GeneNotes Extension to Firefox
Version 1.0

A powerful tool for biologists to collect and manage a variety of biological information as notes from Internet
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1. Overview

GeneNotes extension to Firefox (http://combio.cs.brandeis.edu/genenotesextension/) is a gene-oriented tool developed to help biologists collect and manage a variety of biological information as notes from the Internet. It greatly helps biologists during the decision making processes in large-scale functional genomics projects. Users can organize hits (genes) identified in their experiments into lists, which can be loaded into GeneNotes. GeneNotes can automatically retrieve the up-to-date annotation information of genes from our server. Users can freely surf the Internet in a gene-centric mode. Web content can be captured as notes linking to either genes or projects. Notes are editable and are stored locally on users’ computers so that they can be accessed off-line.

2. How to Install and Uninstall

2.1. How to install

(a) Download genenotes-firefox-extension-1.0.0.zip from http://combio.cs.brandeis.edu/GenenotesExtension/download.html.
(b) Uncompress the ZIP file to get genenotes-firefox-extension-1.0.0.xpi.
(c) In Firefox menu, use “File” → “Open File …” to open the extension installation file genenotes-firefox-extension-1.0.0.xpi, and then a dialog will show up (see Figure 1). Follow the installation instruction provided in the dialog to install GeneNotes extension.

![Software Installation](image)

**Figure 1.** Install GeneNotes extension to Firefox.

2.2. How to uninstall

(a) In Firefox menu, use “Tools” → “Add-ons” to bring up the Add-ons window (Figure 2).
(b) Choose “GeneNotes Firefox Extension” and click “Uninstall”.

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3. Interfaces

The interfaces of GeneNotes Extension consist of a toolbar and a sidebar.

3.1. GeneNotes Toolbar

The toolbar (Figure 3) has three items: a drop-down menu Q-links, a Search box, and a Workspace button.

- **Q-links** provides a set of useful biological website links allowing users to quickly jump to those databases.
- The **Search Box** is a portal to several useful searching engines such as NCBI, Flybase, MGI, RGD, SGD, Wormbase, and so on.
- The **Workspace** Button is used to toggle the GeneNotes sidebar on or off, which will be explained in the next section.

![GeneNotes toolbar](image1)

**Figure 3. GeneNotes toolbar.**

3.2. GeneNotes Sidebar

The GeneNotes sidebar (Figure 4) can be toggled on or off by the Workspace button in the GeneNotes toolbar (see Figure 3). It has three sub windows: **Workspace View**, **Gene List View**, and **Gene Information View**. The **Workspace View** shows all gene lists in the current workspace. If a gene list is selected, the **Gene List View** will show all the...
genes in it. Users can select a gene in the *Gene List View* to view its annotation information in the *Gene Information View*.

**Figure 4.** GeneNotes sidebar.
4. Workspace

Workspace contains a set of gene lists. Each gene list consists of genes, which can be differentially expressed genes in a microarray experiment, hits in a high content screening, and so on. Once loaded, a workspace is shown in the GeneNotes sidebar (Figure 4). The menu to manage a workspace is located at the top of the sidebar (Figure 5).

A workspace is stored as an XML file. An example is given below.

```
<?xml version="1.0" encoding="ISO-8859-1"?>
<GeneNotes_Workspace>
  <GeneList>AffyProbeSet.txt</GeneList>
  <GeneList>EntrezGeneID.txt</GeneList>
  <GeneList>EnsemblID.txt</GeneList>
  <GeneList>OrganismDBID.txt</GeneList>
  <GeneList>SwissProtID.txt</GeneList>
</GeneNotes_Workspace>
```

4.1. Create Workspace

Click the “Create workspace” menu (see Figure 5) to create a new workspace. In the prompt window (Figure 6), input the name of the new workspace and specify where the workspace should be stored. The newly created workspace is an empty one as below:

```
<?xml version="1.0" encoding="ISO-8859-1"?>
<GeneNotes_Workspace>
</GeneNotes_Workspace>
```

The browser will open the editor (Figure 8) for the user to edit the new workspace.
4.2. Gene List

A gene list contains a list of gene IDs of the same ID type. GeneNotes use those IDs to retrieve gene annotation information. GeneNotes currently supports six ID types: “Entrez Gene ID”, “Ensembl ID”, “Organism Database ID”, “SwissProt ID”, “UniGene ID”, and “Affymetrix Probe Set”. A gene list file is a text file that starts with a line specifying the ID type, which is followed by gene IDs. Each line contains only one ID. An “Organism Database ID” gene list example is given below.

    Organism Database ID
    WBGene00001609
    FBgn0000137
    HGNC.17
    MGI.107704
    S00000580
    RGD.2004

4.3. Load a Workspace

Click the “Load workspace” menu item (Figure 5) to load an exiting workspace. In the prompt window (Figure 7), choose the workspace file and click the “Open” button.
4.4. Edit Workspace

Click the “Edit workspace” menu item (Figure 5) to edit the current workspace. The browser will load a webpage for the user to edit the workspace (Figure 8).

Figure 8. The interface for editing a workspace. There are three panels in the edit workspace interface. (a) “Gene List” panel. Toggle the checkboxes to select or deselect gene lists. The genes in the selected list are shown in the middle panel (the
“Gene” panel). The buttons at the bottom of the “Gene List” panel allow the user to import a gene list, create a new gene list, or delete the selected gene list. (b) The “Gene” panel shows the genes in the selected gene list. Genes can be selected by toggle the corresponding checkboxes. Use the “delete” button at the bottom of the panel to delete the selected genes. (c) The third panel is the “Add Gene” panel. The user can input a list of gene IDs and add them to the selected gene list by clicking the “Add” button. The gene IDs to be added must be of the same ID type to those in the selected gene list. See the next section for the explanation of gene ID types.

4.5. Create Gene Lists

Use the “Create” button in the “Gene List Panel” (Figure 8) to bring up a dialog (Figure 9) for creating a new gene list. In the pop-up dialog (Figure 9), input the gene list name and choose the primary ID type. The new gene list will be created under the same directory with the workspace.

![Figure 9](image9.png)

Figure 9. The interface for creating a new gene list. The user needs to input the filename name of the new gene list and specify the primary ID type.

4.6. Import Gene List

Use the interface shown in Figure 8 to bring up a dialog (Figure 10) for importing a new gene list.

![Figure 10](image10.png)

Figure 10. The dialog for importing a gene list.

4.7. Edit Gene List

Use the interface shown in Figure 8 to edit gene lists. The user can also use the
context menu of the “Gene List View” in the sidebar to quickly add or delete a gene ID. To evoke the context menu, right-click the “Gene List View” (see Figure 11).

![Gene list view context menu.](image)

**Figure 11.** Gene list view context menu.
5. Take Notes

Web content can be captured and stored as notes. There are two types of notes: notes of individual genes and project notes.

5.1. Capture Notes

Choose the web content (high-lighted in Figure 13) to be saved as a note and then right-click the mouse. In the popup menu, select “GeneNotes → Capture Gene Note” or “GeneNotes → Capture Project Note” to save a note of the selected gene or the project respectively. If no gene is selected in the “Gene List View”, the “Capture Gene Note” menu item will be disabled. A note if captured will be associated with the selected gene or the project and save locally on the computer, so that they can be accessed off-line.

![Figure 13. Capture notes.](image)

5.2. Show Notes of a Gene

The Notes of a gene can be viewed using in two ways.

(a) Right click a gene in the “Gene List View” (see Figure 11) and select the “Show Notes of This Gene” option. The browser will open a new page (see Figure 14) containing all notes of the selected gene.

(b) Double click a note in the “Notes” tab of the “Gene Information View” in the sidebar to open the note in the editor.
Figure 14: This is the page which shows all the Notes of the selected Gene, user can click on the radio to see the contents of the Notes.

5.3. Show Project Notes

Click on the “Project Notes” tab (See Figure 15) to view all notes of the current project.

Figure 15. Show notes of a project.

5.4. Edit Notes

To edit any notes, choose the Gene whose notes needs to be edited and in the Gene Information view click on the Notes tabs (See Figure 16) to see a list of all the Notes captured for the selected gene. Double click on a note to open and edit it in an html editor (See Figure 17). Once done, user needs to click the “Save” button of the editor to save the changes.
5.5. Delete Notes

To delete a note, select the note and then click on the “Delete” button as shown in the Figure 18.
Use the “Delete” button to delete the selected note.

**Figure 18:** Delete button to delete selected Note
6. Quick Links

GeneNotes automatically compile a list of quick links to public database for each gene. Click “Quick Links” tab in the Gene Information View (Figure 19) to show a list of quick links which if double-clicked can bring users directly to the corresponding records in public databases.

![Figure 19. Quick links for a gene.](image)