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GATB: a software toolbox for genome assembly and analysis

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GATB

The Open Source Toolbox for Genomic Assembly & Analysis

Erwan Drézen¹, Guillaume Rizk¹, Rayan Chikhi², Charles Deltel¹, Claire Lemaître¹, Pierre Peterlongo¹ and Dominique Lavenier¹

¹ INRIA/IRISA/GenScale, Campus de Beaulieu, 35042 Rennes cedex

² Department of Computer Science and Engineering, Pennsylvania State University, USA

1. What is GATB ?

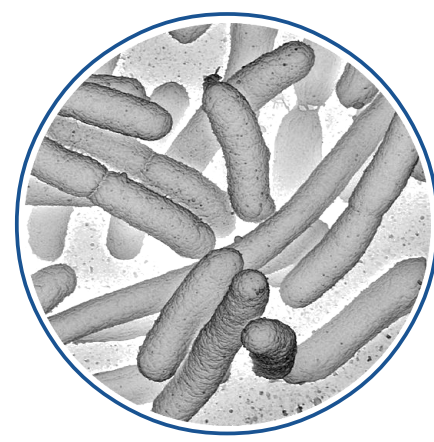
Motivation

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

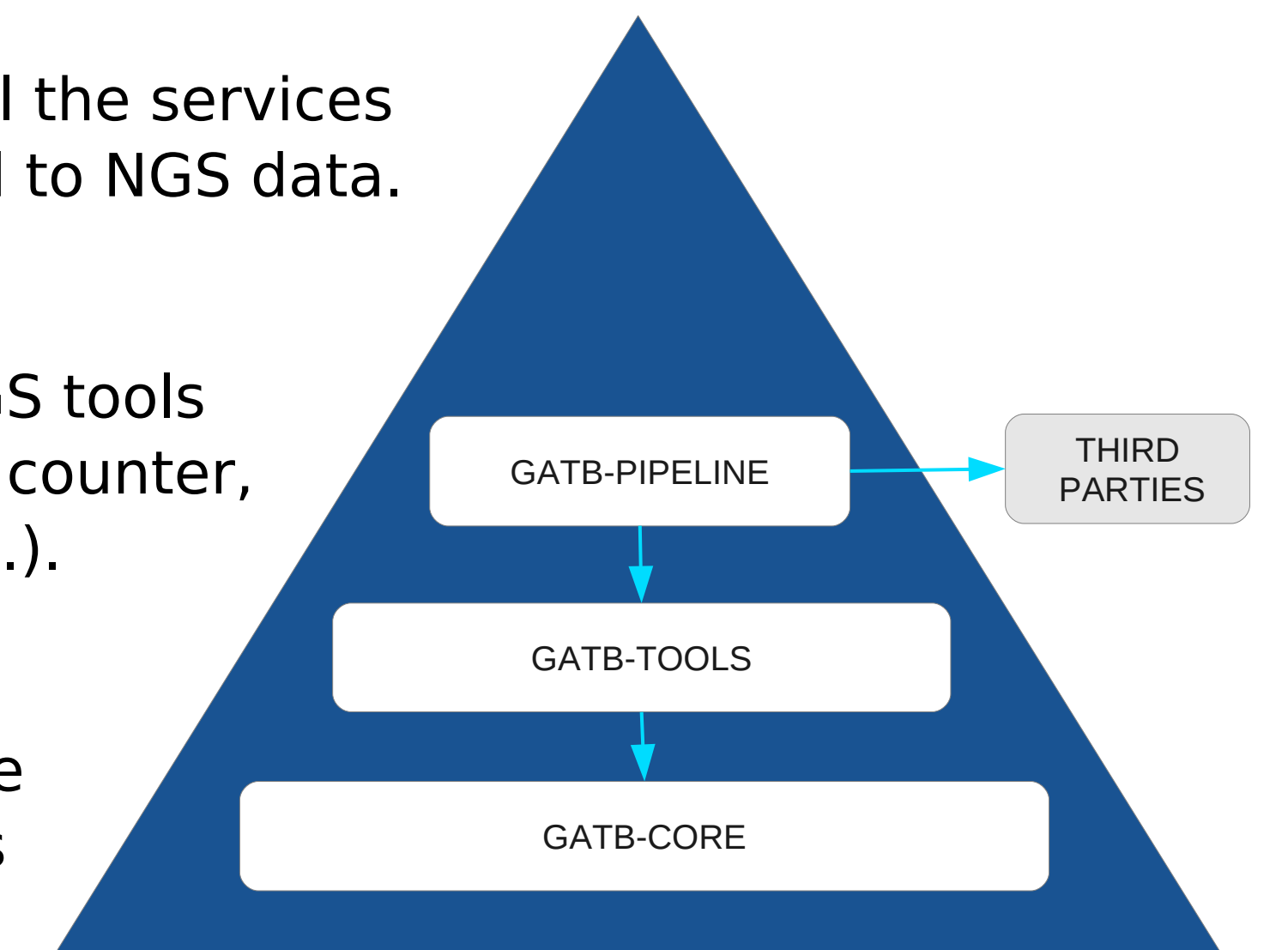


```
>read 1
ACGACGACGTAGACGACTAGCA
AAACTACGATCGACTAT
>read 2
ACTACTACGATCGATGTCGGG
CTGCTCGCTCTCTCGCT
...
>read 100.000.000
TCTCTTAGCGCGGCTATACCC
TCGCTAGCTACGTAGCT
...
```

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, contiger, scaffolder, variant detection, etc.).
3. **GATB-PIPELINE**: a set of NGS pipeline that links together tools from the previous layer.

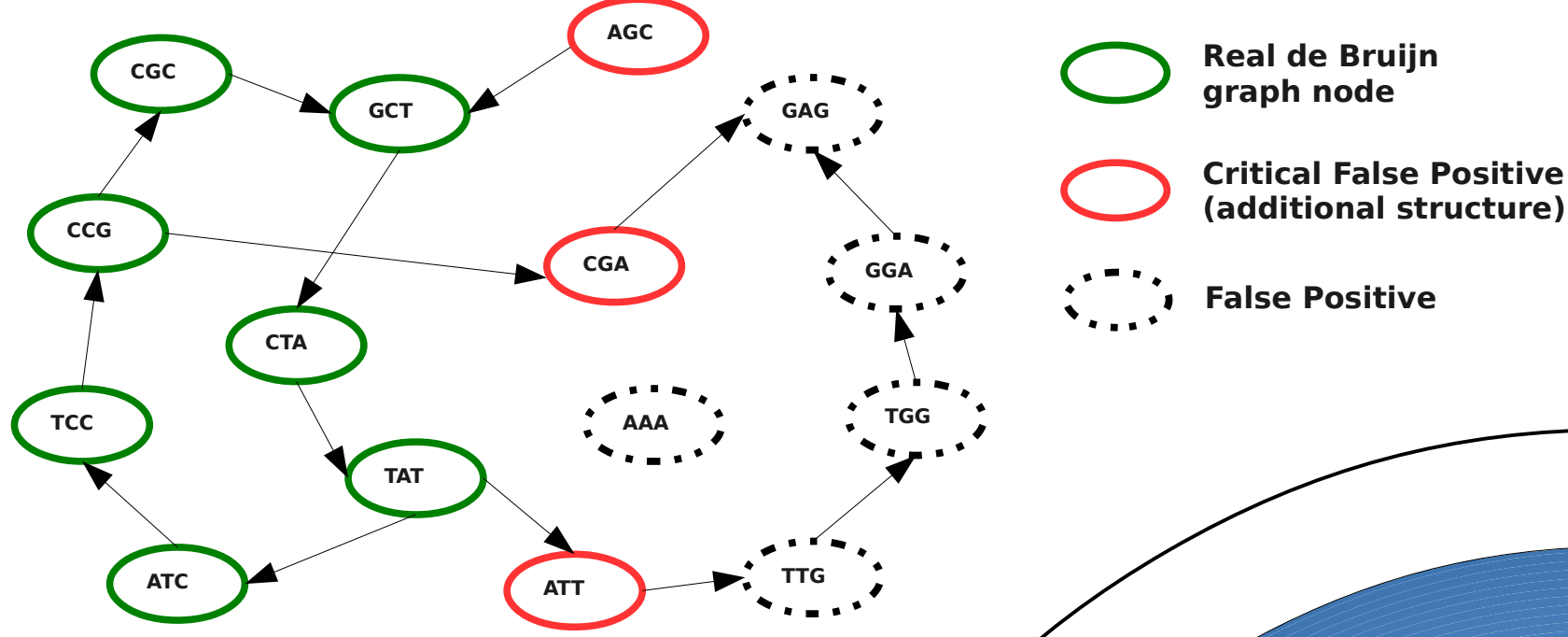


3. Compact de Bruijn graph data structure

The core data structure of GATB is a de Bruijn graph that encodes the main information from the sequencing reads.

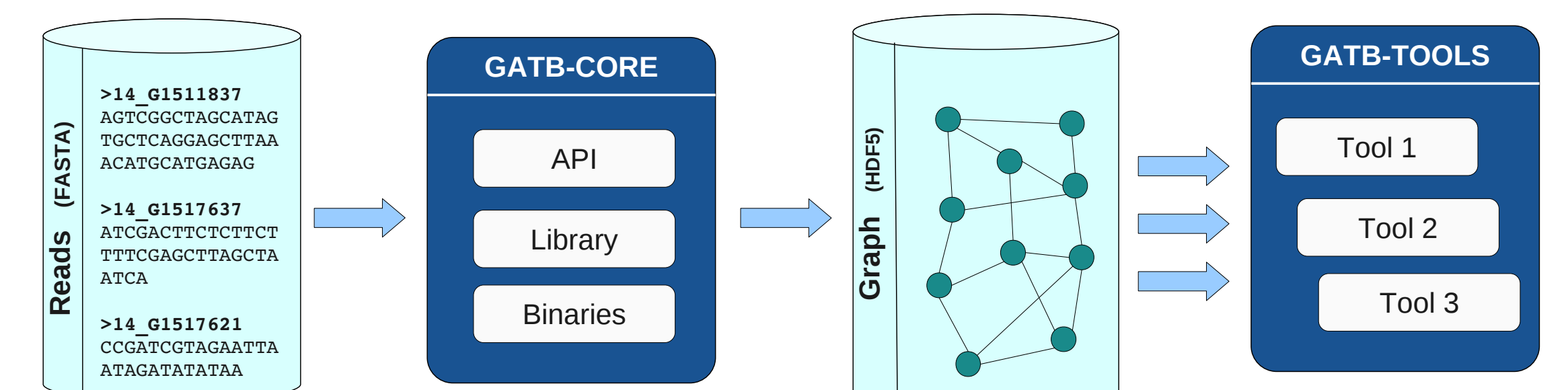
Strength of GATB

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**
- a whole human genome sequencing reads can be handled with 5 GBytes of memory

Several tools based on GATB are already available

- Blooco** 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

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 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

Publications

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

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, G. Rizk, 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.

K.I Salikhov, 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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For more details on GATB:

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