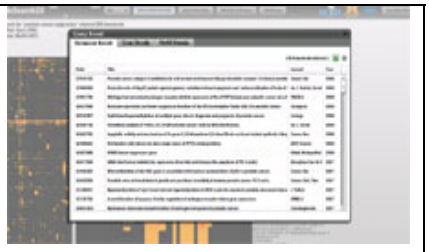
BioSearch 2D

1. Tools screen shots and description

		
This display shows the main search page. It offers users to input a Medline search with Mesh Category options	This display shows search heatmap. It offers users an important way to understand genes tagged by Mesh across all pubmed documents	This display shows the pubmed document retrieval page. It offers users the ability to select clusters from the heatmap and retrieve document info.

Series of screen shots, Figure #s and labels (and referred to in text below)

2. Application uses

2.1. Users can perform the following objectives and tasks with these displays:
- Search using as Medline query
- Get back a clustered map of genes and mesh terms.
- Have the ability to select a cluster and retrieve Pubmed documents
- select a set of genes and send it to the Mimi Netbrowser
- select a set of mesh terms and send it to Conceptgen
- Enlarge the map size dynamically using a sliding bar
- Change the color of the map with the pre-set colors
- filter the map using with a gene list

2.2. The presentation provides methods for users to do the following things:

What users are able to display:
- Users are able to display a clustered heatmap of GENES, MESH and PUBMED docs

What users are able to see and identify:
- They can identify the most cited genes and mesh terms in pubmed with the Medline query they searched with

How users see/can access info about sources of data and how they're searched/processed?

The document retrieval popup allows users to view the documents and be able to download that info as an excel spreadsheet.

How users can facilitate their selection (e.g. sort):
They can filter their result by using a gene list of interest, where the genes will light up (green color). The document retrieval page also allows users to sort by all the data shown.

What users can do once they select:
When they select a cluster of interest on the heatmap they can then send a set of genes to Mimi NetBrowser and a set of Mesh terms to Conceptgen.

For continued work along these lines, users can go next to

- find what info in what tool?:
- carry over what assumptions about gene, sources drawn from:

3. Challenges

3.1. Some difficult problems in addressing users objectives and purposes include:

a. Search across multiple literatures in Pubmed can be difficult on a specific topic as the result set if very large

b. To associate specific targeted gene set with meaningful terms in all the literature is nearly impossible

3.2. The system and presentation address these problems for these reasons as follows:

Using Gene2Mesh Tagging the application is able to parse through the entire Pubmed database and retrieve results that are displayed in a way that users have the ability to discern large amounts of data.