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CARNAC-LR: De novo Clustering of Gene Expressed Variants in Transcriptomic Long Reads Data Sets

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► **To cite this version:**

Camille Marchet, Lolita Lecompte, Corinne da Silva, Corinne Cruaud, Jean-Marc Aury, et al.. CARNAC-LR: De novo Clustering of Gene Expressed Variants in Transcriptomic Long Reads Data Sets. RECOMB-seq 2018 - Eighth RECOMB Satellite Workshop on Massively Parallel Sequencing, Apr 2018, Paris, France. pp.1-2. hal-01929963

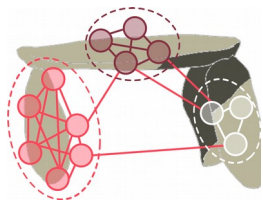
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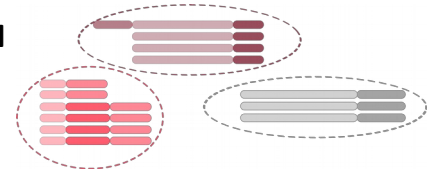
Submitted on 21 Nov 2018

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CARNAC-LR: De novo Clustering of Gene Expressed Variants in Transcriptomic Long Reads Data Sets



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Goal: *de novo* cluster Nanopore reads per expressed genes

Data: Nanopore 1D reads from mouse transcriptome sequenced with MinION (accession number: ERP107503)

Results:

- ★ State of the art does not perform well on ONT reads
- ★ We introduce CARNAC-LR, a new clustering approach designed for long reads
- ★ Validations on mouse transcriptome

Benchmark 1: community detection algorithms

	Recall	Precision	Jaccard index
Single link	76%	<15%	<0.1
Louvain	89%	<15%	<0.1
Modularity	61%	<75%	<0.5
CPM	79%	<75%	<0.5
CARNAC-LR	65%	98%	0.79

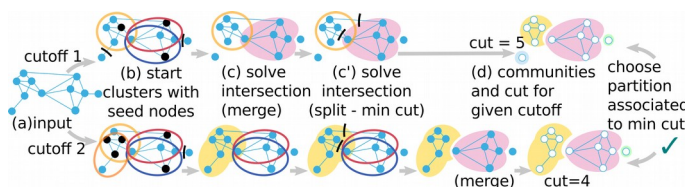
Benchmark 2: sequence clustering tools

	Recall	Precision	Status
Starcode	NA	NA	error
Tofu	NA	NA	not applicable
SEED	0	0	run
CD-HIT	27%	99%	run
CARNAC-LR	65%	98%	run

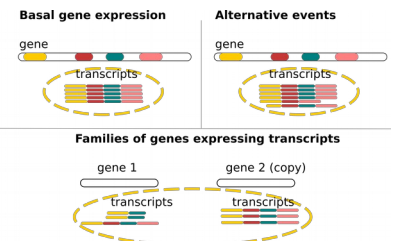
Algorithm overview:

Key ideas:

- maximize local edge density
- minimize cut size
- partition the graph

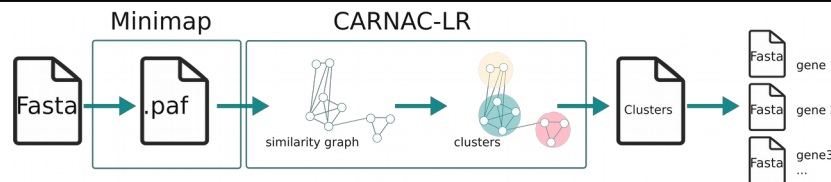


Expected clusters:



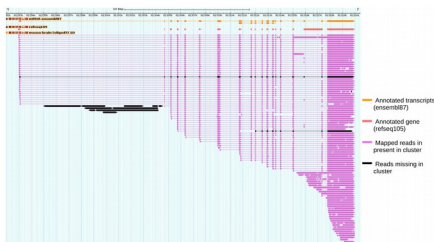
Pipeline overview:

From reads to clusters per expressed gene



- ★ C++11 and Python 3
- ★ GPL license
- ★ available on Github

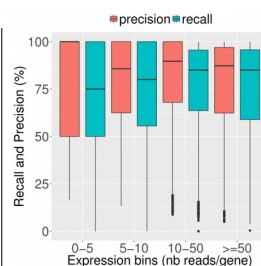
Results on whole mouse transcriptome:



Output graphical example for mouse Picp5 gene

Performances:

- For 1 million reads
- wallclock 3 hours (40 threads)
- memory: 30G



Clusters **purity** and **completeness** assessed using mapping strategy (BLAT+est2genome)

Work in progress:

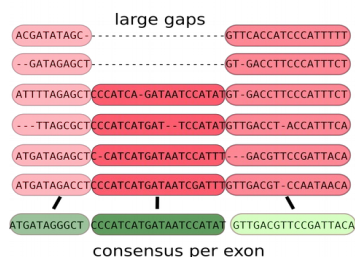
Goals:

- Identify alternative isoforms from CARNAC-LR's clusters
- Propose one consensus per isoform

Key ideas:

- intra-cluster multiple sequence alignment
- detect alternative blocks (exons)
- separated block consensus computation

MSA with sequences from 1 cluster



Main achievements

- ★ Clusters *de novo* ONT reads by expressed genes
- ★ Scales a whole mouse transcriptome
- ★ Performs better than state of the art on ONT reads
- ★ Validated using comparison by mapping strategy on real data

Tool:

github.com/kamimrcht/CARNAC-LR

Preprint:

[biorxiv.org/content/early/2018/03/26/170035](https://www.biorxiv.org/content/early/2018/03/26/170035)

Contact : camille.marchet@irisa.fr

Acknowledgments



- ★ Genoscope platform
- ★ ASTER ANR
- ★ Genouest team & infrastructures