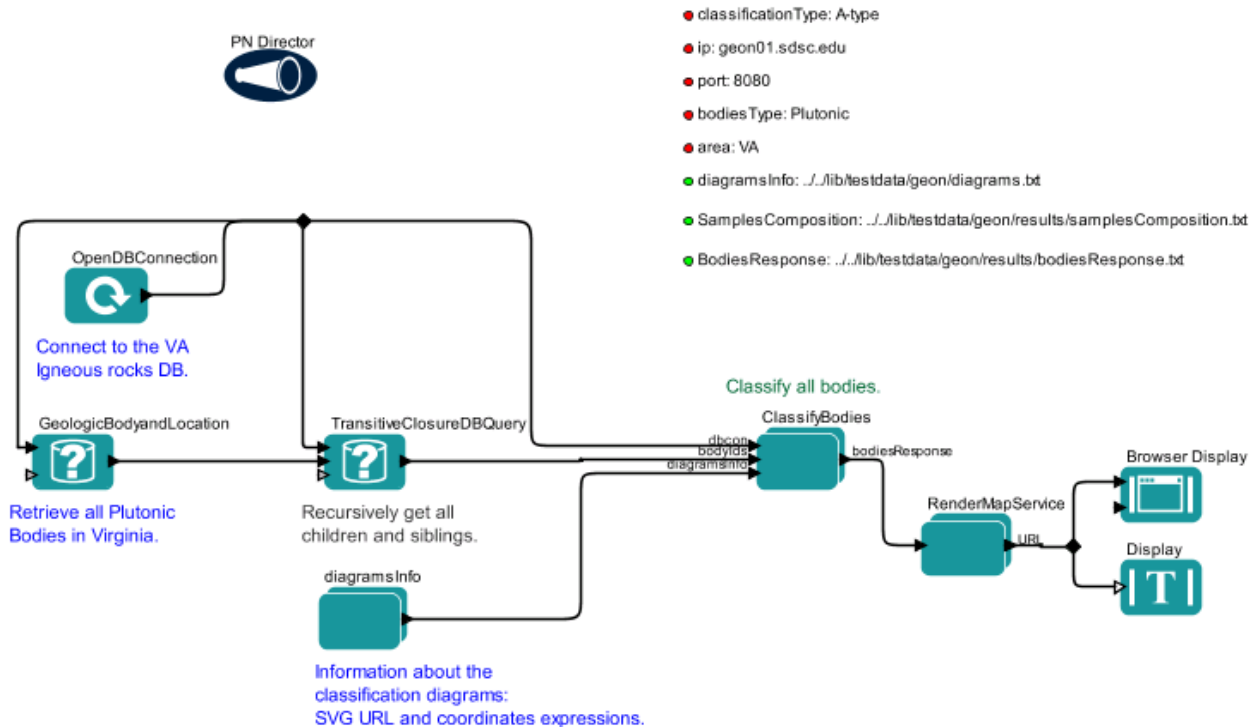
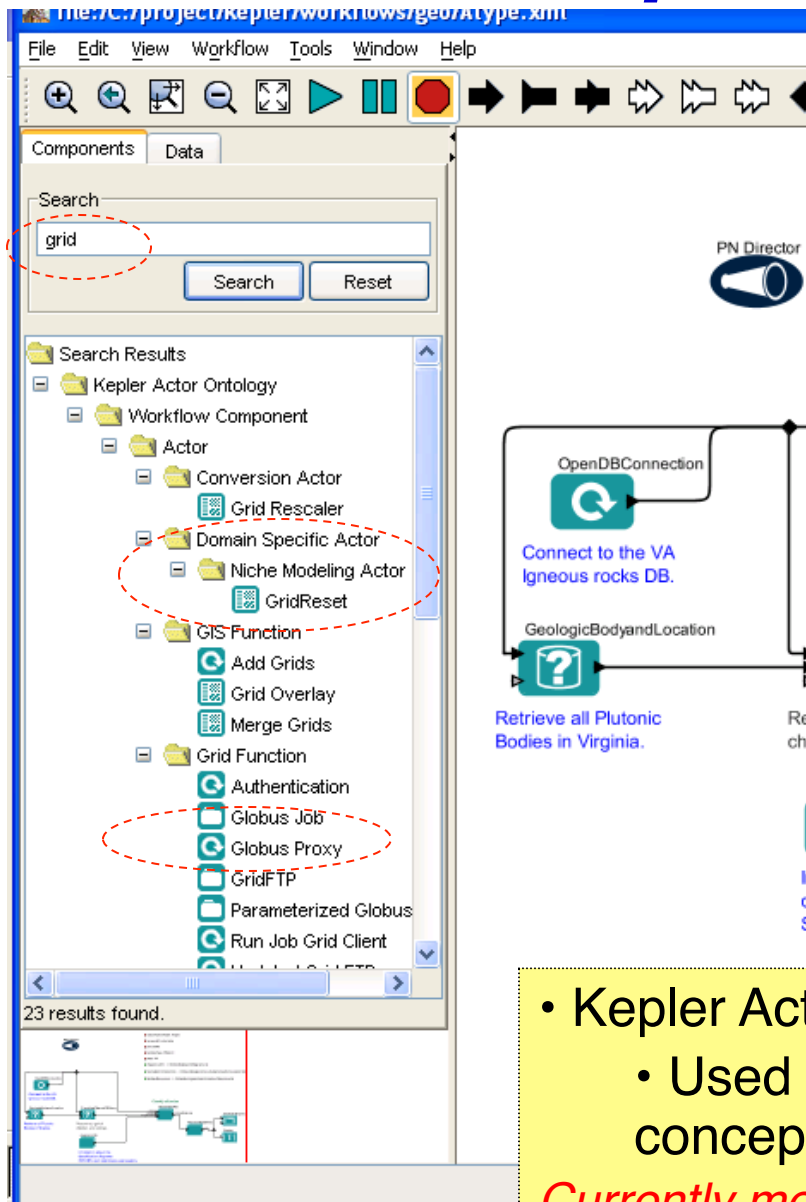

Introduction to the Kepler User Interface and Actor-Oriented Modeling

Daniel Crawl

The Kepler User Interface

... but Kepler can also run in batch mode as a command-line engine.

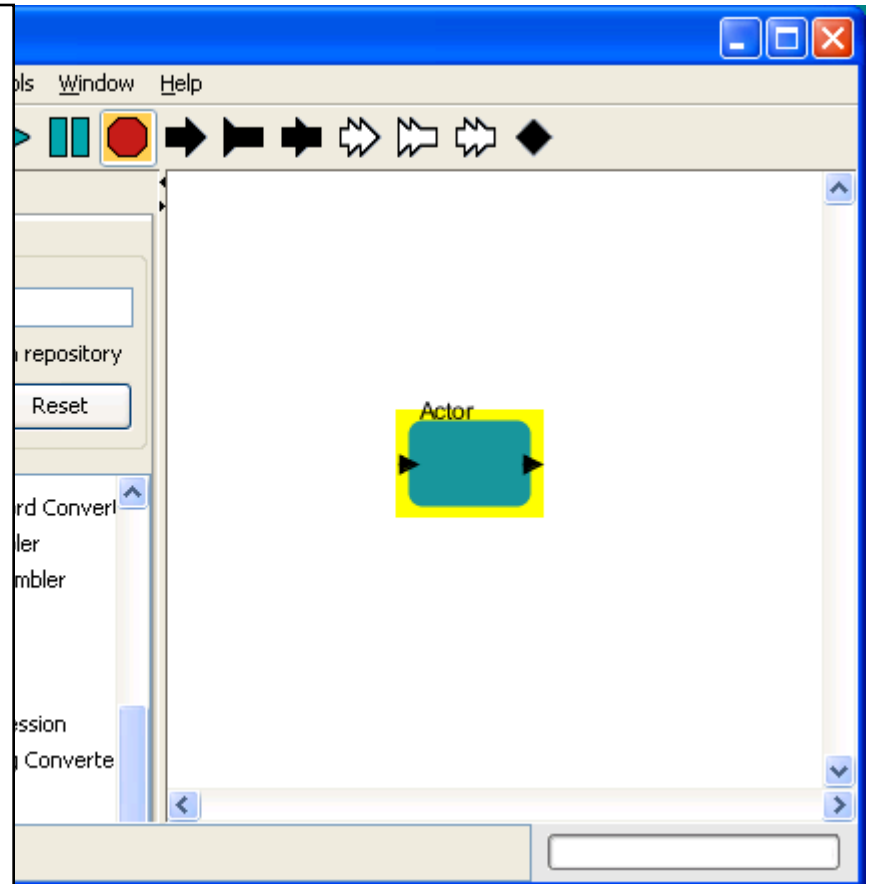


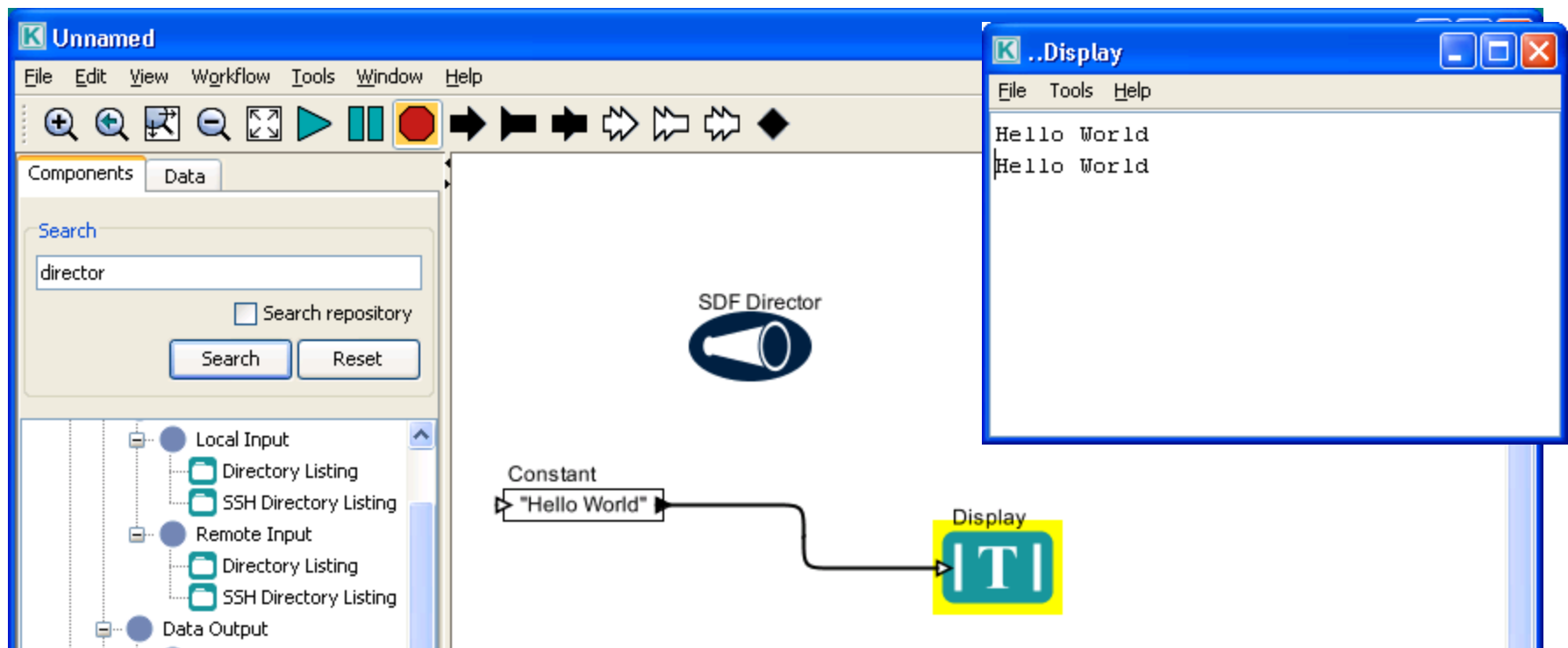
- Kepler Actor Ontology
 - Used in searching actors and creating conceptual views (= folders)

Currently more than 200 Kepler actors added!

Actor-Oriented Modeling in Kepler

- Actors
 - Single component or task
 - Well-defined interface (signature)
 - Given input data, produces output data
 - Configured with parameters
 - “Composite” actor for [sub-workflows](#)
- Ports
 - Each actor has a set of input and output ports
 - Denote the actor’s signature
 - Produce/consume data (a.k.a. tokens)
 - Can be [semantically annotated](#) with domain-specific concepts





- Dataflow Connections
 - Actor “communication” channels
 - Directed edges
 - Connect output ports with input ports
- Directors
 - Execution models, define the execution semantics of workflow graphs
 - Executes workflow graph (some schedule)
 - **Sub-workflows** may have different directors

Directors Provide Execution Semantics

- Define the semantics of
 - execution of actors and workflows
 - interactions between actors
- Synchronous Dataflow (SDF)
 - Connections have queues for sending/receiving fixed numbers of tokens at each firing. Schedule is statically predetermined.
- Process Networks (PN)
 - Actors execute in separate threads with queues of unbounded size. Related to Kahn/MacQueen semantics. The workflow is executed in parallel pipeline.
- Discrete Event (DE)
 - Actors communicate through a queue of events in time. Used for instantaneous reactions in physical systems.
- Dynamic Dataflow (DDF)
 - Connections have queues for sending/receiving arbitrary numbers of tokens at each firing. Schedule is dynamically calculated.

Ptolemy and Kepler are unique in combining different execution models in heterogeneous models.



Demo: Building a Simple Workflow

The screenshot shows the SDF Director interface with a workflow editor. The workflow consists of three components connected in a sequence:

- String Constant**: A yellow box containing the text "Hello \$name". It has a "trigger" input on the left.
- CompositeActor**: A teal rounded rectangle.
- Display**: A teal box with a white "T" inside.

Arrows indicate the flow from the String Constant to the CompositeActor, and then to the Display. The interface includes a toolbar at the top, a search panel on the left, and a status bar at the bottom showing "execution finished: 16 ms. Memory: 189368K Free: 75836K (40%)".

Kepler Provenance Framework

- **What** provenance is recorded:
 - Workflow Specification: actors, ports, connections, parameters, etc.
 - Workflow Evolution: parameter values that change over time, addition/removal of actors, ports, etc.
 - Workflow Execution:
 - Start/stop of workflow, individual actor executions
 - Data exchanged between actors
- **Where** provenance is recorded:
 - Modular interface supports saving to different output types.
 - Currently implemented: Text file, SQL, Ignore

Reporting and Workflow Run Manager

file:/Users/crawl/repos/kepler/k/kepl. . .each/resources/demos/SEEK/Elk_Wolf.xml

Tag run:select or type tag and press enter View: Report Designer

Report Designer Report Viewer

Title: **Elk Wolf Growth/Death Rates**

Items Of Interest

- Elk_Wolf
 - Net Growth Rate per
 - TimedPlotter
 - Rate of Elk Increase
 - Elk death rate per E
 - Wolf death rate per
 - Elk kill rate per Wolf
 - Elk eaten rate

Show Ports
 Show Attributes
 Show Relations

Report Formatting Items

- section
- hr
- text
- image

Properties

Property	Value
ALIGNMENT	
SCALE	

Workflow Run Manager

click to enter search term	workflow search	> Jan 01, 2004 12:00:00 AM	> 00:00:00	username	> 0
Tags	Workflow Name	Run Date	Duration	User	Id
	Elk_Wolf	Jan 28, 2010 7:30:54 PM	00:00:35	crawl	6
	Elk_Wolf	Jan 28, 2010 7:29:29 PM	00:00:34	crawl	5
	Elk_Wolf	Jan 28, 2010 7:28:20 PM	00:00:35	crawl	4
	00-StatisticalSummary	Jan 28, 2010 7:27:18 PM	00:00:12	crawl	3
	ebi	Jan 28, 2010 7:26:43 PM	< 1s	crawl	2
	1	Jan 28, 2010 7:26:04 PM	< 1s	crawl	1

TimedPlotter

execution finished.

Command-Line Execution

- Execute from command-line:

```
kepler.sh -runwf demo1.xml
```

- Set parameters:

```
kepler.sh -runwf -name "Kepler" -x 20 demo1.xml
```

NEXT:
***Building a Metagenome Annotation Workflow
using Kepler and bioKepler***

1st Workshop on bioKepler Tools and Its Applications