itcrispr

Interface to assemble and track progress of CRISPR sequence experiments in BioNumerics (6.5 - 6.6).

Version: `0.1.4`

Setup and configuration

Install Python 2.6

Download (x86 version): http://www.python.org/download/releases/2.6.6/

Install PyQt

Download (x86 version for Python 2.6): http://www.riverbankcomputing.co.uk/software/pyqt/download

Install itcrispr

Download the latest version of itcrispr from https://github.com/vkvn/itcrispr/downloads

Run `itcrispr-*version*.win32.exe`

Configure script

1. Change configuration in

   `C:\Python26\Lib\site-packages\itcrispr\itcrispr.cfg`

   `DATABASES`, `EXPERIMENTS` and `PRIMER_PATH` are all **required** for the program to work.

   `DATABASES`

   The database name as in BioNumerics. Multiple databases can be specified as comma-separated values. This option is to prevent the script from being executed accidentally in other databases.

   `EXPERIMENTS`

   List of CRISPR sequence experiments - comma-separated.

   `PRIMER_PATH`

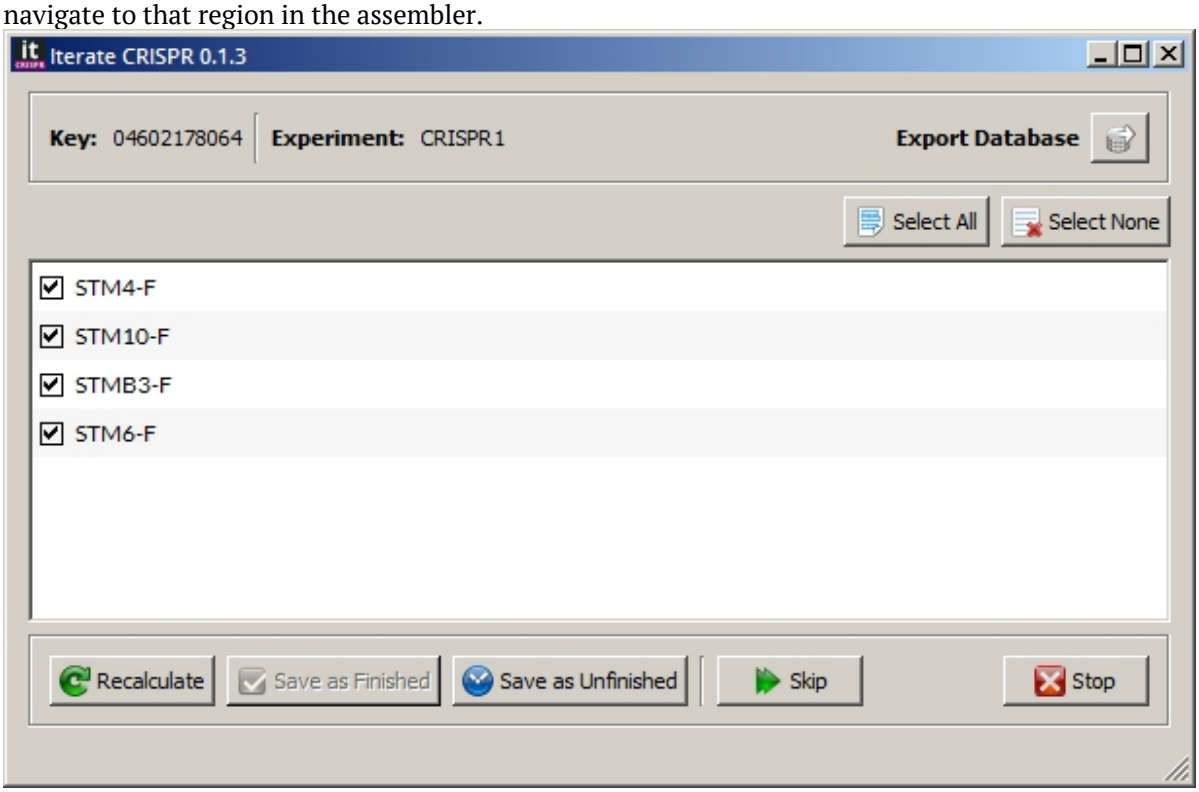
   PATH to the directory containing primer files in text format. File extension should be `.txt` and file should contain only the sequence (FASTA and other formats not supported).

Usage

1. Select entries in BioNumerics. If no selection is made, program runs through all entries in the database.
2. Run script using the `Script --> Run script from file` option in BioNumerics. Navigate to the `C:\Python26\Scripts` folder and select `run_itcrispr.py`

> ***Note***
>
> As easier method to run the script would be to add a button to the toolbar. Steps for doing this is described in Add a button to the toolbar.

3. An assembly will be done using the CRISPR sequences and primers. A dialog window will then be displayed with the list of primers that aligned with the sequences. Double-click on a primer to navigate to that region in the assembler.



4. If you consider an experiment for an entry as finished, click the **Save as Finished** button. No primer should be checked. Use the **Select None** button to deselect all primers.
5. To save an experiment as unfinished, check the primers for regions that need to be repeated and click the **Save as Unfinished** button.
6. If you made some changes in the assembler window, use the **Recalculate** button to redo the assembly.
7. Use the **Skip** button to redo this entry at a later time.
8. Use the **Export Database** button to export the entire database to a `CSV` file.
9. **Stop** button will terminate the program.

Notes

- If the experiment for an entry is saved as finished, it will not be displayed in subsequent runs.
- Primer sequences are read, an assembly is done after changing the minimum score to the smallest length of primer.
- Primers selected previously appear checked when the window is shown.
- Closing the window skips to the next experiment. Use the **Stop** button to exit the program.
- Sequence approval status in BioNumerics is not taken into consideration for deciding which entries to check. Sequences are made approved if they are saved as finished using the program.

Add a button to the toolbar

This needs to be done whenever the program is updated!

1. Copy

   `C:\Python26\Lib\site-packages\itcrispr\itcrispr-menu.bns` to

   the *scripts home* directory under your BioNumerics Home directory. For example,

   `C:\Users\vimal\BioNumerics\Data\Scripts Home\`
2. Load this file in the **BNS** Script editor

   `Script --> BNS Script editor`

   followed by

   `File --> Load Script`
3. Open `File --> Attachments` and click **Add new**
4. Select `C:\Python26\Scripts\run_itcrispr.py` and click **Open**. Enter `run_itcrispr` in the dialog that appears and click **OK**.
5. Save the script.
6. Restart BioNumerics. An icon 

should now be available in the toolbar. Click this icon to launch the program.

Add or remove primer sequences

Primer files are plain text files with just the sequence of the primer.

Add or remove primers to/from the location specified in the configuration file - the `PRIMER_PATH` variable.