

Enabling Plant Sciences Research with the iPlant Discovery Environment and Condor

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Outline





- What is iPlant?
- iPlant Discovery Environment
- Architecture overview
- Tool integration and analysis creation APIs
- Execution environment
- Simple analysis example



What is iPlant?

- Is a cyberinfrastructure collaborative rather than purely a cyberinfrastructure.
- Enables multidisciplinary teams to address grand challenges in plant science.
- Is an entity that is by, for, and of the community.
- Helps train the next generation in computational thinking is designed to be able to reinvent itself as the needs of the community and technologies change.







Perform Analyses





Overview

 Choose Analysis
 More Actions ▾

Name	Description	Start Date	End Date	Status
No Analyses to display				


Find SNPs




Select SAM File(s)





Select SAM File(s):


Add
 Delete

File Name
No files to display.

Select the reference genome


Base calling


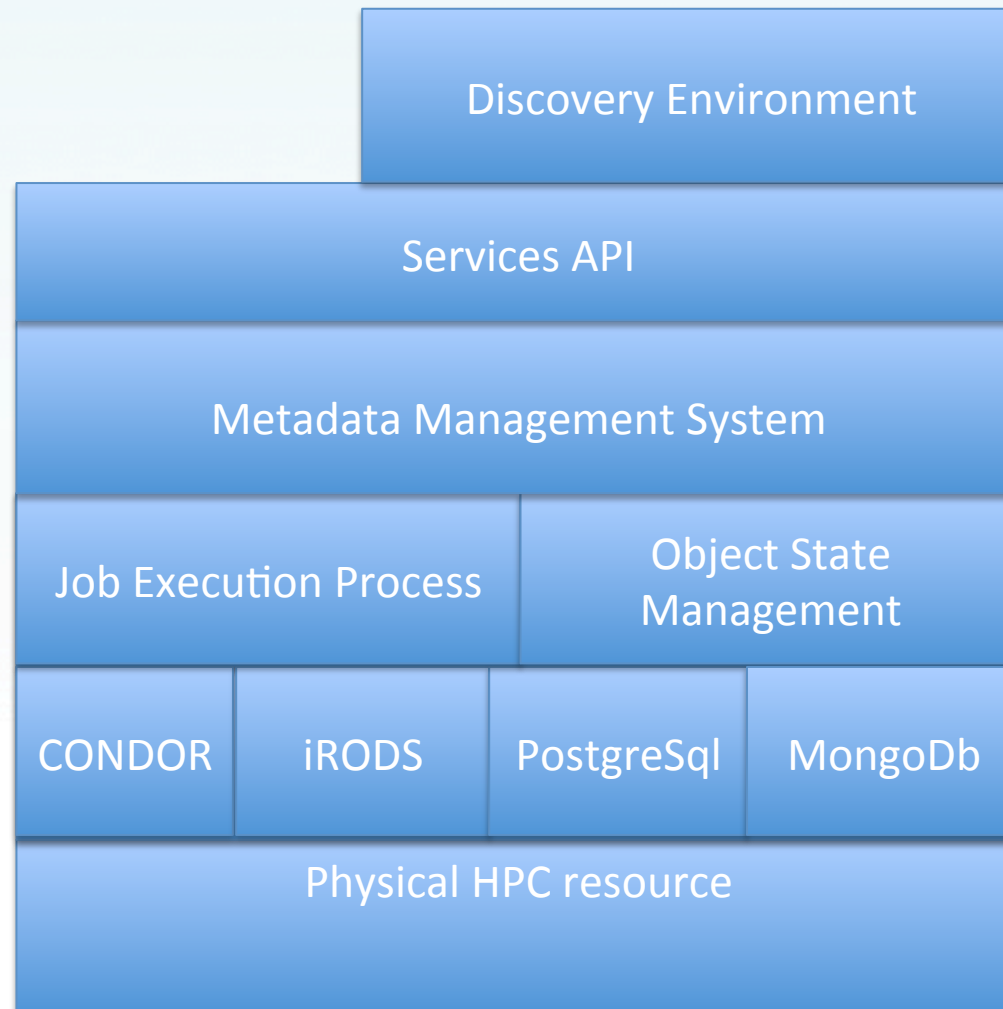
Filtering


Options


Launch Job



Architecture Overview



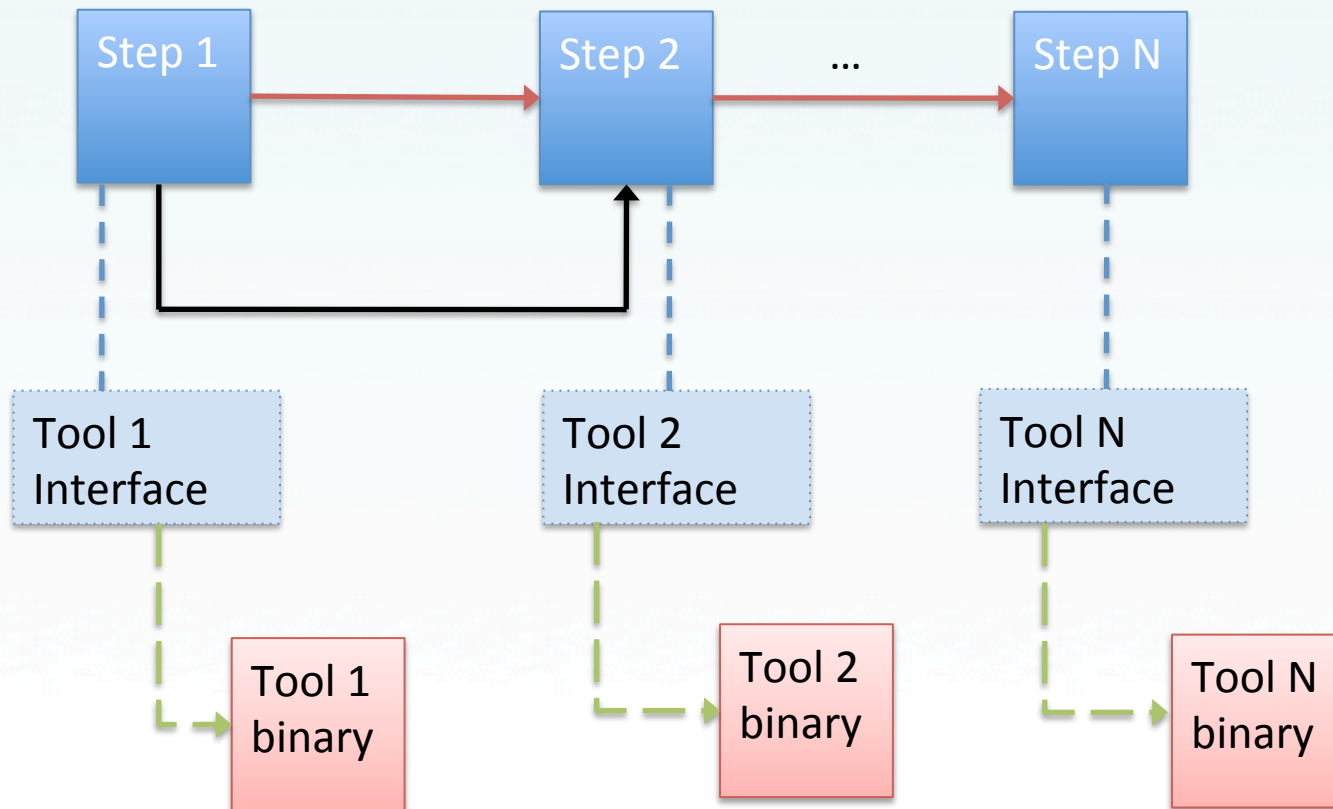
Tool integration and analysis creation API

- Is a textual description of a command line tool's interface and workflow definition in JSON format.
- Allows Scientists to run off-the-shelf tools with the resources provided by iPlant.
- Drives the building of user interfaces shown to the user for a specific tool or analysis.
- Is the *lingua franca* within iPlant for Job Execution.



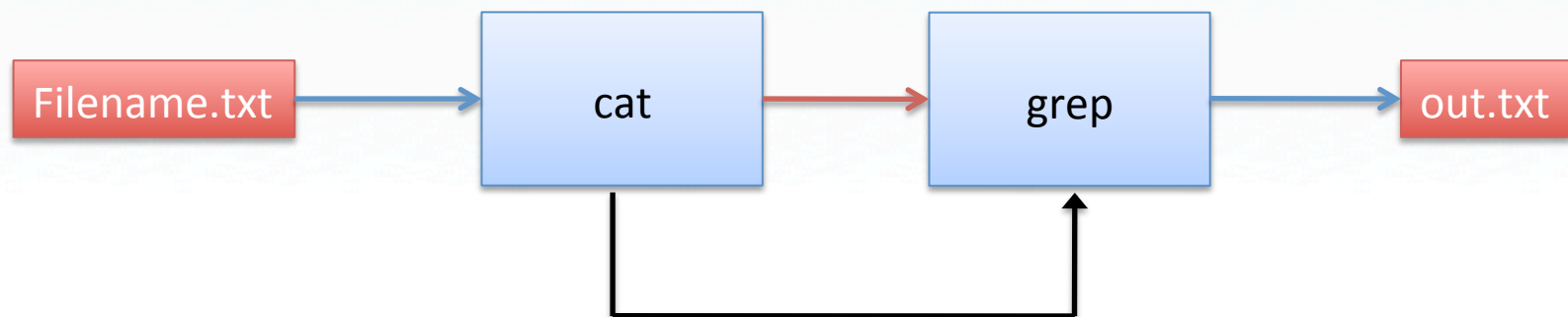
Conceptual Components

Analysis



```
>cat -b filename.txt | grep text > out.txt
```

```
>cat -b filename.txt >cat.out  
grep cat.out text > out.txt
```



>cat

```
{  
  "id": "ahoi3uheralsdkfjasl8ked3",  
  "name": "",  
  "type": "cat",  
  "input": [  
    {  
      "id": "catin",  
      "name": "File to read:",  
      "type": "File",  
      "multiplicity": "single",  
      "order": 2  
    },  
  ],  
}
```



```

"groups": [
  {
    "name": "",
    "id": "",
    "type": "step",
    "properties": [
      {
        "id": "bflag",
        "name": " -b ",
        "type": "Flag",
        "label": "Show line numbers",
        "visible": false,
        "value": true
        "validator": {
          "name": "",
          "required": true
        },
        "order": 1
      }
    ]
  }
],
"output": [
  {
    "id": "catout",
    "name": "cat.txt",
    "type": "file",
    "multiplicity": "single",
    "order": 2
    "switch": " > "
  }
]

```



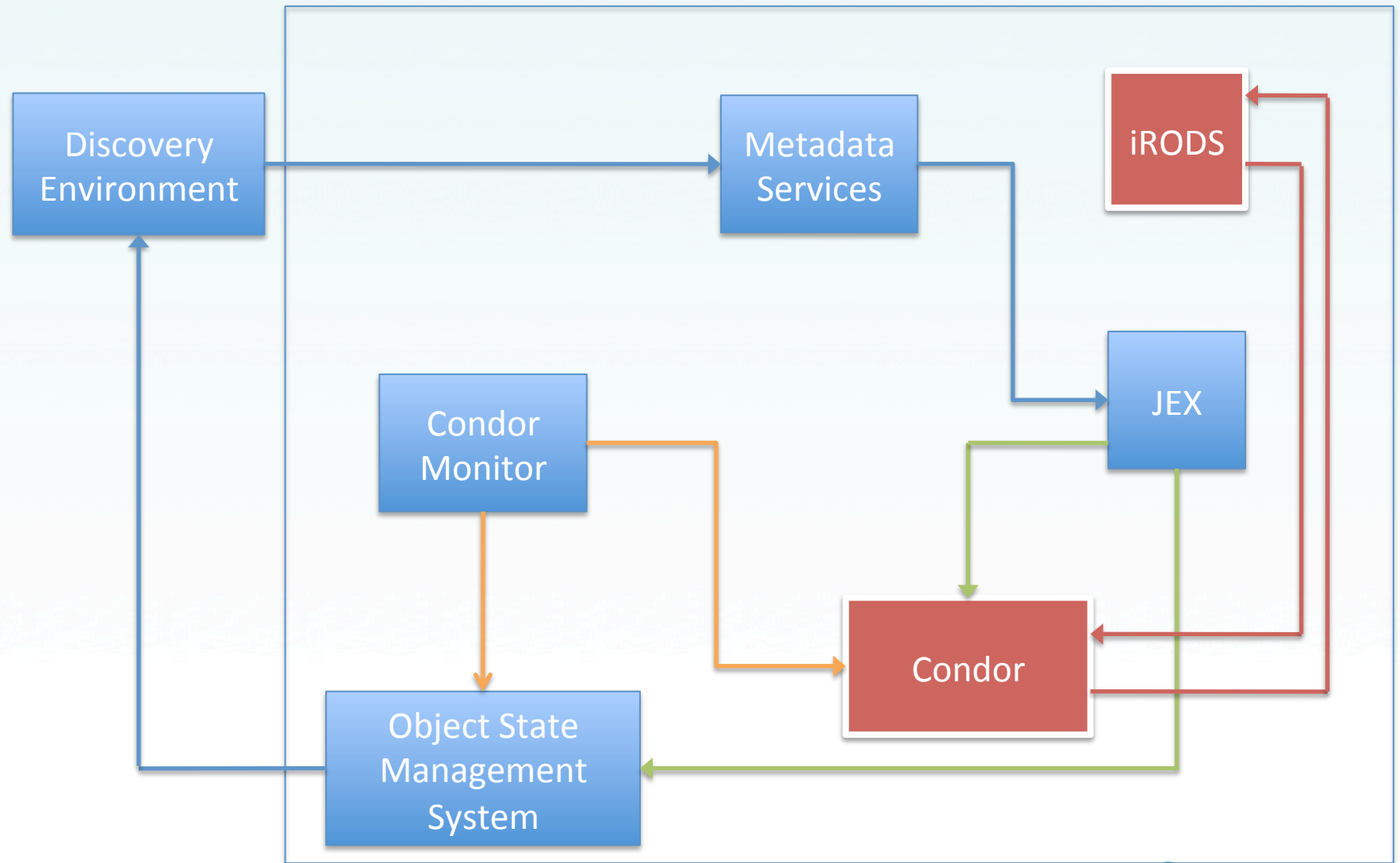
```
{
  "analysis_id": "",
  "analysis_name": "File Read and Filter",
  "type": "unix",
  "description": "Reads a file and filters it",
  "steps": [
    {
      "name": "cat",
      "description": "Reads a file and prints to standard output",
      "template_id": "ahoi3uheralsdkfjasl8ked3",
      "config": {
      }
    },
    {
      "name": "grep_search",
      "description": "Searches within a file for supplied text",
      "template_id": "",
      "config": {
      }
    }
  ]
}
```



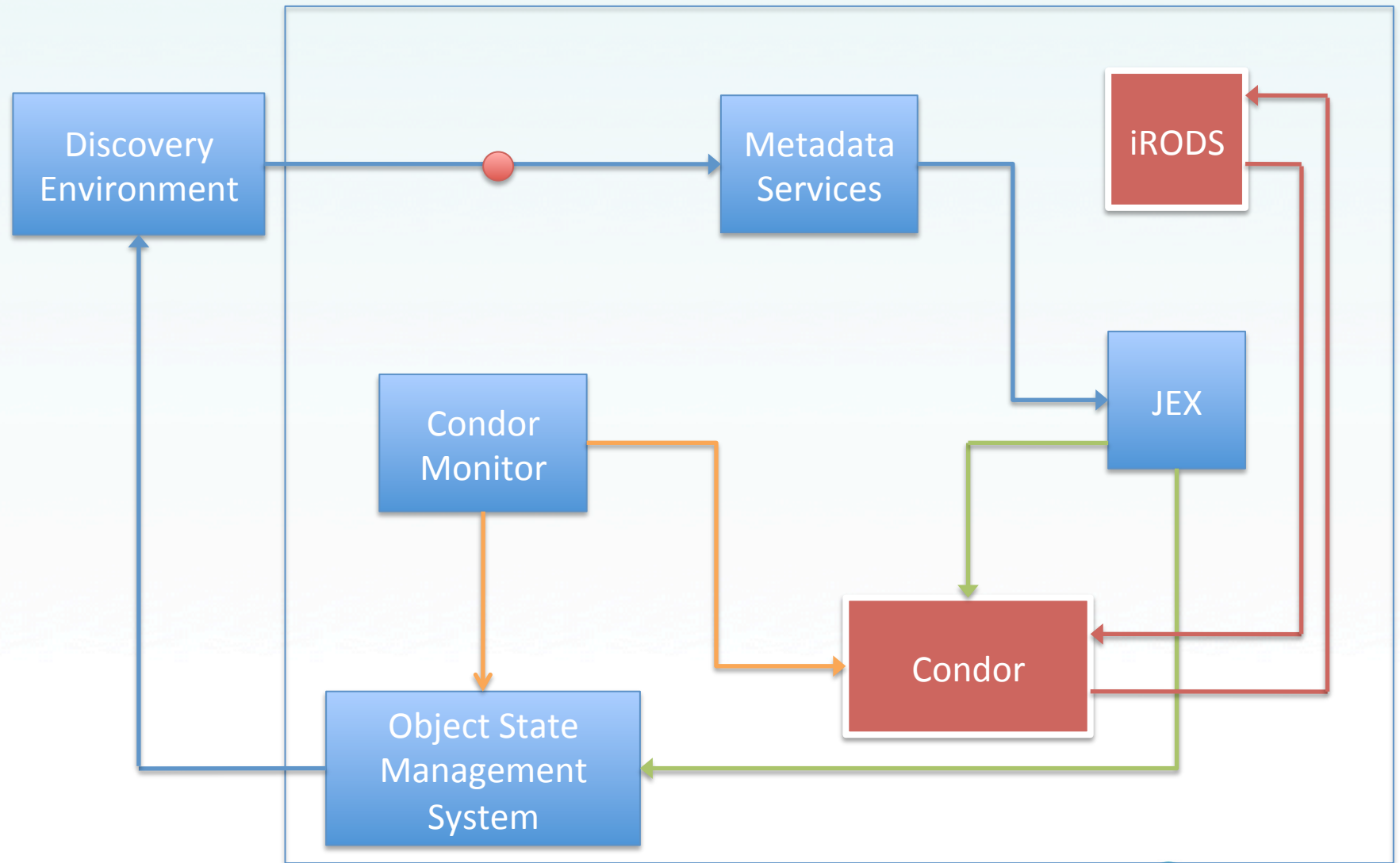
```
"mapping": [
  {
    "source_step": "cat",
    "target_step": "grep_search",
    "map": {
      "catout": "grepin"
    }
  },
]
```



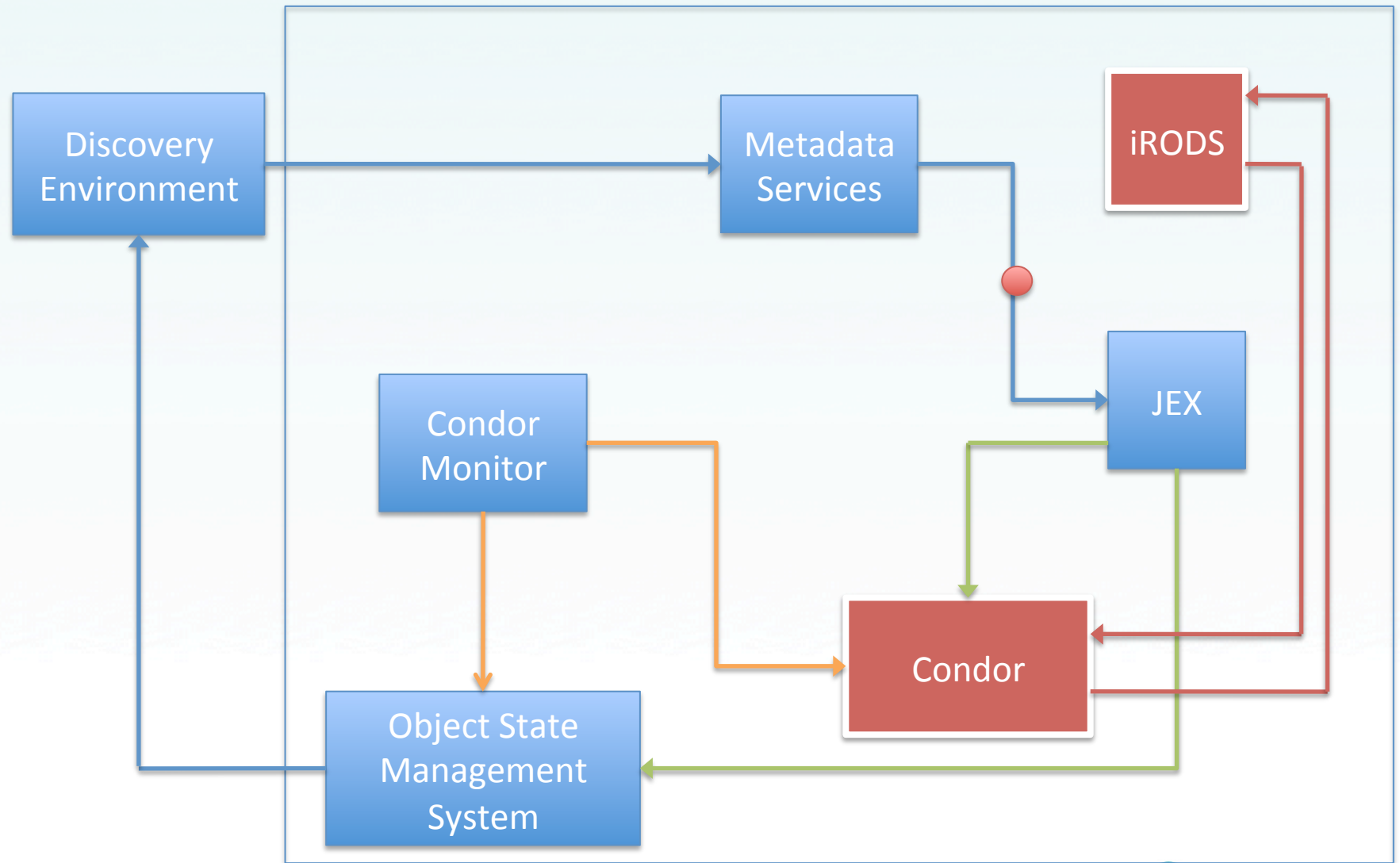
Execution flow



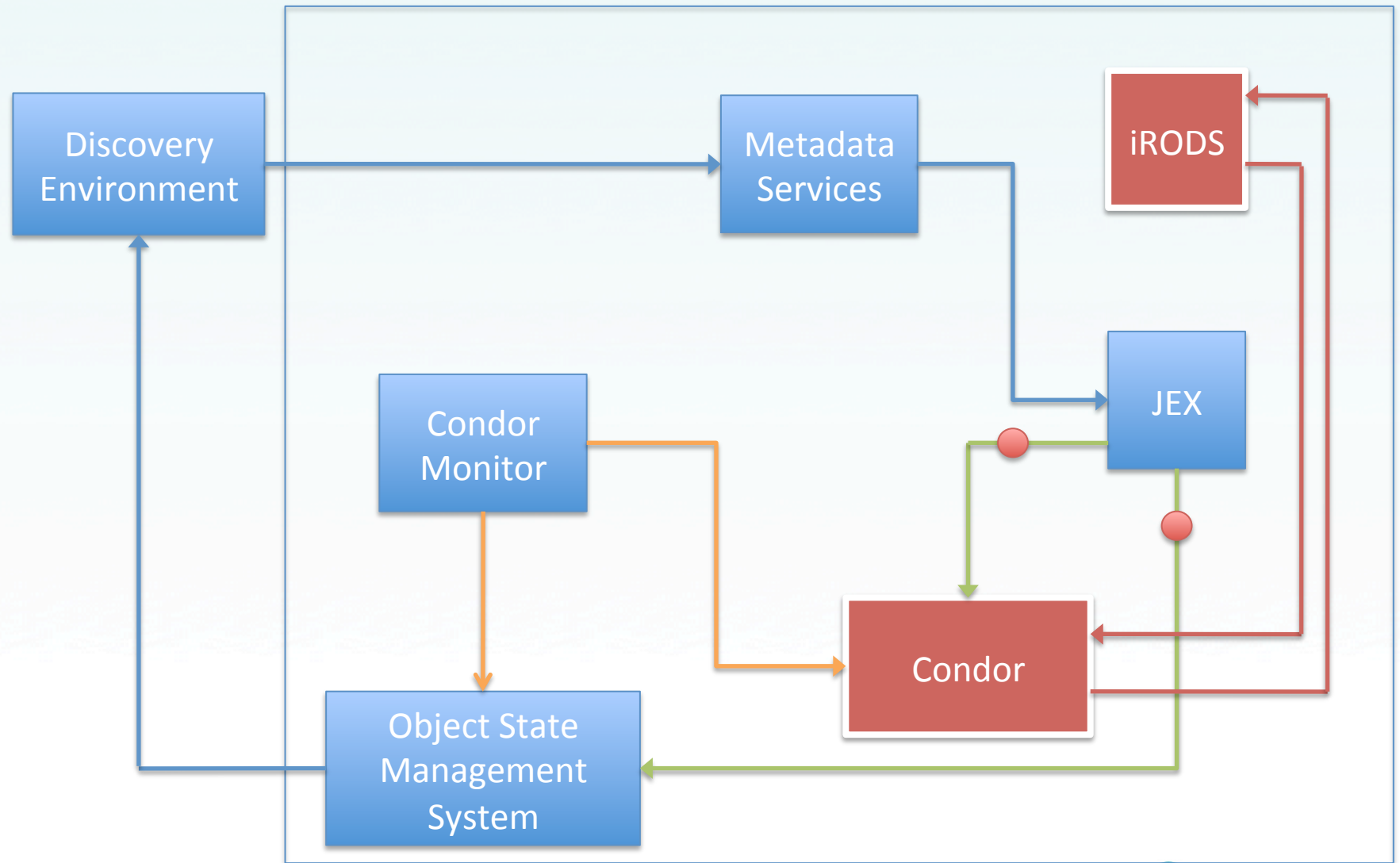
Execution flow



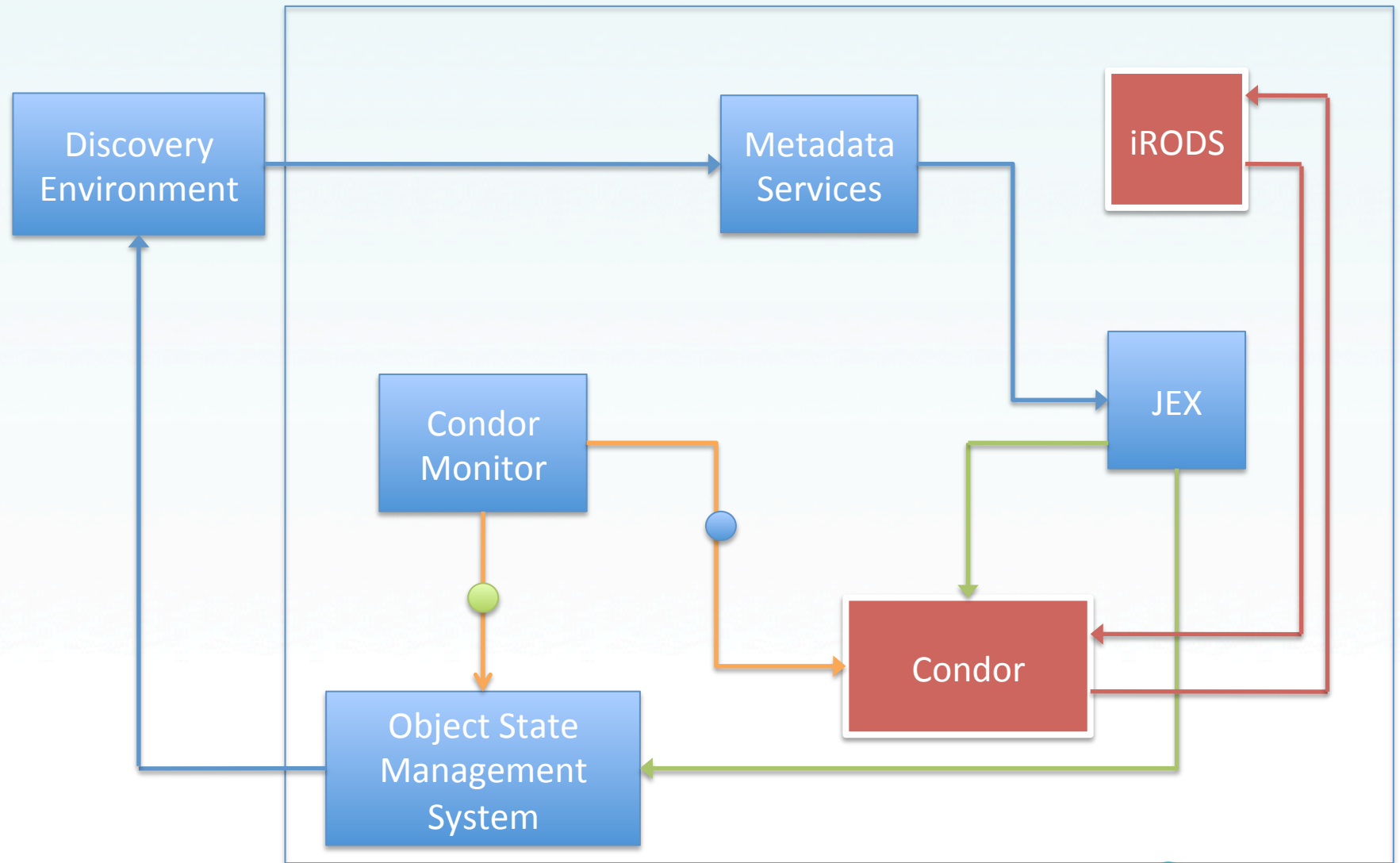
Execution flow



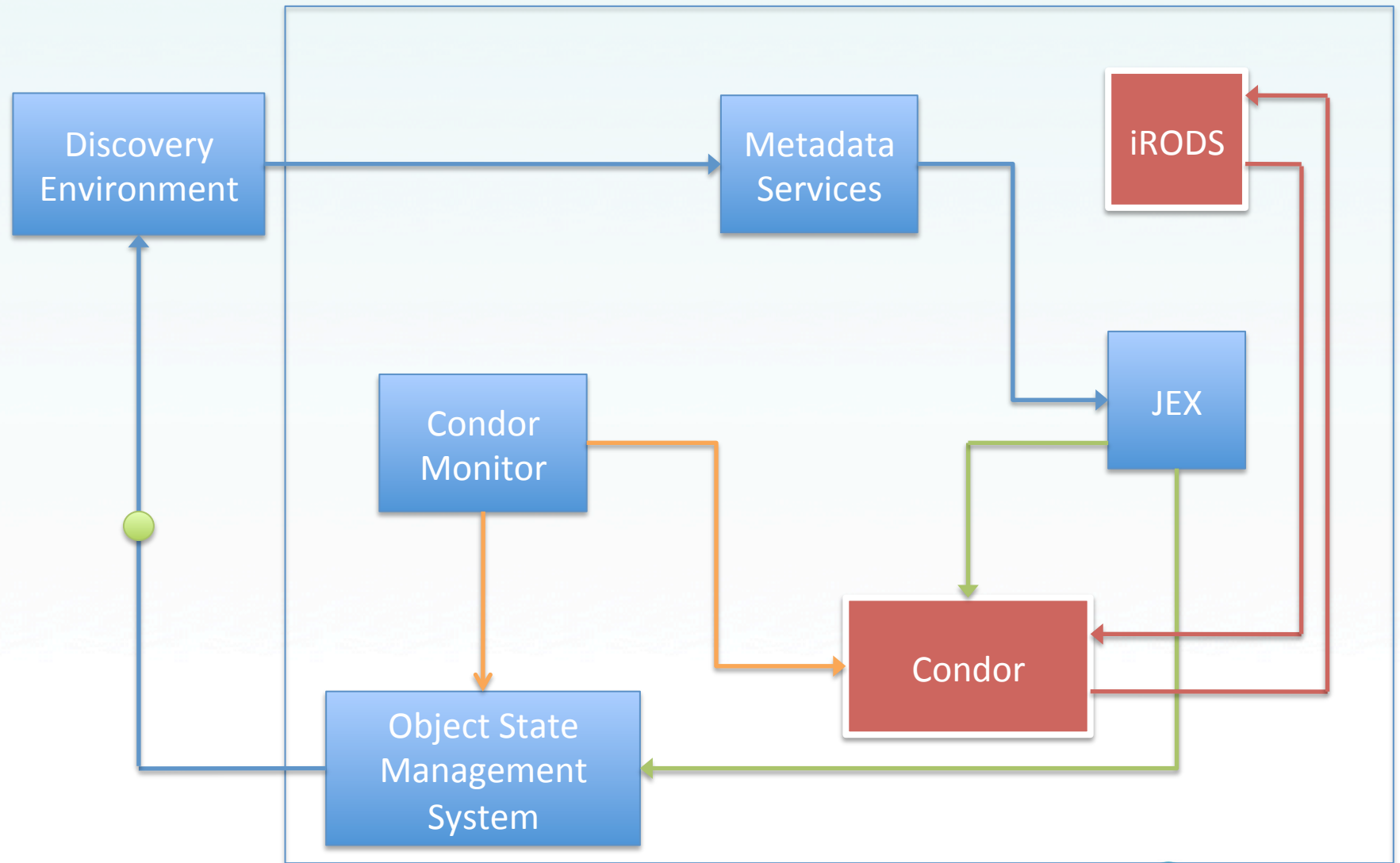
Execution flow

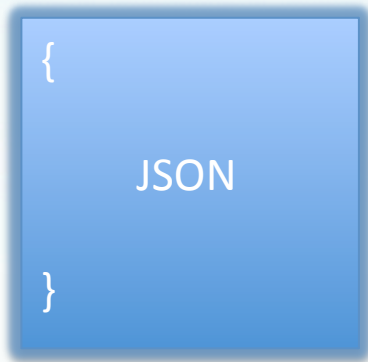


Execution flow



Execution flow





Cufflinks Transcript Quantification

Select SAM File(s)

Select SAM File(s):

Add Delete

File Name

No files to display.

Select Reference Annotation

Parameters for analysis

Launch Job



Complete material & tutorials at:

<http://www.iplantcollaborative.org>

<https://pods.iplantcollaborative.org/wiki/display/docs/Tool+Integration+Tutorial>

<https://pods.iplantcollaborative.org/wiki/display/docs/Analysis+Authoring+Tutorial>



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