User's Guide

Version 1.0

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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. This guide with the provided source code will help you to learn about the developing and understand the requirements for creating i2b2 cells.

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Prerequisites

Downloads

a. Java JDK

Make sure that you have Java 1.5 version 7 or higher installed. If you need to get and install the 1.5 JDK, go to
http://java.sun.com/javase/downloads/index_jdk5.jsp

Run the installer.

2

Install

Installing the i2b2 Workbench application

Download and extract i2b2Workbench-10.zip into a target area, e.g.
C:\i2b2workbench.

In your target's eclipse directory, edit the file workbench.ini so that the value of
Xmx is equal to the amount of physical memory. The default setting is 512m
For example, if you are running with 1GB of RAM:

```
-Xmx=1024m
```
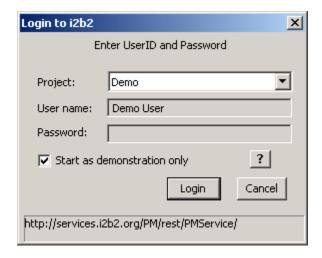
Launch C:\i2b2workbench\i2b2Workbench.exe

Logs are written to C:\i2b2workbench\i2b2.log and can also be viewed by
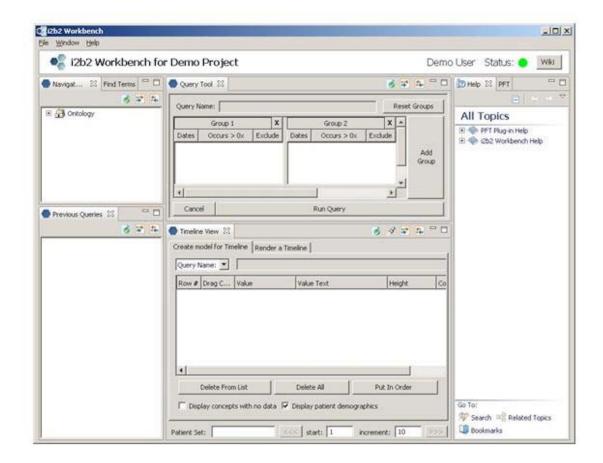clicking on the Status icon.

3

Execute

Running the i2b2 Workbench application

Double click on the i2b2Workbench icon.

You will see a splash screen followed by a Login dialog box.
Select "Start as demonstration only" or log in. The User name is demo
and the Password is demouser.

Once the workbench is running, an i2b2 workbench tutorial may be accessed via Help->Help Contents.

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License

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