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Bioclipse Workshop: short but productive

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Abstract

The Bioclipse Workshop has ended and, for just three days, turned out quite productive. We have first bits of scripting support for JavaScript using Rhino. At this moment the scripting plugin needs to explicit depend on plugins to be able to access their classpath, but we plan to solve that.

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```
// to have short identifiers
Array = Packages.java.lang.reflect.Array;
String = Packages.java.lang.String;
msgBox = Packages.net.bioclipse.plugins.bc_rhino.ShowBcMsgBox;
DbfetchServiceServiceLocator =
  Packages.uk.ac.ebi.www.ws.services.urn.Dbfetch.DbfetchServiceServiceLocator;

// get data
service = new DbfetchServiceServiceLocator();
strarray = service.getUrnDbfetch().fetchData("refseq:NM_210721", "refseq", "raw");

// make readable
str = new String();
for (i = 0; i < Array.getLength(strarray); i++) {
  if (i != 0)
  str = str + ("\n");
  str = str + strarray[i];
}

// show
msgBox.ShowStatic(str);
```

It's just a short example that uses webservice technology in Bioclipse to fetch a sequence.

QSAR support

QSAR support is getting along too, with a new DescriptorProvider extension point in trunk/ and work is progressing on a wizard that allows selecting descriptors and a CDK backend. The output of the wizard is a matrix resource, for which we already have a rich editor. A JOELib plugin has been suggested, as it has a good deal of QSAR descriptors too; Jörg, interested in doing a tiny bit of Bioclipse hacking?

A full proceedings is available online.