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

| Software | a) Input [*] [*] |
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| CAMBerVis v1.2 | b) Closure (), (), |
| • CAMBerViS software (zip package, executables in the <i>bin</i> folder) | iterations Y Y |
| • <u>Manual</u> for CamberVis | |
| • Example 1 of CAMBerVis usage to identify inconsistent annotations of TISs (Translation Initiation | transitive closure |
| Sites) | c) (|
| • Example 2 of CAMBerVis usage to identify highly conserved gene families, but annotated in very | Multigens graph representation |
| few strains | |
| • <u>Video - example</u> 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/camberz/. | |
| CAMBerVis v1.0 platform-dependent installers | |
| • CAMBerViS <u>Windows</u> installer | |
| • CAMBerViS <u>Linux</u> installer | |
| • CAMBerViS <u>MAC OS</u> installer | |

• CAMBer

Executable scripts and source code for the CAMPer 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-pathsdefault.txt)

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| 📮 🕞 camber2 [trunk/camber2] | S import sys |
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| in the analysis | from soft.utils.mtb utils import overwriteParameters, readParameters |
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| 🖶 🖶 closure-gse | parameters = overwriteParameters(sys.argv) |
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| 🗰 🖶 refinement | for param in parameters: |
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| parameters-resources.txt 102 9/5/11 6:40 PM mw219725 | print ("Customize the file: parameters-paths-default.txt") |
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Retrive information from GenBank files into a simpler format running the script: *genbanks_into_anns.py*

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Initiate the directory structure for the closure procedure running script:

prepare-anns.py

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| <terminated>E:\camber\trunk\camber2\src\soft\closure\prepare-anns.py</terminated> | |
| Initialization of the closure procedure. Creates folders to store results | |
| Creates file iteration.txt to info which iteration of the closu | are procedure |
| Creates files with list of genes used as BLAST queries | |
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Create BLAST databases for queries running script: *prepare-databases.py*

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Iteration 1:

Compute BLASTs to transfer annotations

(1 iteration of the closure procedure) running script:

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| Computes BLASTs to transfer annotations between strains. | | |
| Current iteration: O | | |
| Reading sequences: | | |
| Reading new annotations: | | |
| Save BLAST queries: | | |
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Iteration 1: Parse and rate (accept or reject) BLAST hits running script: *parse-blasts.py*

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| Parses computed BLASTs to transfer annotations between strains. | |
| Current iteration: 0 | |
| Reading sequences: | |
| Prepare rev-sequences: | |
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Iteration 1:

Merge transfered annotations running script: *merge-anns.py* 1 iteration will be finished with 574 newly annotated ORFs

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| <terminated> E:\camber\trunk\camber2\src\soft\closure\merge-anns.py</terminated> | |
| Merges accepted BLAST hits with annotations. Current iteration: O | |
| Reading sequences: | . |
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Iteration 2: Compute BLASTs to transfer annotations (2 iteration) running script: *do-blasts.py (it may take around 1 min)*

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Iteration 2: Parse and rate (accept or reject) BLAST hits running script: *parse-blasts.py*

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| Current iteration: 1 | |
| Reading sequences: | |
| Prepare rev-sequences: | |
| Reading all annotations: | 1 |

Iteration 2:

Merge transfered annotations running script: *merge-anns.py* 2 iteration will be finished with 11 newly annotated ORFs

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| Merges accepted BLAST hits with annotations. | |
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Iteration 3: Compute BLASTs to transfer annotations running script: *do-blasts.py* (only a few seconds)

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| Computes BLASTs to transfer annotations between strains. | |
| Current iteration: 2 | |
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| BLASTs: | . |

Iteration 3: Parse and rate (accept or reject) BLAST hits running script: *parse-blasts.py*

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Iteration 3:

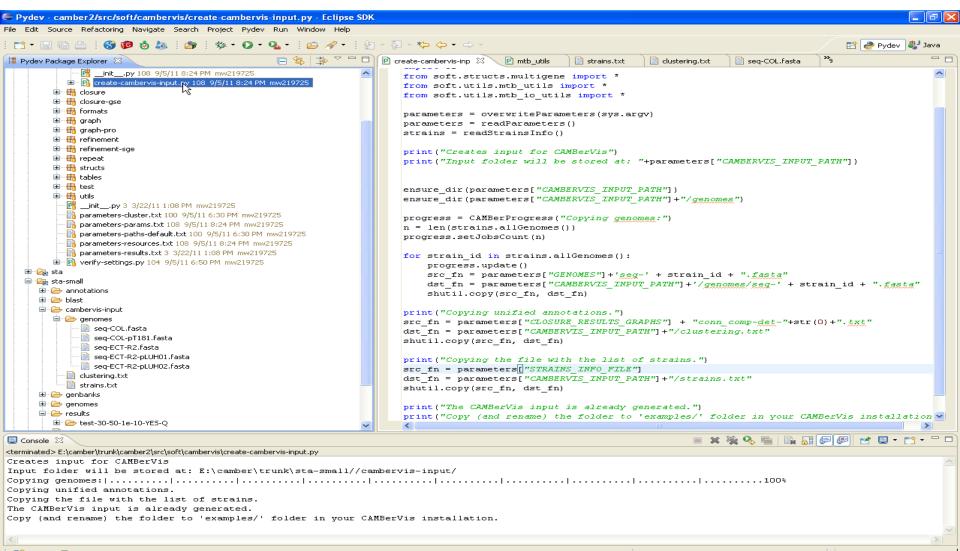
Merge transfered annotations running script: *merge-anns.py The closure procedure is computed.*

| Pydev - Eclipse SDK | |
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| <terminated> E:\camber\trunk\camber2\src\soft\closure\merge-anns.py</terminated> | |
| Merges accepted BLAST hits with annotations. | 1 |
| Current iteration: 2 | |
| Reading sequences: | |
| The closure procedure is already computed. | |
| The Globale procedure is arready compact. | |
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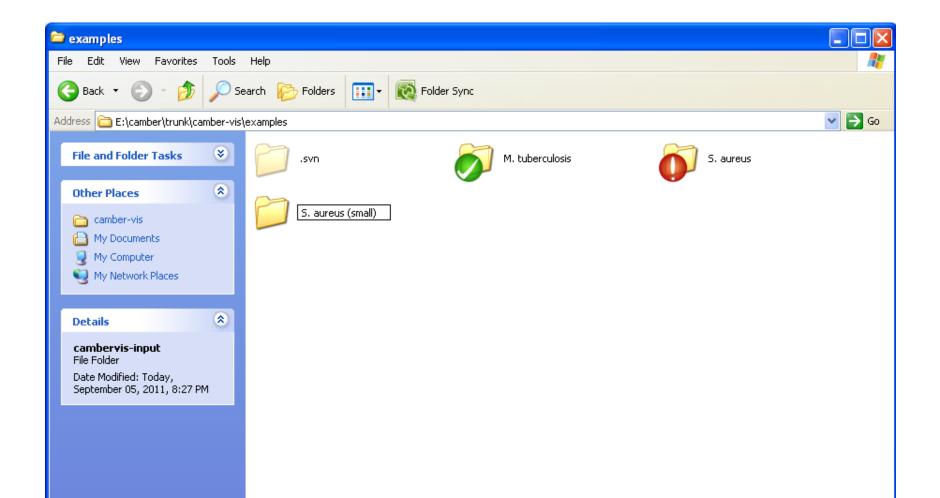
Run subsequently scripts:

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

Generate the input data for CAMBerVis running the script: *create-cambervis-input.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

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