Eulimnogammarus verrucosus genome

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34th Herbstseminar
14 Feb 2019
Bled
Study objects

_Eulimnogammarus verrucosus_ (Gerstf. 1858)

ca. 1 cm / 100 km
Previous results & available data

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- Transcriptome (Illumina) reads and assembly (C:89.2%[S:43.0%, D:46.2%], F:8.6%, M:2.2%, n:1066)

- Nanopore reads: about 0.5x coverage.

- Genome size estimate: \( \approx 10 \text{ Gb} \).
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Algorithm overview

Illumina genome / transcriptome assembly → Blast → Low coverage Nanopore reads

filter only reliable results (e.g. bitscore > 1000 & indels > mm)

Reliable hits → Ovelap graph

Select path

Extend scaffolds → Align NP reads

Correct errors

Hybrid genome assembly! (+bonus exome annotation)
Algorithm overview

Illumina genome / transcriptome assembly

Blast

Low coverage Nanopore reads

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Reliable hits

Overlap graph

Select path

You are here

Correct errors

Extend scaffolds

Align NP reads

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First results
First results

Genome assembly
Algorithm overview

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Reliable hits

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Hybrid genome assembly!
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Long... (days)

(minutes)

Correct errors

?
Acknowledgements

Peter F. Stadler
Thomas Gatter
Lorena Rivarola-Duarte

Maxim Timofeyev
Daria Bedulina
Denis Axenov-Gribanov
Anton Gurkov
Yulia Lubyaga
Kseniya Vereshchagina

Till Luckenbach
Stephan Schreiber
Hans-Otto Pörtner
Magnus Lucassen
Franz Sartoris
Lena Jakob

Thank you for your attention!