polars-bio: High-Performance Python DataFrame Operations for Genomics

Demystify AI & Data Management Series

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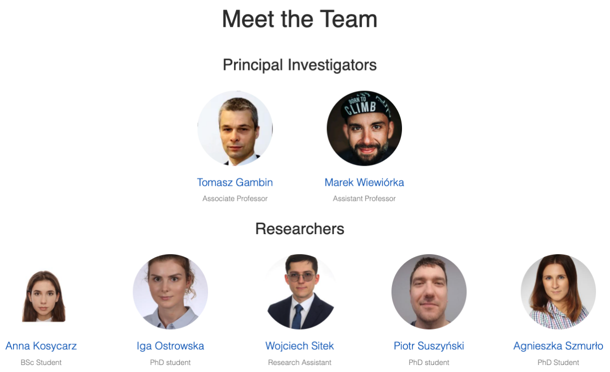
About me

- Assistant Professor[a] at Warsaw University of Technology
- Chief Architect @Xebia Data Poland, 20+ years building data-intensive systems
- distributed and data-intensive systems, artificial intelligence and cloud computing for large scale genomic studies.
- road and gravel bikes enthusiast
- https://marekwiewiorka.org/

[a] Institute of Computer Science

Biodatageeks lab

- Warsaw University of Technology, Faculty of Electronics and Information Technology
- 🔬 current research topics:
  - AI for analyzing biomedical literature
  - Meta-calling for gene fusion detection in RNA-Seq
  - Optimizing RVAS
  - Open genomic data lakehouse
- https://biodatageeks.org/
- https://github.com/biodatageeks/



Agenda

1. 🤔 Rationale and motivation
2. 🗺️ Context and alternatives for `polars-bio`
3. 🔬 Deep dive into internals
4. 📊 Benchmarks
5. 🔮 Future directions

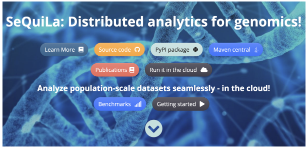
Introduction to polars-bio

- polars-bio is a novel Python DataFrame library for genomics that is *fast* and *memory-efficient*, introduced in 2025, built on top of Polars, Apache DataFusion and Apache Arrow.
- main focus areas:
  - 🧬 genomic interval operations
  - 🚀 scalable data processing and querying
  - 💾 fast I/O for bioinformatics file formats
  - ☁️ cloud storage interoperability
  - 🧱 genomic data lakehouse readiness

POLARS-BIO

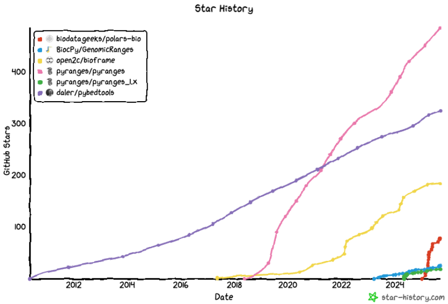
Rationale, History, and Challenges

- 📈 Growing bioinfo dataset sizes vs. increasing capacity of commodity hardware
- ⚖️ Trade-off: scalability of distributed systems (e.g., Apache Spark - Hail, Glow) vs. simplicity and performance of single-node libraries (e.g. DuckDB)
- 🖥️ Single-node solutions: constrained in both performance and scalability
- 🧪 First attempt (2019–2023): SeQuiLa project on top of Apache Spark
- 🔀 Conclusion: towards a *hybrid* approach



Landscape of tools for genomic interval operations in Python

- several widely used libraries exist in this space:
  - Pyranges and new Pyranges1
  - Pybedtools
  - Bioframe
  - GenomicRanges
- employing an *eager*, *in-memory* execution model with Pandas DataFrames/ NumPy arrays
- sweep-line (Bioframe, Pyranges1) or Nested Containment List (Pyranges, GenomicRanges) or genome binning algorithm (Pybetools)
- focus *primarily* on optimizing genomic operations rather than end-to-end processing and IO operations



Market trends in data systems

- out-of-core (streaming) processing
- single node vectorized engines – e.g. DuckDB, Polars
- *lazy* evaluation and query optimization – e.g. Polars
- open data standards and interoperability, such as Apache Arrow or Apache Iceberg
- composability and reusability, e.g. query parsers, optimizers, query engines, memory and file/table formats
- data lakehouse architecture

DuckDB

Composable Data Management Systems (CDMS) Manifesto

- **Problem**: Data systems are *fragmented*, *duplicated*, hard to maintain
- **Vision**: Break *monoliths* into *modular*, *reusable* components (frontends, Internal Representation, optimizers, execution engines, runtime environments)
- **Why Now**: Already existing *open standards* (Arrow, Parquet, Iceberg) enable composability
- **Examples**: Velox, Apache DataFusion
- **Benefits**: *Faster* innovation, *reduced* engineering effort, consistent user experience

Limitations of Current Approaches to Genomic Interval Processing

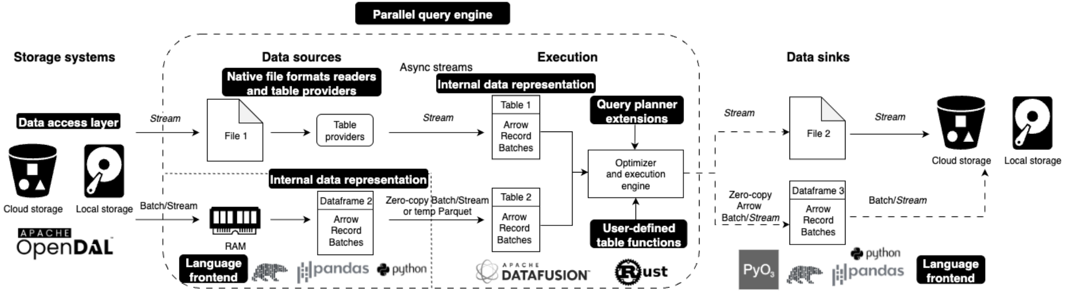
Genomic intervals processing is closer to BI/DWH/ETL-style workloads than to numerical computing!

- Relying on libraries (e.g., NumPy) not designed for efficient bioinformatics data handling
- Re-implementing algorithms and reinventing the wheel instead of leveraging mature *query engine*: optimizers, operators and open data standards
- *Parallelism* and *out-of-core* not treated as a first-class concern (limited scalability)
- *Naive* Python implementations (slow, limited scalability)
- Missing *end-to-end optimization* including reading, processing and writing data

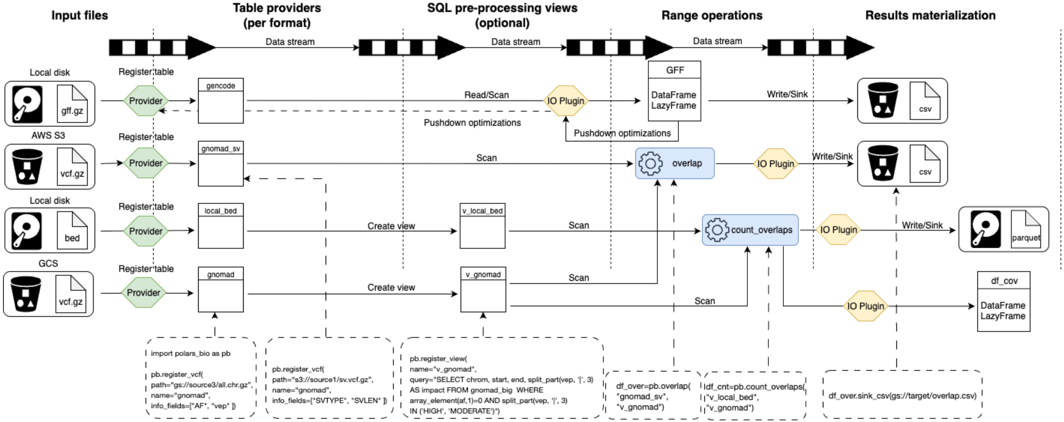
Why polars-bio is different?

- Composable and best of breed approach
  - query engine (Apache DataFusion)
  - DataFrame library (Polars)
  - columnar memory format (Apache Arrow)
  - data structure for interval intersection queries (COITrees and Superintervals)
  - bioinformatics file formats (noodles)
- Builtin *lazy*, *out-of-core* and *parallel* computational model
- IO layer optimizations for analytical queries, such as *projection* and *predicate* pushdowns

polars-bio high-level architecture



Architecture deep-dive - core components

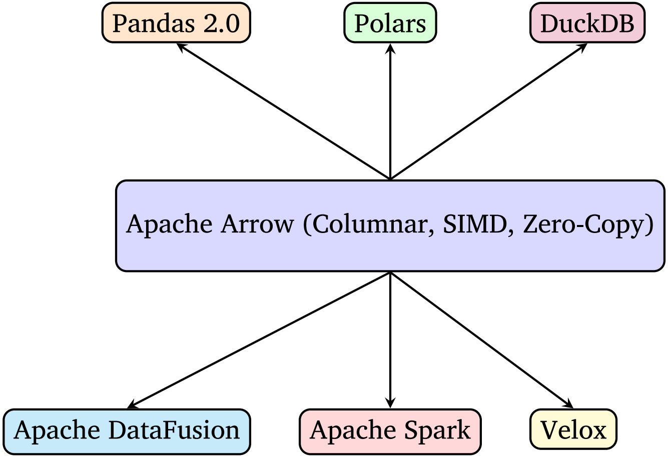


Architecture deep-dive - Polars and Apache DataFusion primer

- Polars and Apache DataFusion exhibit significant similarities, such as Apache Arrow columnar memory model, lazy evaluation and out-of-core computational model, great performance
- different main focuses:
  - Polars – feature-rich end-user DataFrame library
  - DataFusion – extremely extensible query engine for building custom data systems
- do we really need both?
  - Polars' great data wrangling capabilities but hard to extend
  - DataFusion's codebase reusability (e.g. hybrid execution) and more robust abstractions for query and IO optimizations
  - additional integration complexity (e.g. pushdown optimizations, parallelism control)

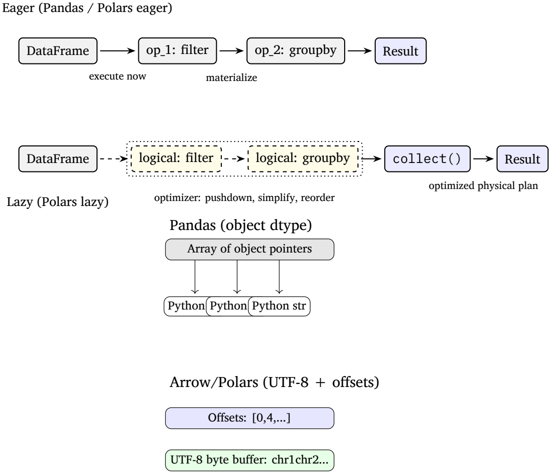
Architecture deep-dive - Apache Arrow

- Standardized columnar memory format – zero-copy sharing
- Vectorized execution: SIMD and CPU cache efficiency
- Cross-language interoperability (e.g. Python and Rust)
- Integration with open standards – Parquet, Iceberg
- Foundation for modern data systems – Polars, Ray, Rapids, Apache Spark



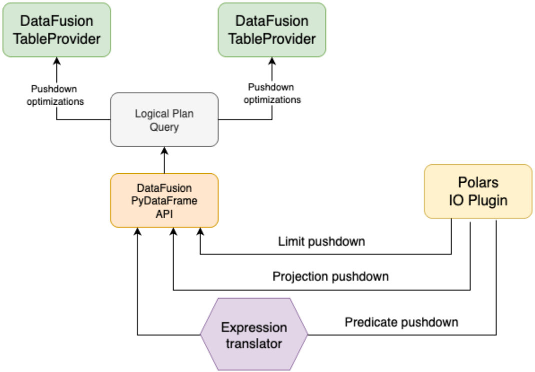
Architecture deep-dive - Polars vs. Pandas

- Execution model: Pandas is eager-only; Polars supports eager *and* lazy.
- Optimization: Pandas has no query optimizer; Polars (lazy) performs projection/predicate pushdown, simplification, reordering.
- Parallelism: Pandas mostly single-threaded (Python/GIL); Polars is multi-threaded (Rust).
- Memory/layout: Pandas uses NumPy blocks; Polars is columnar and Arrow-friendly.
- Out-of-core/streaming: Pandas primarily in-memory; Polars supports streaming/out-of-core in lazy plans.
- String handling: Pandas often stores Python objects (high memory overheads); Polars stores UTF-8 natively with efficient kernels (SIMD).



Architecture deep-dive - Polars IO plugin

- arbitrary function that returns a generator (Iterator) producing pl.DataFrame batches and gets back LazyFrame
- used for both files scanning and interval operations results streaming
- zero-copy and streaming using Arrow RecordBatchStream with DataFusion PyDataFrame
- support for limit, projection and predicate pushdowns (currently only GFF)



Architecture deep-dive - input file formats

- subproject datafusion-bio-formats
- exposed using custom TableProviders
- support for parralel reading of BGZF inputs
- local and cloud storage (AWS S3, GCS and Azure Blob
- cloud storage supported features

Format	Single-threaded	Parallel	Limit pushdown	Predicate pushdown	Projection pushdown
BED	✅	❌	✅	❌	❌
VCF	✅	🚧	✅	🚧	🚧
BAM	✅	❌	✅	❌	❌
FASTQ	✅	✅	✅	❌	❌
FASTA	✅	❌	✅	❌	❌
GFF3	✅	✅	✅	✅	✅

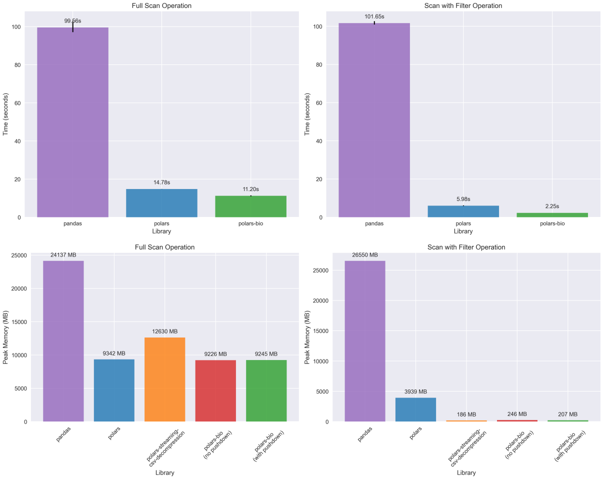
Benchmarking dataset

- AILIst real dataset converted into Parquet format – details
- GFF3 GENCODE release 49

Dataset#	Name	Size(x1000)	Description
0	chainRn4	2,351	Source
1	fBrain	199	Source
2	exons	439	Dataset used in the BEDTools tutorial.
3	chainOrnAna1	1,957	Source
4	chainVicPac2	7,684	Source
5	chainXenTro3Link	50,981	Source
6	chainMonDom5Link	128,187	Source
7	ex-anno	1,194	Dataset contains GenCode annotations with ~1.2 million lines, mixing all types of features.
8	ex-rna	9,945	Dataset contains ~10 million direct-RNA mappings.

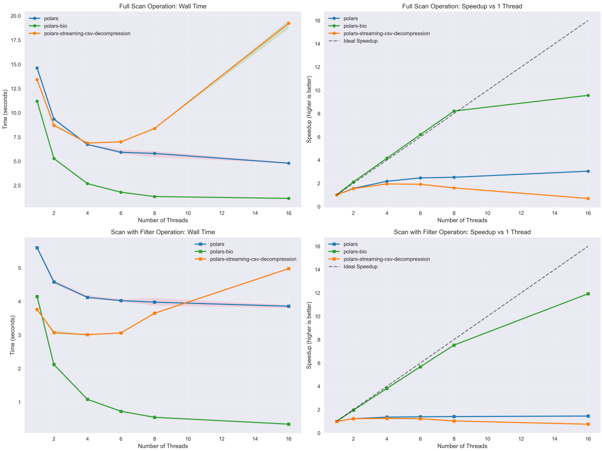
Source: Jianglin Feng , Aakrosh Ratan , Nathan C Sheffield, *Augmented Interval List: a novel data structure for efficient genomic interval search*, Bioinformatics 2019.

File formats: GFF (scan_csv vs polars-bio) – results 1/2



- in full-scans Polars and polars-bio significantly outperform Pandas
- Polars problem with `scan_csv` and compressed files)
- streaming decompression plugin

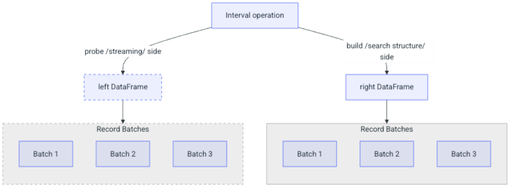
File formats: GFF (scan_csv vs polars-bio) – results 2/2



- polars-bio achieves near-linear scaling up to 8 threads
- Polars and streaming decompression plugin scale poorly

Architecture deep-dive – genomic interval operations 1/2

- inspired by the Hash Join implementation in DataFusion
- the *entire* (coordinates) build side is read into the interval search data structure
- batches from the probe side are *streamed* through and checked against the contents of the search data structure

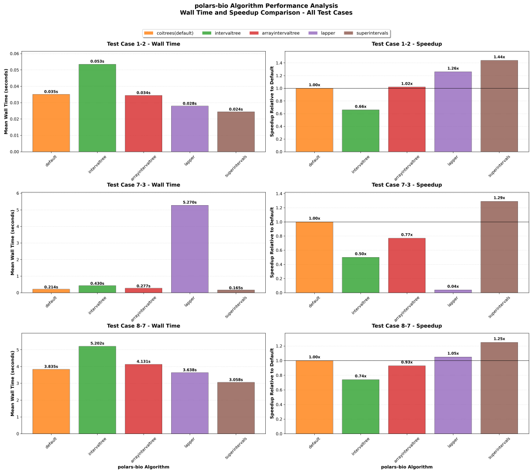


Architecture deep-dive – genomic interval operations 2/2

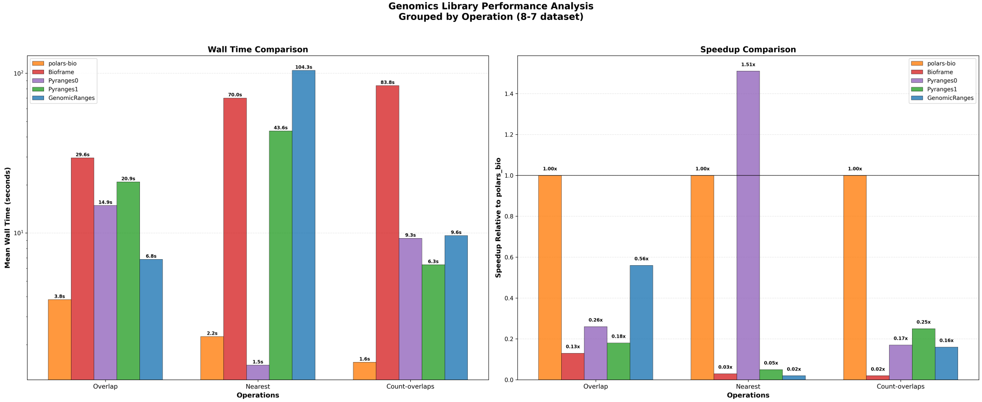
- subproject sequila-native
- custom PhysicalPlanner and PhysicalOptimizerRule for detecting and rewriting generic interval join operation (overlap or nearest)
- User-Defined Table Function (UDTF) for operations, such as coverage or count overlaps
- several data structures available:
  - COITrees
  - IITree
  - AVL-tree
  - rust-lapper
  - Superintervals

Genomic interval operations – structures comparison results 1/6

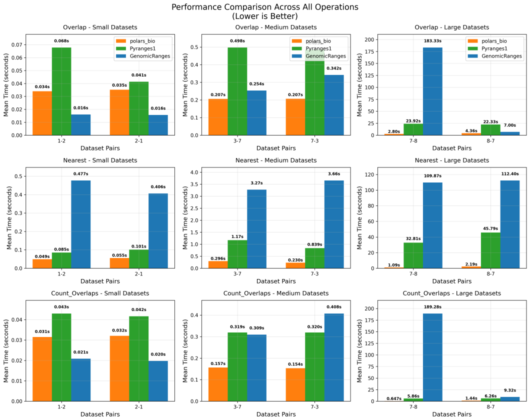
- COITrees (polars-bio default) and Superintervals fastest in all test cases
- configurable in runtime
- more tests using different datasets characteristics needed

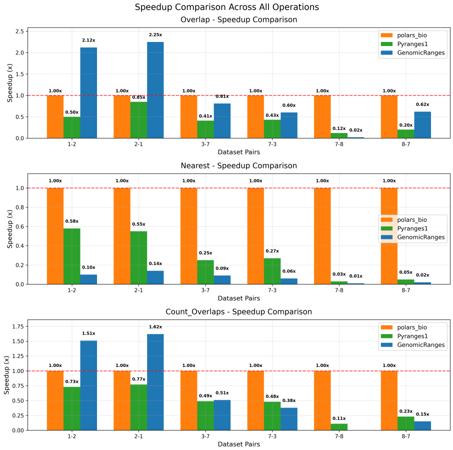


Genomic interval operations – results 2/6

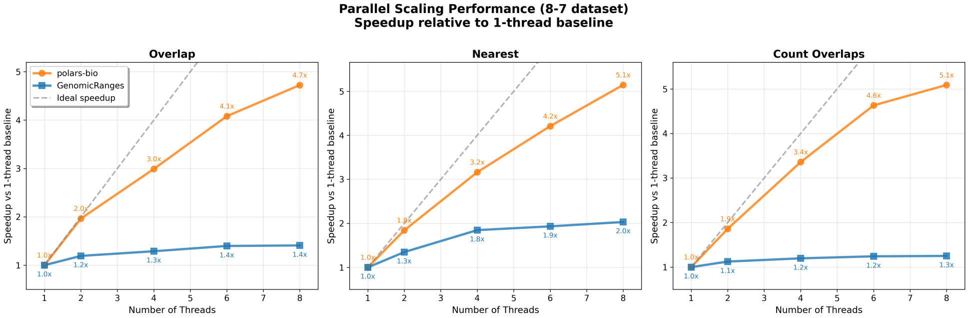


Genomic interval operations – results 3/6

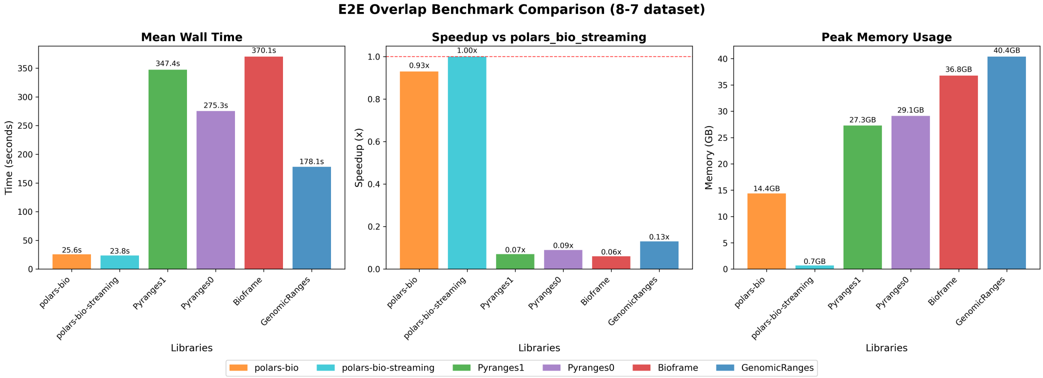




Genomic interval operations – scaling – results 4/6



Genomic interval operations – e2e pipeline – results 5/6



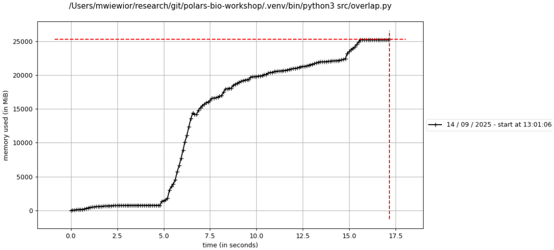
Genomic interval operations – results 6/6

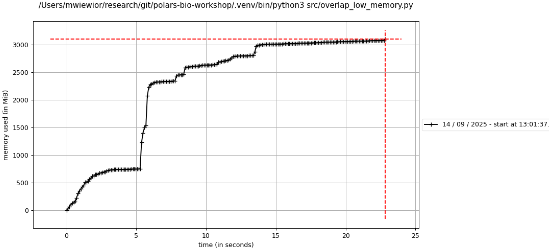
```
import pandas as pd
>> df = pd.read_parquet("/tmp/exons/")

# GenomicRanges - int32
GenomicRanges(number_of_ranges=438694, seqnames=[],
ranges=IRanges(
    start=array([], shape=(438694,), dtype=int32),
    width=array([], shape=(438694,), dtype=int32)),

# Bioframe - int32
cols=["contig","pos_start","pos_end"]
>> bf.from_any(df, cols=cols).info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 438694 entries, 0 to 438693
Data columns (total 3 columns):
 #   Column     Non-Null Count   Dtype
---  ------     --------------   -----
 0   contig     438694 non-null  object
 1   pos_start  438694 non-null  int32
 2   pos_end    438694 non-null  int32
dtypes: int32(2), object(1)
```

```
# Pyranges0 - int64 !!!
>> df2pr0(df)
+--------------+------------+-----------+
| Chromosome   | Start      | End       |
| (category)   | (int64)    | (int64)   |
|--------------+------------+-----------|
| chr1         | 11873      | 12227     |
| chr1         | 12612      | 12721     |
| chr1         | 13220      | 14409     |
| chr1         | 14361      | 14829     |
| ...          | ...        | ...       |
+--------------+------------+-----------+
Unstranded PyRanges object has 438,694 rows and 3 columns.

# Pyranges1 - int32
>> df2pr1(df)
index    |    Chromosome    Start     End
int64    |    object        int32     int32
-------  ---  ------------  --------  --------
0        |    chr1          11873     12227
1        |    chr1          12612     12721
2        |    chr1          13220     14409
3        |    chr1          14361     14829
...      |    ...           ...       ...
PyRanges with 438694 rows, 3 columns, and 1 index columns.
```

Overlap operation low memory mode for ~ 10^9 wide rows

Capped (max rows per batch) streaming-friendly emission – ~ 30 – 50% slower but with significantly lower memory utilization.





polars-bio roadmap

- 🏠 Lakehouse support with open standards
  - 🧊 Apache Iceberg integration with open-source (e.g. Apache Grvaitino, Lakekeeper, Apache Polaris, Unity Catalog OSS) and proprietary catalogs
- 💾 Feature parity across all supported bioinformatics formats
- 📝 Write-back into table formats (e.g. Apache Iceberg)
- 🤖 Spec-driven agentic development for automated pipelines
- 🚀 Hybrid execution: SeQuiLa + Apache Comet accelerator
- ✨ **Your use case!**

Summary

- 🧬 `polars-bio`: a new Python DataFrame library for genomics
- 🚀 Combines Polars, Apache DataFusion, and Apache Arrow for speed and scalability
- 💾 Efficient I/O for popular bioinformatics formats
- ⚖️ Addresses limitations of existing interval processing tools
- 🏗️ Towards a hybrid, lakehouse-ready approach for large-scale genomics

Stay Tuned!

- 🔗 GitHub: github.com/biodatageeks/polars-bio
- 🌎 Project page: biodatageeks.org/polars-bio
- 💬 Discord: Join our community
- 📅 Meet us at **ASHG 2025 Annual Meeting, Boston, October 14-18, 2025**

Thank You!

🤝 😊

Questions

Hands-on Demo

github.com/biodatageeks/polars-bio-workshop