GATB: 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

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.

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.

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.

Major facts about the GATB C++ library
- Object oriented design
- Simple and powerful de Bruijn graph API
- Simple and powerful multithreading model
- HDF5 usage for data storage
- Full Doxygen documentation including many code samples
- Test suite that checks the correct behavior of the library