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, contigger, 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-PIPELINE 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 an 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

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

How to Analyze Complex Genomes on a Simple Desktop Computer?

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

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. Collet, D. Rizk, R. Chikhi, D. Lavenier: Mina on Raspberry Pi, assembling a 100 Mbp genome on a Credit Card Sized Computer. Poster at the JGMH conference, 2013 jul 4 (Nabissi) Best poster award

License & Web Site

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Proprietary licencing for software editors or services providers is currently being studied.

For more details on GATB:

http://gatb.inria.fr

Partners

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