
Informatics for Integrating Biology and the Bedside



Developer's Guide
VISTA Browser Tools

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Table of Contents

<i>About this Guide</i>	<i>iii</i>
<i>Prerequisites and Third-Party Software</i>	<i>1</i>
Downloads and Installation.....	<i>1</i>
<i>Install & Configure</i>	<i>2</i>
Setting up the VISTA browser plugin within the eclipse i2b2 workspace	<i>2</i>
Building the VISTA browser Project within the i2b2 Workbench	<i>5</i>
<i>Install Data</i>	<i>7</i>
<i>Run within eclipse</i>	<i>11</i>
<i>License</i>	<i>12</i>

About this Guide

Informatics for Integrating Biology and the Bedside (i2b2) is one of the sponsored initiatives of the NIH Roadmap National Centers for Biomedical Computing (<http://www.bisti.nih.gov/ncbc/>). One of the goals of i2b2 is to provide clinical investigators broadly with the software tools necessary to collect and manage project-related clinical research data in the genomics age as a cohesive entity—a software suite to construct and manage the modern clinical research chart.

The guide provides installation and source code compilation and building steps for the VISTA browser plugin.

1

Prerequisites and Third-Party Software

Downloads and Installation

a. i2b2 Workbench

The VISTA browser plugin is compatible with i2b2Workbench version 1.6. Download the i2b2Workbench from <https://www.i2b2.org/software/>. Follow installation and configuration instructions as given in the *i2b2 Workbench Developers' Guide* which can be found under the Docs tab.

2

Install & Configure

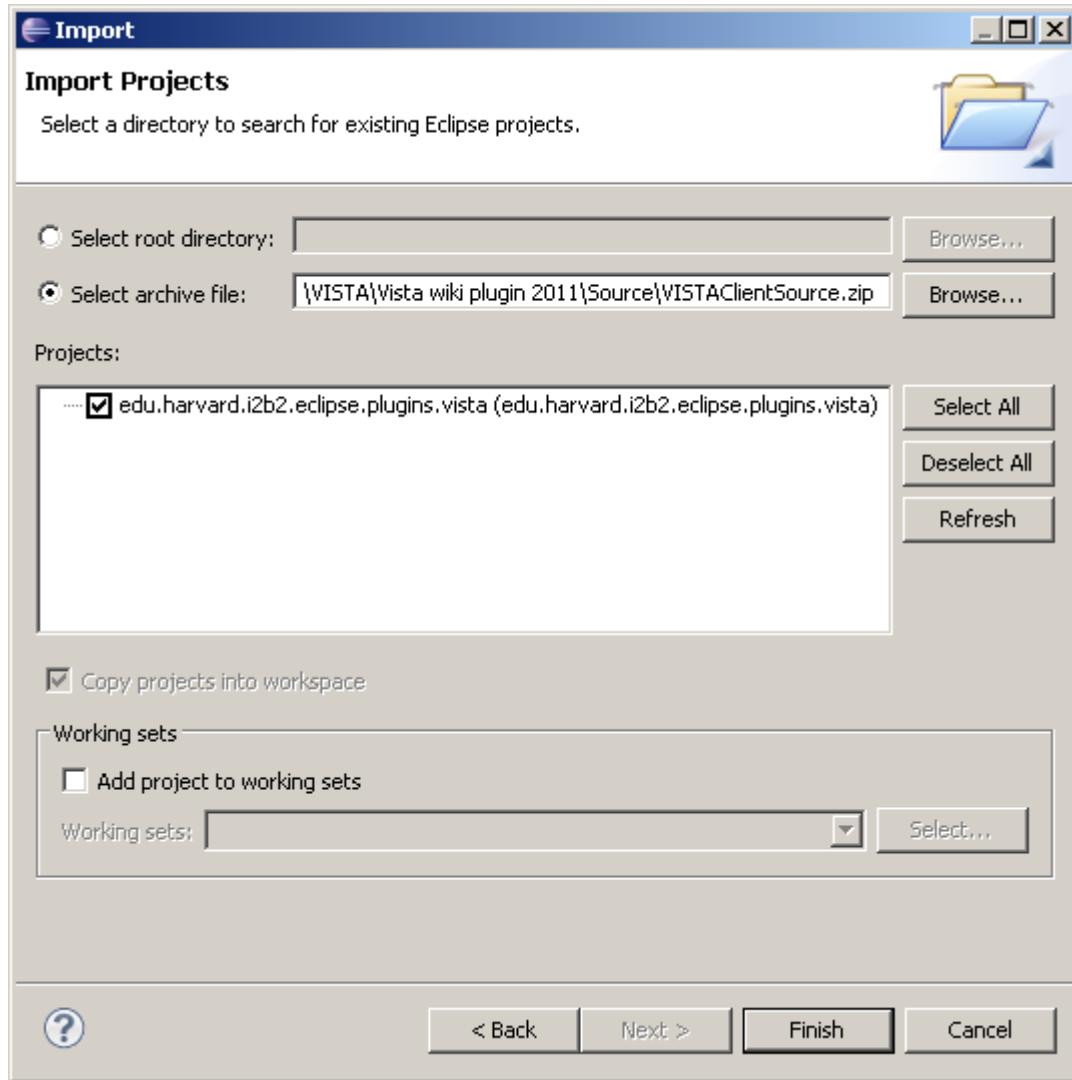
Setting up the VISTA browser plugin within the eclipse i2b2 workspace

You should have already installed the Eclipse environment and imported the i2b2 Workbench projects into it as detailed in the *i2b2 Workbench Developers' Guide*.

Importing the VISTA browser project

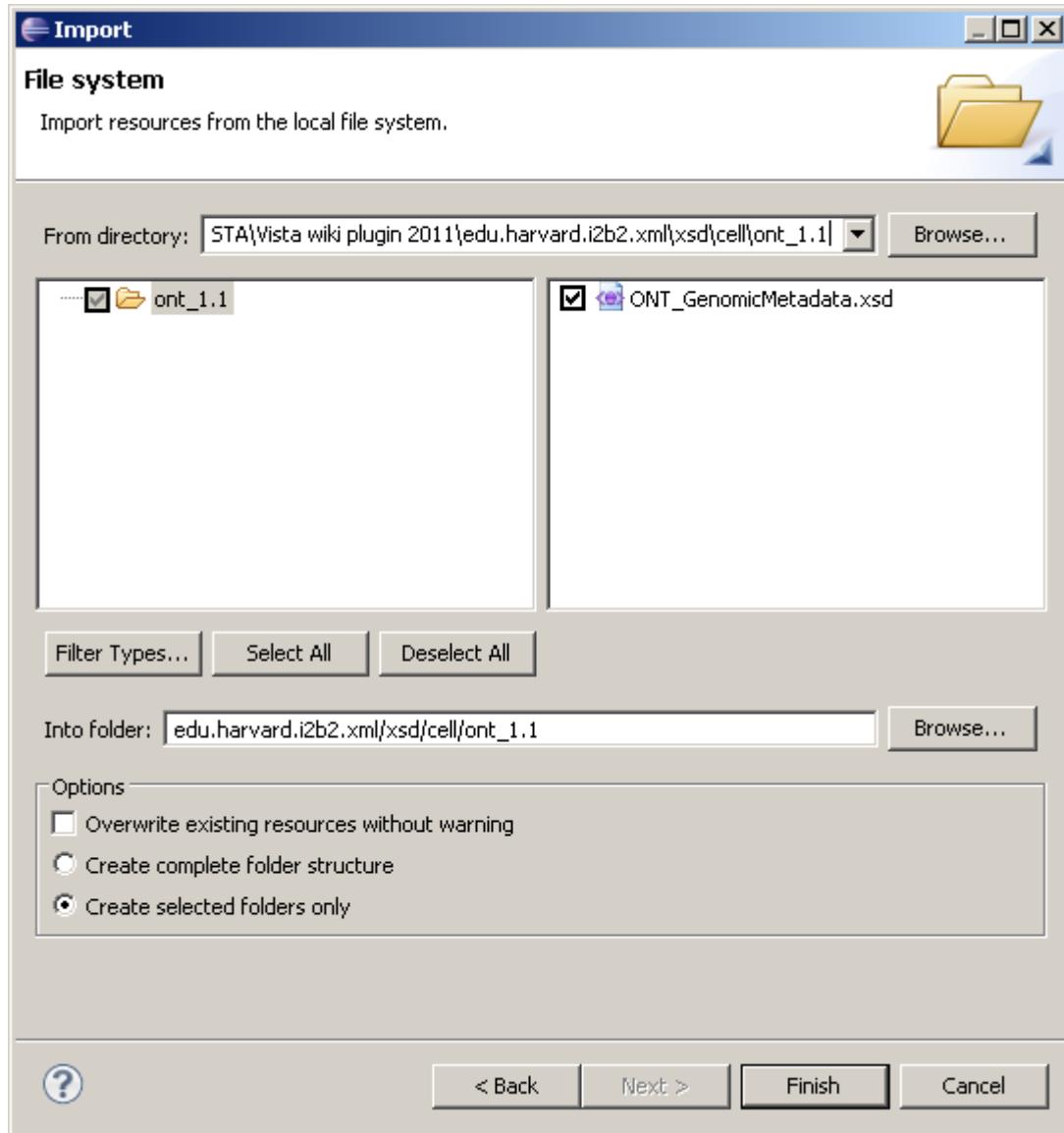
This project software is contained in the Eclipse archive files called “VISTAClientSource.zip” and VISTAXsdSource.zip.

From the File Menu of the i2b2 Workbench select *Import->General->Existing Project into Workspace* and navigate to the place where the archive was saved to disk. Import the file “VISTAClientSource.zip” into eclipse.



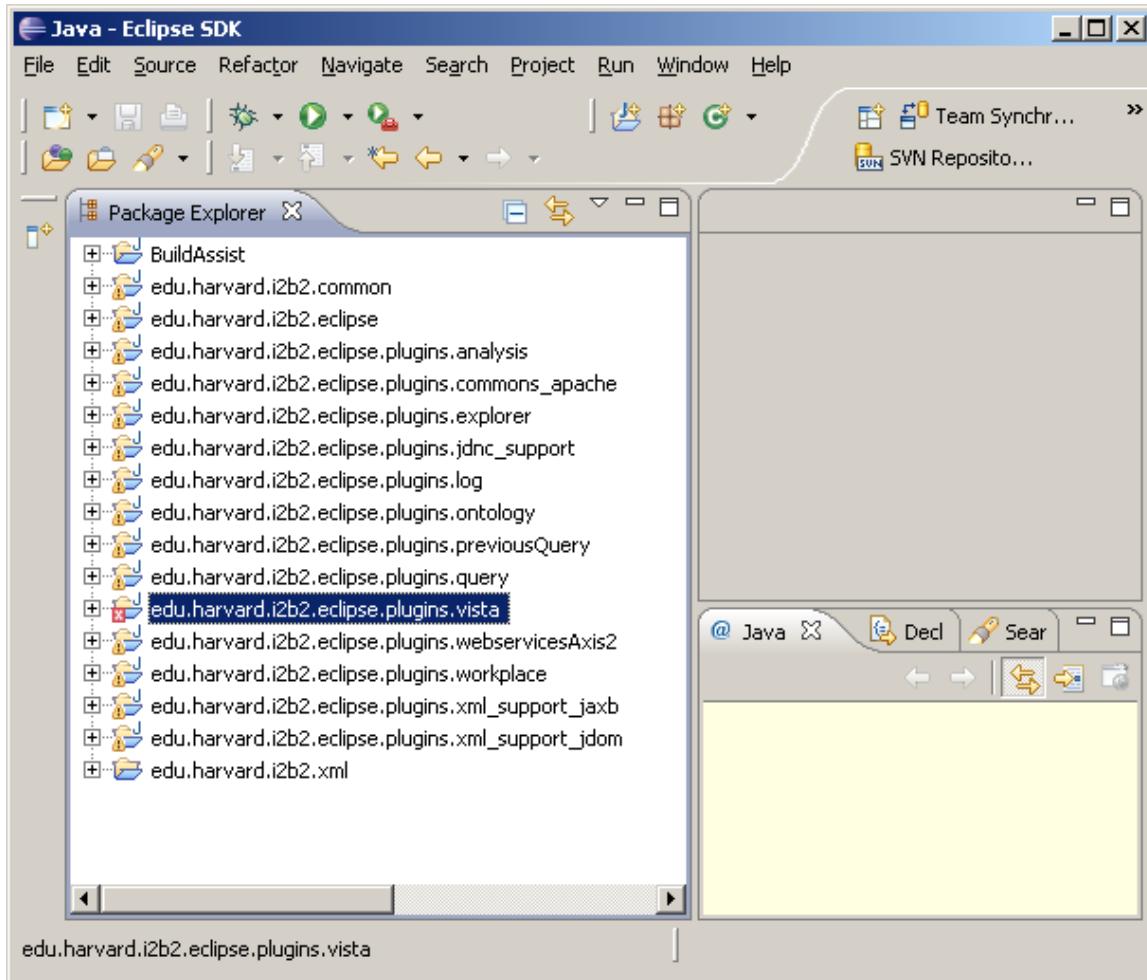
Click *Finish* and let eclipse import the VISTA plugin archive into the workspace.

In addition, unzip the file VISTAXsdSource.zip. Locate and extract the file edu.harvard.i2b2.xml/xsd/cell/ont_1.1/ONT_GenomicMetadata.xsd and place it in your edu.harvard.i2b2.xml project within eclipse if the file does not already exist. From the File Menu of the i2b2 Workbench select *Import->General->File System* and navigate to the place where the archive was saved to disk. Import the file “ONT_GenomicMetadata.xsd” into eclipse.



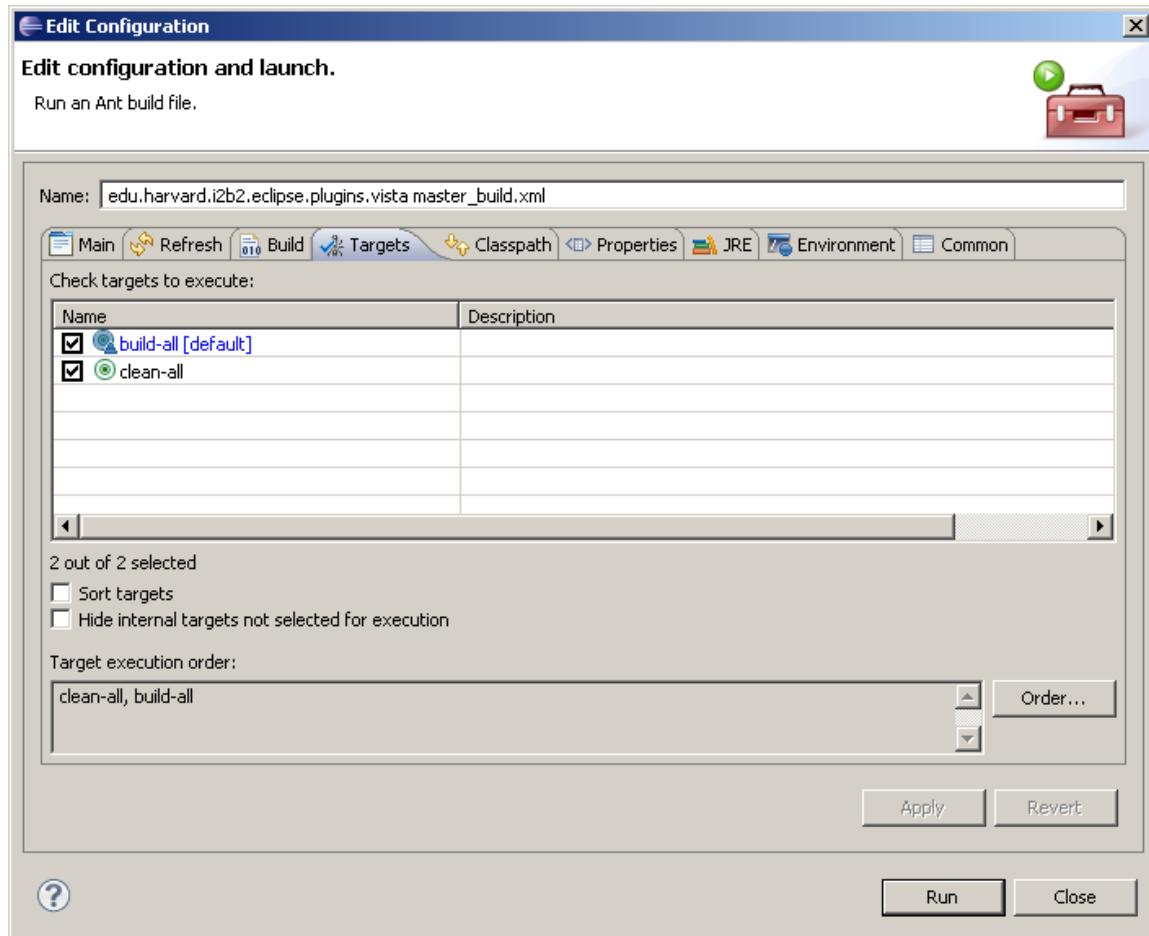
Click *Finish* and let eclipse import the VISTA Genomic metadata xsd file into the workspace.

When you are complete you should have an eclipse workspace with the core i2b2 plugins and the VISTA browser plugin plus the additional ont xsd file.



Building the VISTA browser Project within the i2b2 Workbench

Open the `edu.harvard.i2b2.eclipse.vista` project. Open the folder `buildFiles` and its file `master_build.xml`. Right-click within the file editor, and select `RunAs-> 2 Ant Build`. Select target execution order `clean-all; build-all` and select `Run` to build the vista project code. Refresh the vista project when the build is complete.



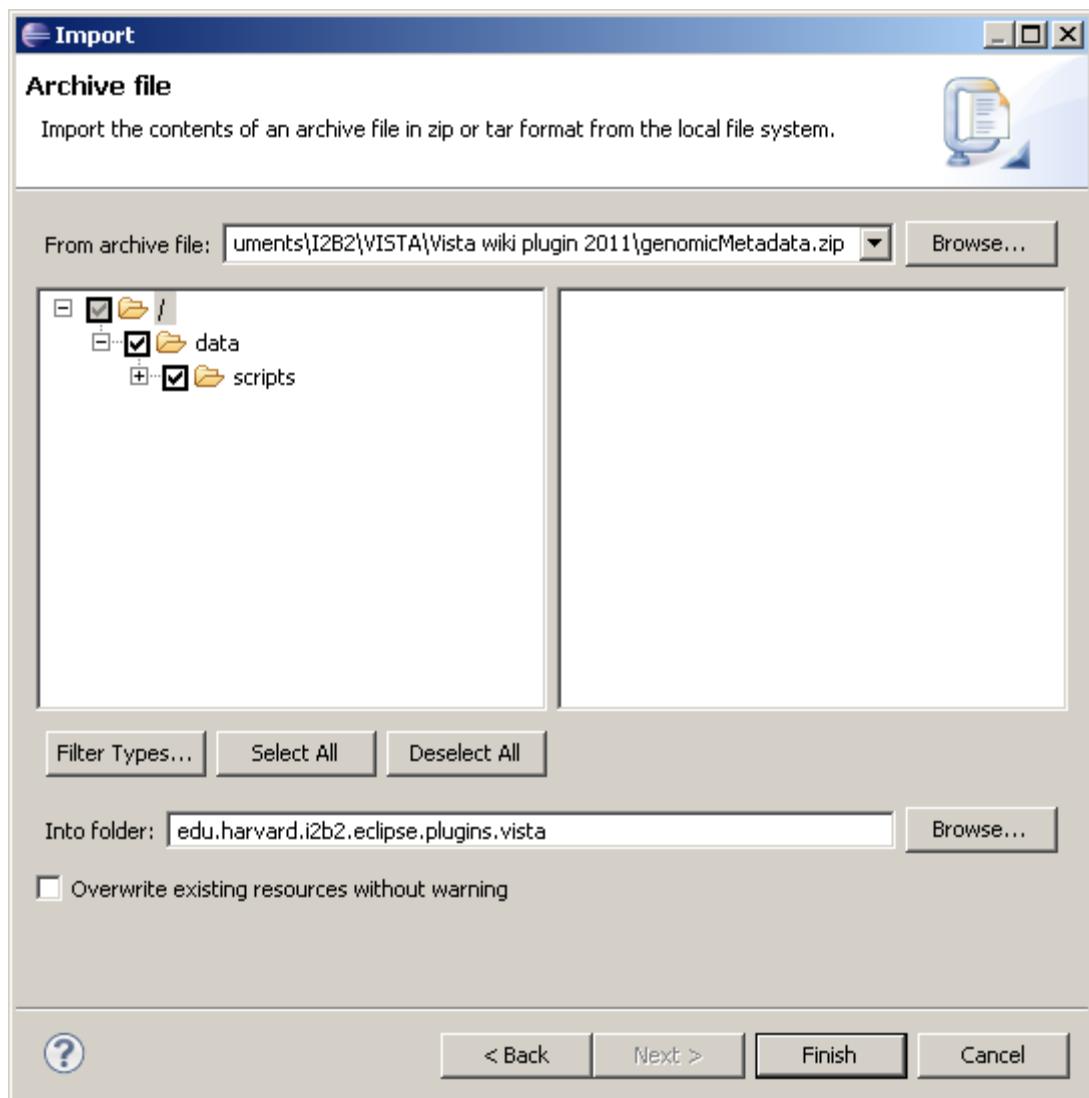
3

Install Data

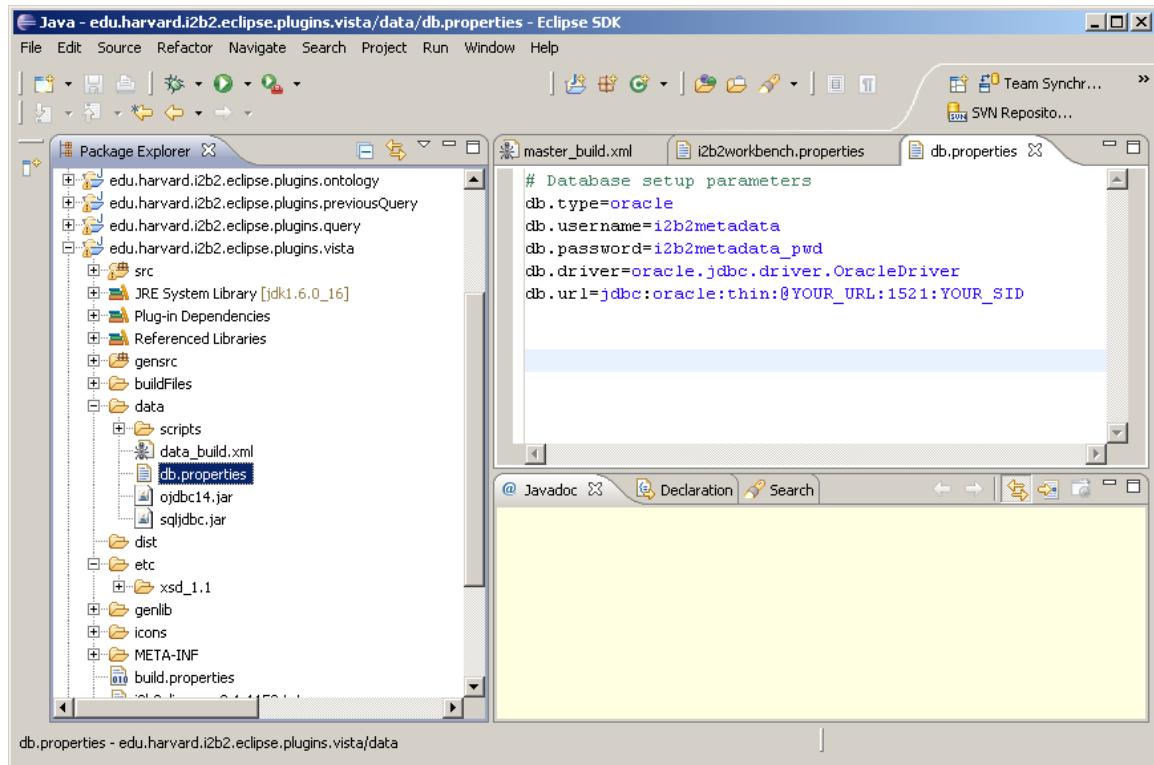
The VISTA browser plugin utilizes and accesses genomic metadata terms. A script is provided to load this data into an existing CUSTOM_META metadata table. See data installation scripts for how to set up a CUSTOM_META table if you do not already have one.

From the File Menu of the eclipse workspace select *Import->General->Archive File* and navigate to the place where the archive was saved to disk. Import the data folder within the file “genomicMetadata.zip” into the edu.harvard.i2b2.eclipse.plugins.vista package within eclipse.

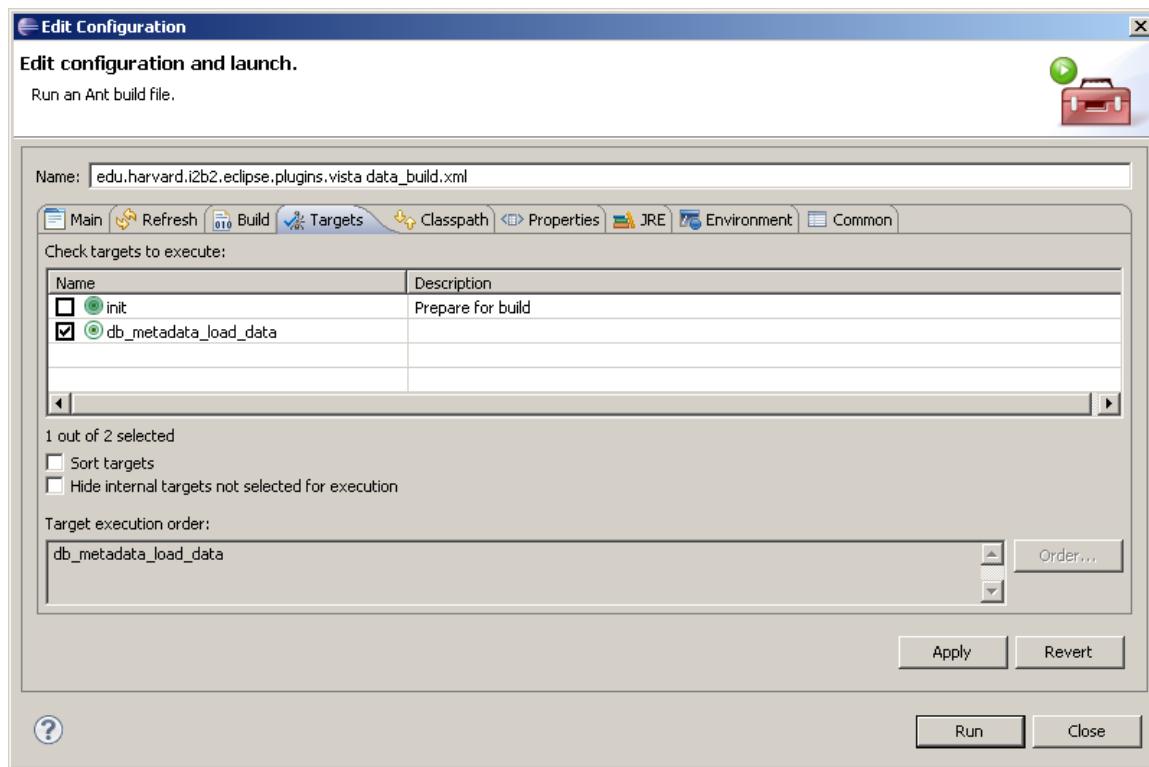
Click on Finish and allow eclipse to import the data folder. When complete you will see a folder called data that contains a scripts folder and a data_build.xml file.



Modify the content of the db.properties file to point to your database. Drivers (jars) for Oracle and SqlServer are provided.



Open the file data_build.xml in the eclipse and right-click within the edit window of the file. Select Run As -> 2 Ant Build. Choose target db_metadata_load_data and run to load new genomic metadata into your CUSTOM_META table.



4

Run within eclipse

Launch the i2b2Workbench from within eclipse as you normally would. Once the workbench is up, select Window->Show View -> Other -> Vista Category -> Variant View bring the view into focus.

Drill down into the Genomics folder of Custom Metadata and select a SNP. Drag the variant into the Variant View. Please refer to the Users Guide for details about the new view.

5

License

The i2b2 source code is licensed under the i2b2 Software License 2.1. This includes but is not limited to all code in the edu.harvard.i2b2.* package namespace.