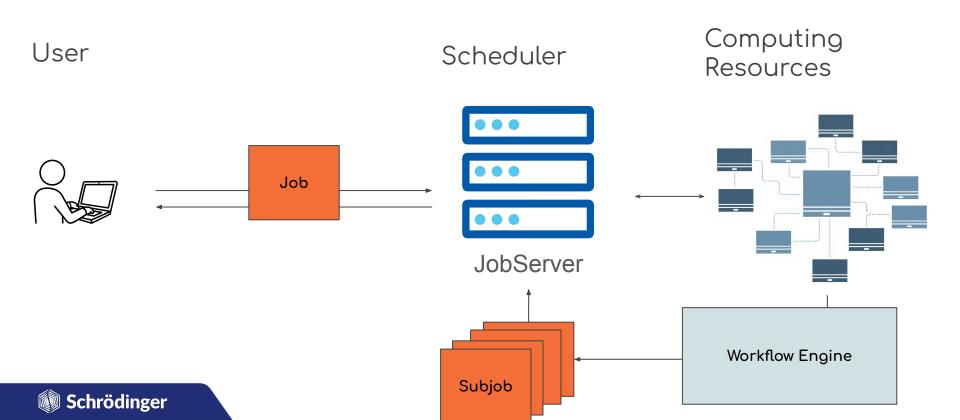


Computing User Scheduler Resources Job \$SCHRODINGER/run **JobServer** glide input.mae An abstraction over queueing systems









Workflow Engines at Schrödinger

EpikX Local Train



FragmentVSWorkflow

Jaguar MultiStage



Workflow Engine Feature Matrix

	Observability	Worker Autoscaling	Cloud Integrations	Text-based declarative workflows	Checkpointin g	Expressive and usable API
stepper	~	V	V	×	×	×
active learning	×	×	~	×	V	×
meta	×	×	×	V	×	×
multisim	×	×	×	V	×	×
						×

Workflow Engines at Schrödinger

SeamRunner

Beam runner built to execute workflows on JobServer-enabled compute





1990

2008

2008

2019

and beyond...

Workflow Engine Feature Matrix

	Observability	Worker Scaling	Cloud Integrations	Text-based declarative workflows	Checkpointing	Expressive and usable API
SeamRunner	V	V	V	V	V	
Apache Beam						V

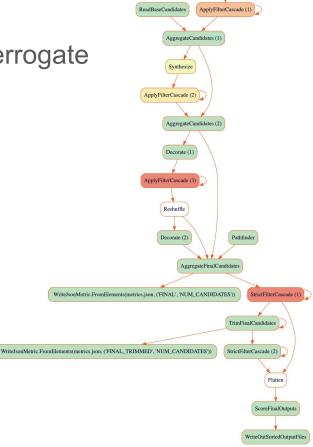
SeamRunner Features

Log aggregation

```
2025-05-07T00:15:28.005 seam_log pipeline.clean.log[0]
      12:15:28AM [seam orchestrator]
May07 12:15:28AM [seam_orchestrator]-|- USER
                                                Executing pipeline
May07 12:15:28AM [seam_orchestrator]-|- USER
                                                Using following non-default SeamRunner options:
May07 12:15:28AM [seam_orchestrator]-|- USER
May07 12:15:28AM [seam_orchestrator]-|- USER
May07 12:15:28AM [seam_orchestrator]-|- USER
May07 12:15:28AM [seam_orchestrator]-|- USER
May07 12:15:49AM [seam_orchestrator]-|- USER
May07 12:15:49AM [seam_orchestrator]-|- USER
                                                Running stage 1/171
May07 12:15:49AM [seam orchestrator]-|- INFO
                                                (EXECUTABLE STAGE)
May07 12:15:49AM [seam_orchestrator]-|- USER
May07 12:15:49AM [seam_orchestrator]-|- USER
May07 12:15:49AM [seam_orchestrator]-|- USER
May07 12:15:49AM [seam_orchestrator]-|- DEBUG
May07 12:15:49AM [seam orchestrator]-|-
                                       DEBUG
May07 12:15:49AM [seam_orchestrator]-|- INFO
May07 12:15:49AM [seam_orchestrator]-|- INFO
May07 12:15:49AM [seam orchestrator]
```

SeamRunner Features

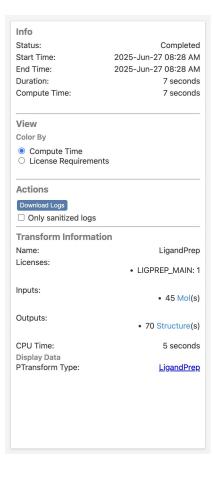
- Workflow Watcher
 - Visualize and interrogate your pipelines



ReadAdditionalTrimmedInputs

MMP Transform

ReadMolsFromFile



Seam Tooling

Resource Management

- Per-transform licenses
- GPU requirements
- Memory requirements

```
@with_license_requirements({license.LIGPREP_MAIN: 1})
@requires_min_ram("16GB")
class PrepareLigand(beam.PTransform):
...
```

Seam Transform Catalog

Seam Transform Catalog

See also:

- · Beam transform catalog
- Seam YAML transform catalog

Transform	Description
<u>ReadStructuresFromFile</u>	Read a file (or files) containing structures and return a PCollection of Structure objects.
<u>WriteStructuresToFile</u>	Write a PCollection of Structure objects to a file.
<u>ReadMolsFromFile</u>	Read a file (or files) containing molecules
<u>WriteMolsToFile</u>	Write a PCollection of Mol objects to a file.
<u>FixedSample</u>	Split a PCollection into two PCollections: a random sample of the input PCollection and the remaining elements.
<u>Тор</u>	Split a PCollection into two PCollections: the largest n elements of the input PCollection and the remaining elements.
<u>RandomSample</u>	Create a PCollection made up of a random sample of the input PCollection.
<u>Smallest</u>	Create a PCollection containing the smallest element(s) of the input PCollection.
<u>IPythonInspect</u>	Starts an IPython shell to interactively inspect the contents of a PCollection.

Scientific Transforms

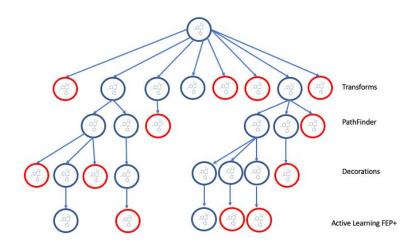
Transform	Description	
Dock	Dock ligands into a receptor using Glide.	
<u>ProteinPrep</u>	Clean up and prepare a protein using PrepWizard	
<u>LigandPrep</u>	Clean up and prepare a ligand and generate tautomers	
Refine	Refine a protein receptor using Prime.	

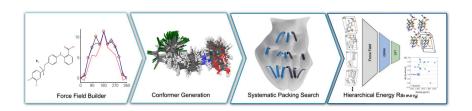


Seam-based Applications

AutoDesigner: R-Group Enumeration

Crystal Structure Prediction

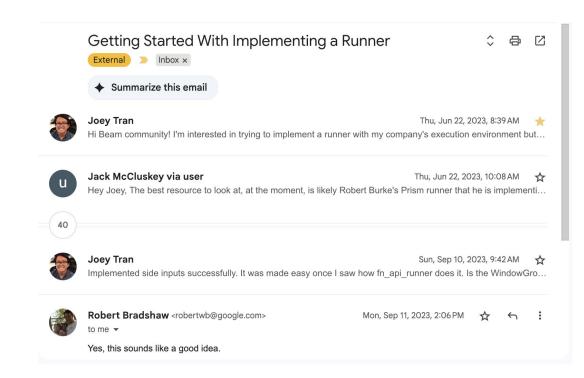




Scaled to 10k CPU cores and TB scale data PCollections

Challenges

Writing a runner is hard!



Challenges

Developer adoption

- Beam learning curve can be steep



Future Direction

- Streaming support
- YAML-based workflows
- Improvements in scientific prototyping usability
- Worker/Server-based execution

```
pipeline:
 type: chain
 transforms:
   type: CreateStructures
     config:
       elements:
         - smiles: "CC(=0)C1=CC=C(C=C1)C(=0)0"
           name: "Aspirin"
         - smiles: "Cn1cnc2c1c(=0)n(C)c(=0)n2C"
           name: "Caffeine"
         - smiles: "CC(C)[C@H]1CCC(C)CC10"
          - smiles: "CC(=0)NC1=CC=C(C=C1)OC(C)C=CC=CC2=CC=C(C=C2)0"
           name: "Capsaicin"
         - smiles: "CN1CCCC1C2=CN=CC=C2"
           name: "Nicotine"
    type: LigPrep
       arg string: "-nt -epik -s 32"
```

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Crystal Structure Prediction Team

Efrem Broun

Ethan Alguire

Ding Wei

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QUESTIONS?

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