GATB: Toolbox for developing efficient NGS software
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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

**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.

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.

4. **Workflow**

Here is a typical workflow when working with GATB

**Tool 1**
- 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.

**Tool 2**
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**Tool 3**
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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

- **Bloomoo**: 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

**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**

**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
- C. Deltel, R. Chikhi, D. Lavenier: **Minia on Raspberry Pi**: assembling a 100 Mbp genome on a Credit Card Sized Computer. Poster at the JOBIM conference, 2013 Jul 1-4 (Toulouse) Best poster award