Speeding up NGS software development
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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 structures 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 Bruijin 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

- **Blocco**: 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 Bruijin 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
- HDFS usage for data storage
- Fully documented with numerous code samples
- Complete test suite

Publications

G. Rizk, D. Lavenier, R. Chikhi, **DSK**: k-mer counting with very low memory usage. Bioinformatics, 2013 Mar 1;29(5):652-3

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

K. J. Sokolov, G. Sacomoto, G. Kucherov, Using Cascading Bloom Filters to Improve the Memory Usage for de Bruijin Graphs. Algorithms in Bioinformatics, Lecture Notes in Computer Science, Volume 8126, 2013, pp 364-376

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For more details on GATB: http://gatb.inria.fr

Partners

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