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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

Algorithm overview:

Key ideas:
- maximize local edge density
- minimize cut size
- partition the graph

Pipeline overview:

From reads to clusters per expressed gene

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)

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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