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

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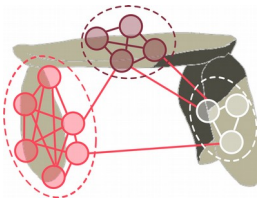
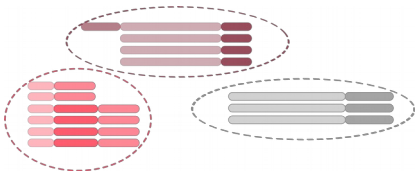


CARNAC-LR:
De novo Clustering of Gene Expressed Variants in Transcriptomic Long Reads Data Sets



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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%		
Modularity	61%	<75%	<0.5
CPM	79%		
CARNAC-LR	65%	98%	0.79

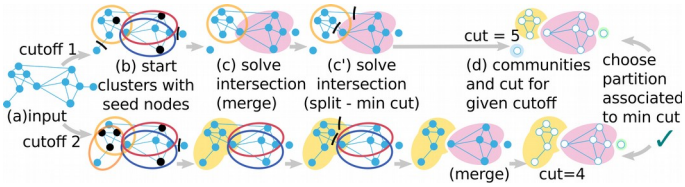
Benchmark 2: sequence clustering tools

	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

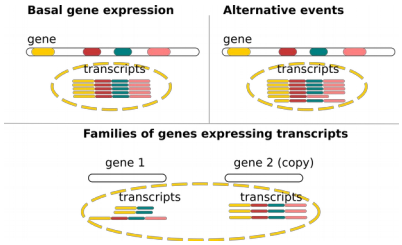
Algorithm overview:

Key ideas:

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

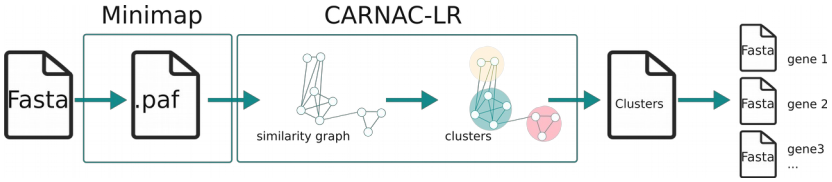


Expected clusters:



Pipeline overview:

From reads to clusters per expressed gene

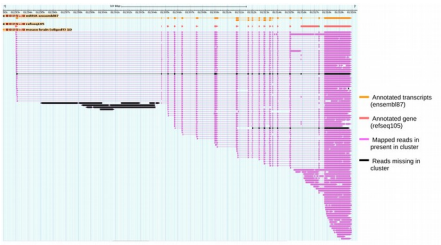


★ C++11 and Python 3

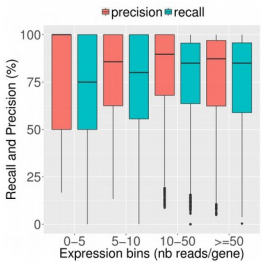
★ GPL license

★ **available on Github**

Results on whole mouse transcriptome:



Output graphical example for mouse Picp5 gene



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

Performances:

For 1 million reads

→wallclock 3 hours (40 threads)

→memory: 30G

Work in progress:

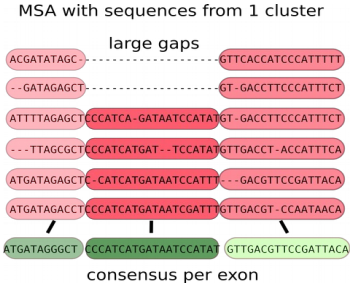
Goals:

-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



Acknowledgments

★ Genoscope platform

★ ASTER ANR

★ Genouest team & infrastructures

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 to mapping strategy on real data

Tool:

github.com/kamimrcht/CARNAC-LR

Preprint:

biorxiv.org/content/early/2018/03/26/170035

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