GA TB: a software toolbox for genome assembly and analysis
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1. What is GATB?

**Motivation**

NGS technologies produce terabytes of data. Efficient and fast NGS algorithms are essential to analyze them.

**Objective**

The Genome Assembly Tool Box (GATB)

- is an open-source software
- provides an easy way to develop efficient and fast NGS tools
- is based on data structure with a very low memory footprint
- allows complex genomes to be processed on desktop computers

3. Compact de Bruijn graph data structure

The core data structure of GATB is a de Bruijn graph that encodes the main information from the sequencing reads.

**Strength of GATB**

GATB makes this graph compact by using a Bloom filter (a space efficient probabilistic data structure) and by using a CFP additional structure that avoids false positive answers from the Bloom filter due to its probabilistic nature.

5. GATB helps you as a NGS user

GATB's de Bruijn graph: a basis for families of tools

- Data error correction
- Assembly
- Biological motif detection

Several tools based on GATB are already available

- Bloocoo: K-mer spectrum based read error corrector for large datasets
- Minia: Short read assembler based on a de Bruijn graph. Results are of similar contiguity and accuracy to other de Bruijn assemblers (e.g. Velvet)
- DiscoSNP: Discover Single Nucleotide Polymorphism (SNP) from non-assembled reads
- TakeABreak: Detects inversion breakpoints without a reference genome by looking for fixed size topological patterns in the de Bruijn graph

4. Workflow

Here is a typical workflow when working with GATB

GATB-CORE transforms the reads into a de Bruijn graph, saves it in a HDF5 file that can be opened by other tools developed with the GATB-CORE API.

6. GATB helps you as a NGS developer

The GATB C++ library gives you the opportunity to quickly develop new NGS tools that fit your needs.

- Proprietary licencing for software editors or services providers is currently being handled with 5 GBytes of memory
- HDF5 usage for data storage
- Full Doxygen documentation including many code samples
- Test suite that checks the correct behavior of the library

License & Web Site

GATB is released under the GNU Affero General Public License. Proprietary licencing for software editors or services providers is currently being studied.

For more details on GATB:

http://gatb.inria.fr

**Publications**

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K. Sakhnov, G. Sacomoto, D. Kucherov, Using Cascading Bloom Filters to Improve the Memory Usage for de Bruijn Graphs, Algorithms in Bioinformatics, Lecture Notes in Computer Science, Volume 8126, 2013, pp 364-378

**Partners**