SADI and Taverna 2 Tutorial

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Preamble

• The Taverna 2 platform is constantly changing; while the look and feel of the workbench may change, the functionality wont!
Using SADI services – installing the plugin

Click on Advanced and then Updates and plugins.
Using SADI services – installing the plugin

Click Find New Plugins.
Using SADI services – installing the plugin

Select **SADI activity plugin 0.2.0**

Click on **Install**.
Using SADI services – installing the plugin

The plugin is being installed.
Using SADI services – installing the plugin

When the plugin is installed a warning about restarting Taverna will be displayed. Click OK.
Using SADI services – installing the plugin

Click on Close and then RESTART Taverna.
Using SADI services – installing the plugin

When Taverna has restarted the Service panel will show a list of SADI services.
Using SADI services

Now that we have SADI service available in Taverna we’re going to build a workflow to answer the questions:

*What genes are involved in KEGG pathway "hsa00232"? What proteins do those genes code for? What are the sequences of those proteins?*

The first step is to find a SADI service that will return the genes involved in a KEGG pathway.
Using SADI services – building a workflow

Type *sadi kegg pathway genes* into the Service panel Filter.
Using SADI services – building a workflow

Right click on the `getKEGGGenesByPathway` service and click Add to workflow.
Using SADI services – building a workflow

The `getKEGGGenesByPathway` service is added to the Workflow diagram.

Click on the Display all service ports button to show the service inputs and outputs.
Using SADI services – building a workflow

The service input and output ports are now shown in the diagram.
Using SADI services – building a workflow

To add an output to the workflow right-click on the workflow diagram and click **Workflow output port**.
Using SADI services – building a workflow

Name the output port gene and click OK.
Using SADI services – building a workflow

Drag a link from the service output port to workflow output gene.
Using SADI services – building a workflow

The next step in the workflow is to find a SADI service that takes the genes from `getKEGGGenesByPathway` and returns the proteins that those genes code for.
Using SADI services – building a workflow

Right-click on the service output port and click **Find services that consume KEGG_Record**...
Using SADI services – building a workflow

Select `getUniprotByKeggGene` from the list of SADI services and click `Connect`. 
Using SADI services – building a workflow

The `getUniprotByKeggGene` service is added to the workflow and automatically connected to the output from `getKEGGGenesByPathway`.
Using SADI services – building a workflow

Add a new workflow output called `protein` and connect the output from the `getUniprotByKeggGene` service to it.
Using SADI services – building a workflow

The next step in the workflow is to find a SADI service that takes the proteins and returns sequences of those proteins. Right-click on the *encodes* output port and click *Find services that consume* UniProt_Record...
Using SADI services – building a workflow

The UniProt info service attaches the property hasSequence so select this service and click Connect.
Using SADI services – building a workflow

The UniProt info service is added to the workflow and automatically connected to the output from `getUniprotByKeggGene`. 
Using SADI services – building a workflow

Add a new workflow output called **sequence** and connect the output from the **hasSequence** output from the **UniProt info** service to it.
Using SADI services – building a workflow

The KEGG pathway we are interested in is "hsa00232", so we’ll add it as a constant value. Right-click on the KEGG_PATHWAY_Record input port and click Constant value.
Using SADI services – building a workflow

Enter the value *hsa00232* and click OK.
Using SADI services – building a workflow

The workflow is now complete and ready to run.
Using SADI services – running the workflow

To run the workflow click on the green arrow in the tool bar. Taverna will switch to the results view and start running the workflow.
Using SADI services – running the workflow

The progress of the workflow is shown in the diagram while the workflow is running.
Using SADI services – viewing the results

To see all the results for an output click on the output tab for that output. To see an individual result click on the value in the result list.