Speeding up NGS software development
Erwan Drezen, Guillaume Rizk, Rayan Chikhi, Charles Deltel, Claire Lemaitre, Pierre Peterlongo, Dominique Lavenier

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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

2. Software Solution

The GATB philosophy proposes a 3-layer construction to analyze NGS datasets

1. **GATB-CORE**: a C++ library holding all the services needed for developing software dedicated to NGS data.

2. **GATB-TOOLS**: a set of elementary NGS tools mainly built upon the GATB library (k-mer counter, contig, scaffold, variant detection, etc.).

3. **GATB-PIPELINE**: a set of NGS pipeline that links together tools from the previous layer.

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.

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.

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

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.

**Major facts about the GATB C++ library**

- Object Oriented Design
- Simple and powerful graph API
- Simple and powerful multithreading model
- HDF5 usage for data storage
- Fully documented with numerous code samples
- Complete test suite

**How to Analyze Complex Genomes on a Simple Desktop Computer?**

GATB helps you as a NGS user

- **GATB-CORE**
- **GATB-TOOLS**
- **GATB-PIPELINE**

**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](http://gatb.inria.fr)

**Partners**

- [INRIA/IRISA/GenScale](http://www.irisa.fr)
- [Department of Computer Science and Engineering, Pennsylvania State University, USA](http://www.cs.psu.edu)

**Publications**

- R. Chikhi, G. Rizk: **Space-efficient and exact de Bruijn graph representation based on a Bloom filter**, Algorithms for Molecular Biology 2013, 8:22
- G. Colin, G. Rizk, R. Chikhi, D. Lavenier: **Minia on Raspberry Pi, assembling a 100 Mbp genome on a Credit Card Sized Computer**, Poster at the TCH conference, 2013 Jul 1-4 (Toulouse) Best poster award
- K. Iskhanov, G. Sacomoto, G. 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 364-376

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**TCC**

**Sequencing, Finishing and Analysis in the Future Meeting, Santa Fé, USA, May 2014**

**Erwan Drézen**, Guillaume Rizk, Rayan Chikhi, Charles Deltel, Claire Lemaitre, Pierre Peterlongo and Dominique Lavenier