The instructions below are for searching and accessing Hemiptera of Canada Library Records on BOLD. Here we will retrieve a specimen record for a seed bug *Neortholomus scolopax*, collected and identified by noted Canadian Heteroperist Geoffrey G.E. Scudder.

Please create a BOLD account, and login at <a href="http://www.boldsystems.org/">http://www.boldsystems.org/</a>

## Once logged in:

1) Choose "Workbench" (at top of page)



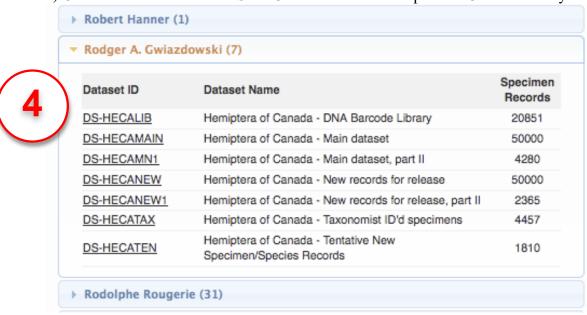
2) Open "Public Datasets" (at center left of page)



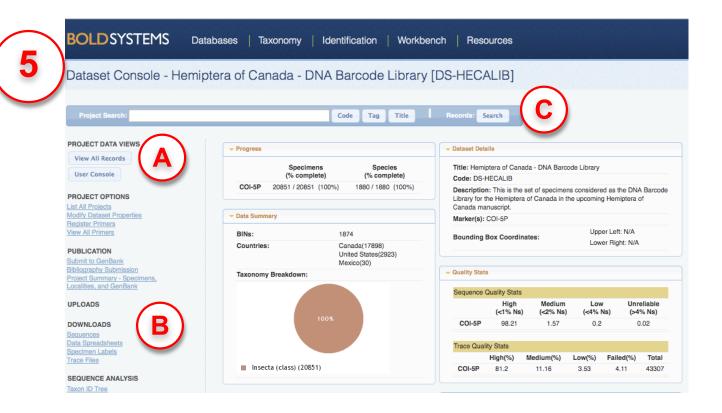
3) Click "Rodger Gwiazdowski" (alphabetically listed by first name)



4) Click on the dataset ID: "DS-HECALIB" for the Hemiptera of Canada Library



- 5) You are now on the Dataset Console, from which you can access all records by:
  - A) Viewing all records
  - B) Downloading all library data as a spreadsheet
  - C) Searching by taxonomy (geography, or other metadata); see details below.



6) On the Record Search page you can search for records in several ways.

To search by taxonomy: click "Search" (C), (for the record search window) entering search terms as "Genus Species" will find that species. Note that you need the include the quotes "", around the binomial name, otherwise the search engine will return all results for that genus species epithet.

\*Note that Record Searches, that search within a dataset [e.g.: DS-HECALIB] occur by default, when engaging a search within that dataset.

Directly access specimen records using the Process ID (and ID number given during the CCDB laboratory processes) Sample ID (an ID number given during the specimen's accession to BOLD) or BIN number from the Record Search window:

Click the "List of Identifiers" tab (adjacent to the "Region of Map" tab), enter (type/paste) the record number (s) in the window and click "Search Records".

Search using either:

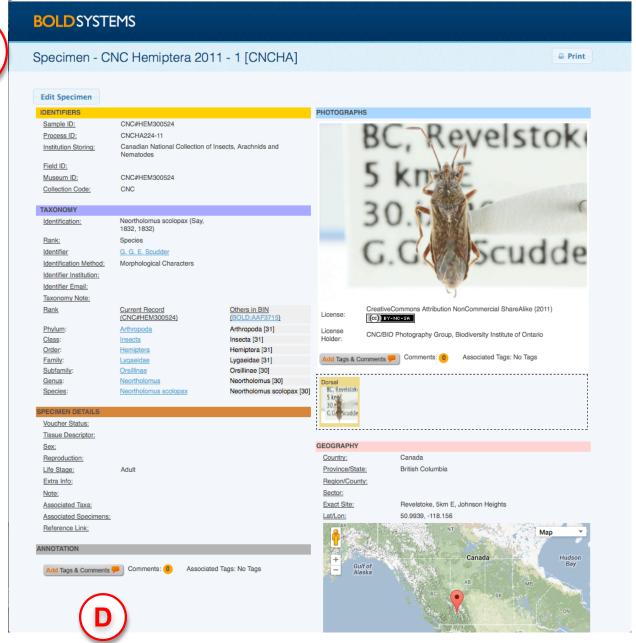
Process ID: CNCHA224-11 Sample ID: CNC#HEM300524

\* Many Process IDs/Sample IDs can be searched at once.



- 7) Commenting on the identification, or any other information on a Library record is welcomed!
- . Currently, there are two ways anyone can add information to records:

1) Direct Annotations: each specimen page, and BIN page has a button for public annotation via posted comments (D).



2) Editorial Access: editing access for public records can be obtained from the BOLD technical staff. We invite those interested to edit records to please contact the authors, or the BOLD team at <a href="mailto:support@boldsystems.org">support@boldsystems.org</a> with the nature of your request or observation, and to please include specimen Process IDs (or Sample IDs) where applicable.