

An example of CAMBer usage to generate input data for CAMBerVis on a small case study of 2 strains with 3 plasmid of *S. aureus* (due to computational time issues)

We download the CAMBer software  
from the project webpage:

<http://bioputer.mimuw.edu.pl/camber/software/camber2.zip>

# CAMBer: Comparative Analysis of Multiple Bacterial Strains

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## Software

- CAMBerVis v1.2

- [CAMBerViS](#) software (zip package, executables in the *bin* folder)
- [Manual](#) for CamberVis
- [Example 1](#) of CAMBerVis usage to identify inconsistent annotations of TISs (Translation Initiation Sites)
- [Example 2](#) of CAMBerVis usage to identify highly conserved gene families, but annotated in very few strains
- [Video - example](#) of an older version of CamberVis (.avi in zip package)

Source code of CAMBerVis is freely available at the project code.google website:

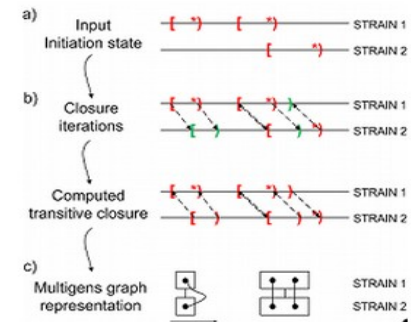
<http://code.google.com/p/camber2/>.

- CAMBerVis v1.0 platform-dependent installers

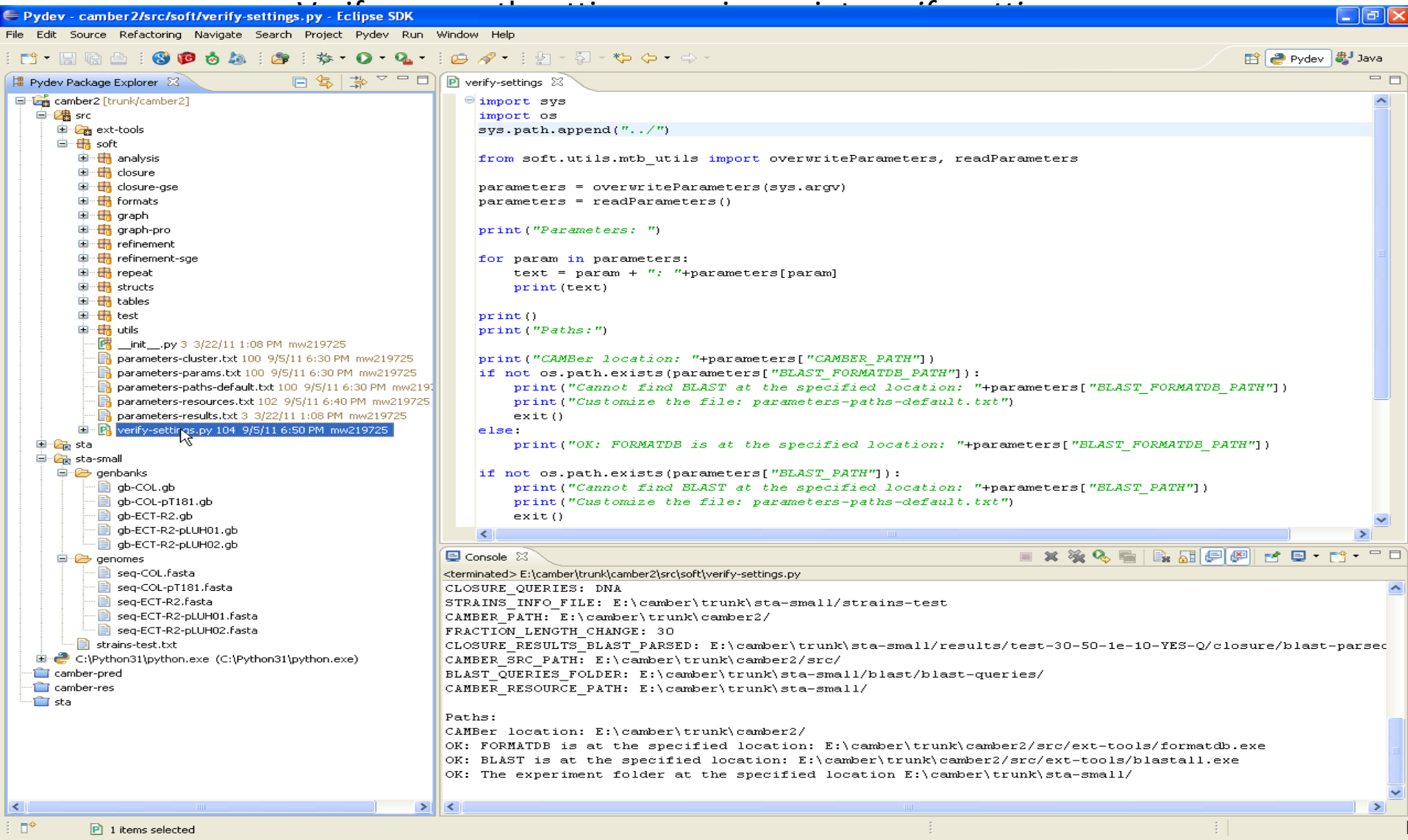
- CAMBerViS [Windows](#) installer
- CAMBerViS [Linux](#) installer
- CAMBerViS [MAC OS](#) installer

- CAMBer

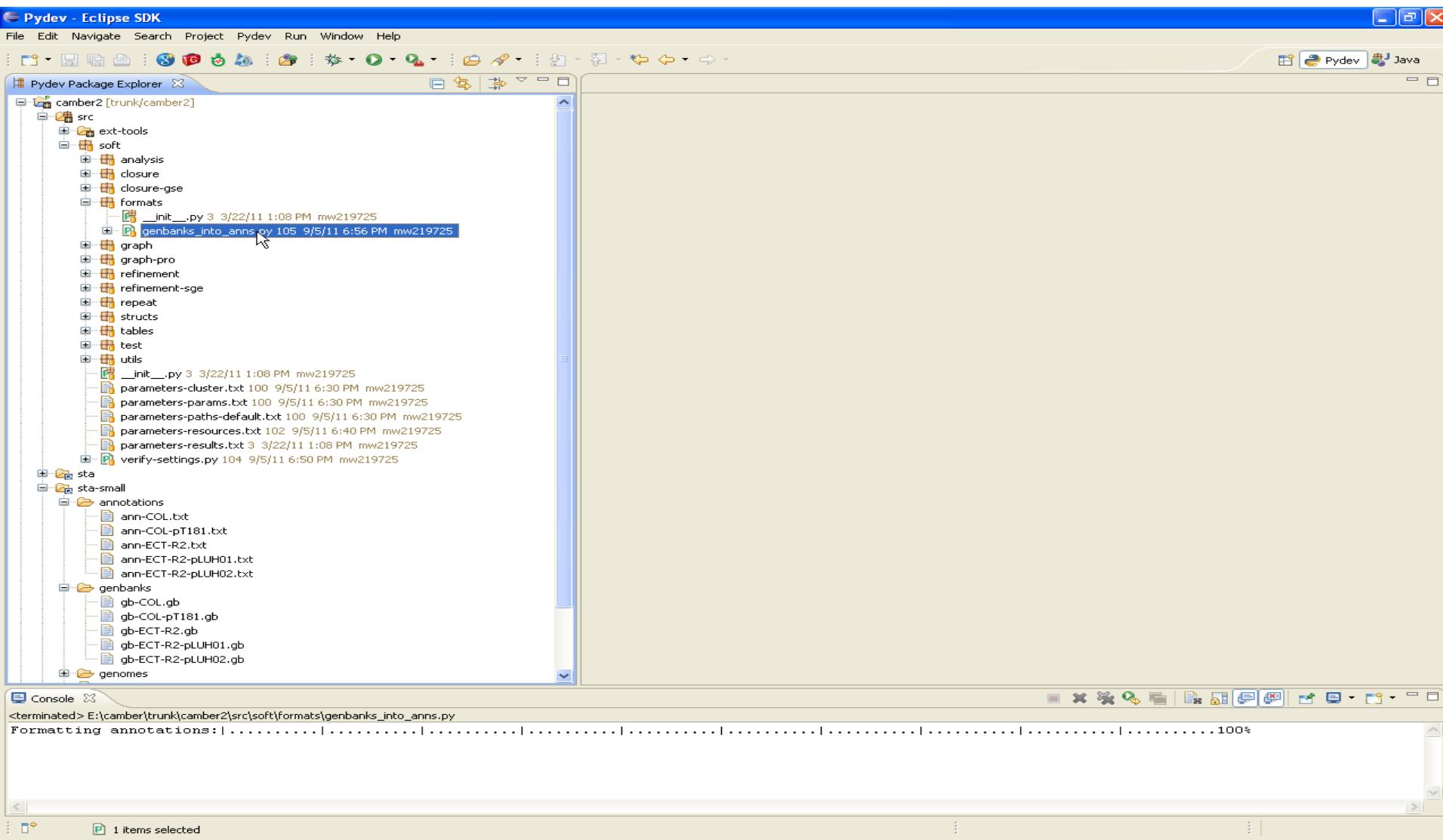
Executable scripts and source code for the CAMBer software. For the most recent version of the software please visit the <http://code.google.com/p/camber2/> project webpage. A draft version of [manual](#)



Open the project in Eclipse (OPTIONAL),  
we present the project opened in Eclipse to show the structure of the directory tree  
Configure paths to external tools (BLAST and BLAST formatdb in the file parameters-paths-  
default.txt)



# Retrieve information from GenBank files into a simpler format running the script: *genbanks\_into\_anns.py*



























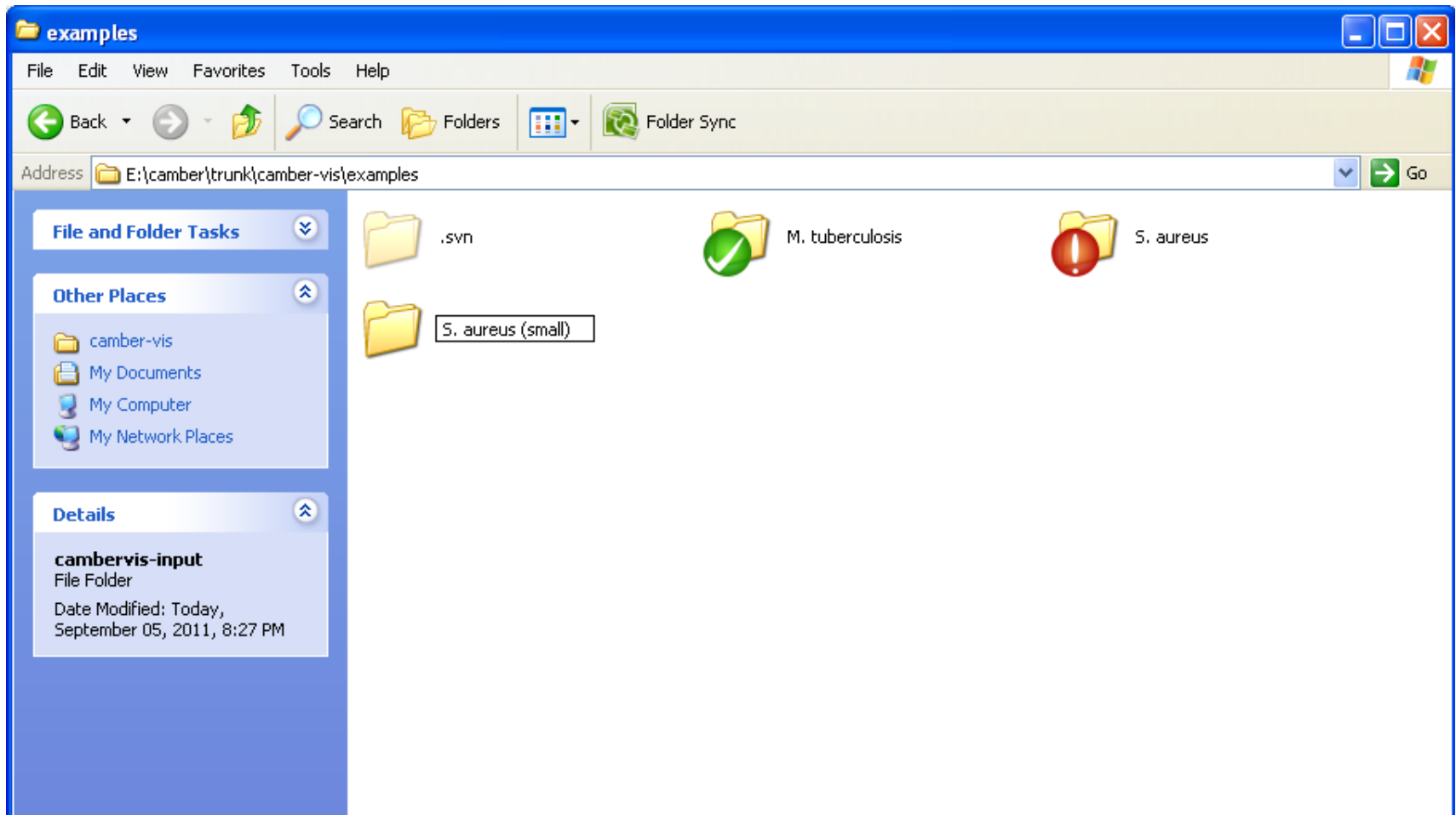
# Run subsequently scripts:

- *create-gene-graph.py*
- *create-multigene-graph.py*
- *save-multigene-details.py*
- *compute-components.py*
- *save-component-details.py*





Last step generated the input folder cambervis-input, copy and rename (OPTIONAL) the the folder into examples folder in CAMBERVis installation.  
In this example we rename it as „S.aureus (small)”



# Run CAMBerVis, the new input data S.aures (small) should be available

