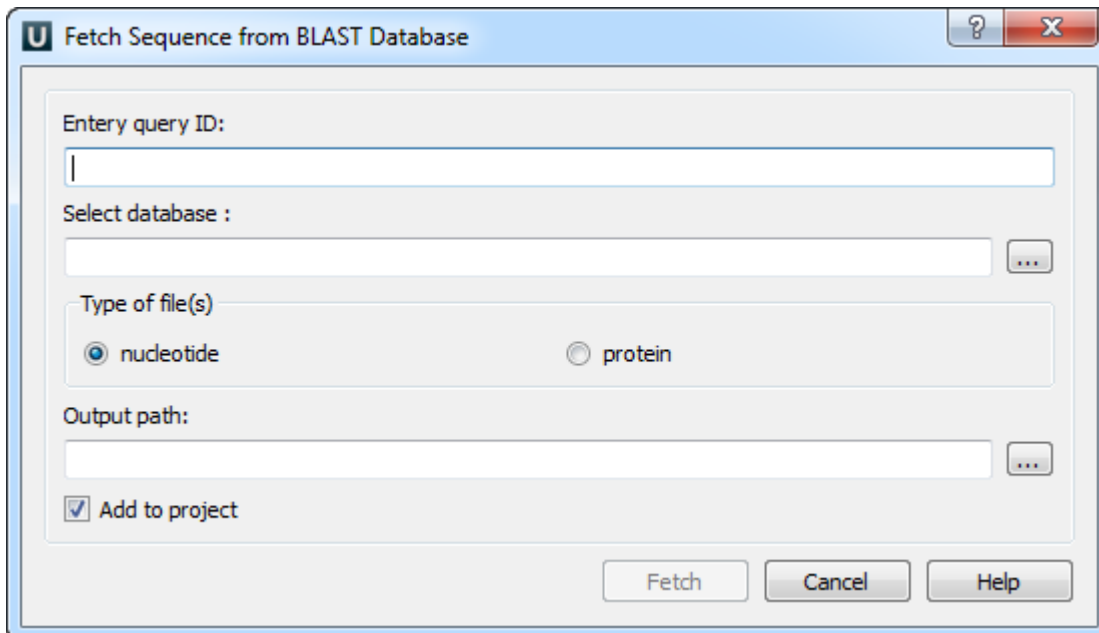


Fetching Sequences from Local BLAST Database

To fetch sequences from local BLAST database use the *Fetch sequences from local BLAST database->Fetch sequences by 'id' from 'blast result'* context menu item of the blast result. The following dialog will appear:



The dialog box is titled "Fetch Sequence from BLAST Database" and contains the following fields and controls:

- Entry query ID:** A text input field.
- Select database :** A text input field with a browse button (three dots) to the right.
- Type of file(s):** Two radio buttons: ☒ nucleotide and ☐ protein.
- Output path:** A text input field with a browse button (three dots) to the right.
- ☒ **Add to project**
- Buttons:** "Fetch", "Cancel", and "Help" at the bottom right.

Here you need select a query ID, database, type of file(s) and output path. After that click on the *Fetch* button. To fetch sequences for several annotations at the same time select the blast results with *Ctrl* key and call the *Fetch sequences from local BLAST database->Fetch sequences by 'id' from 'blast result'* context menu item.