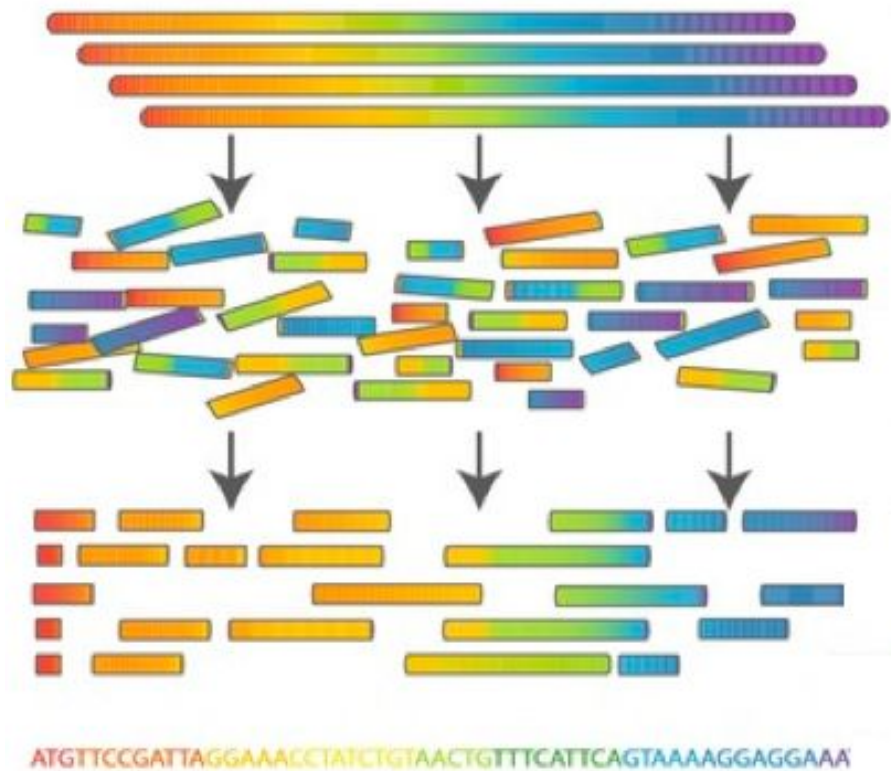




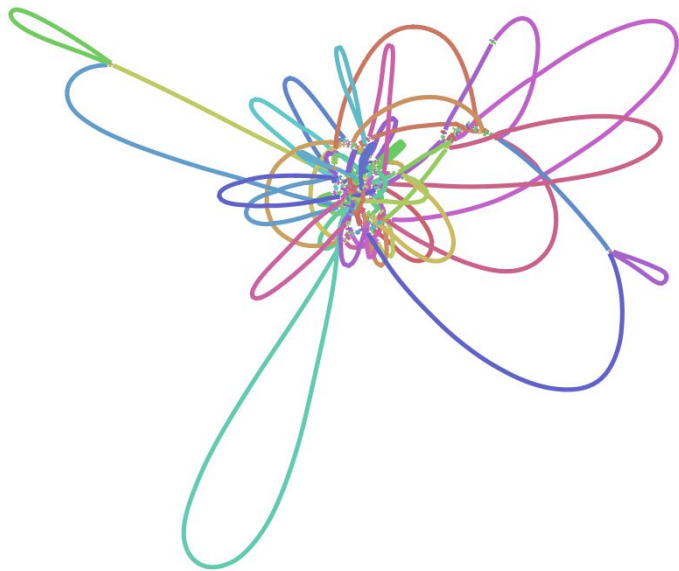
Еще один способ делать метагеномную сборку

Олехнович Е.И.
лаборатория биоинформатики

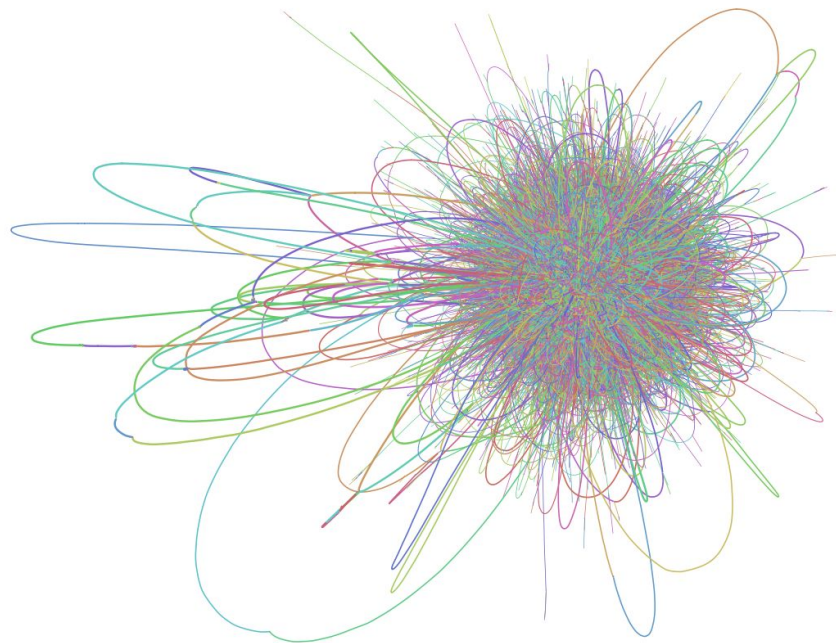
Сборка метагеномов / геномов



Как выглядит собранный метагеном в сравнении с геномом

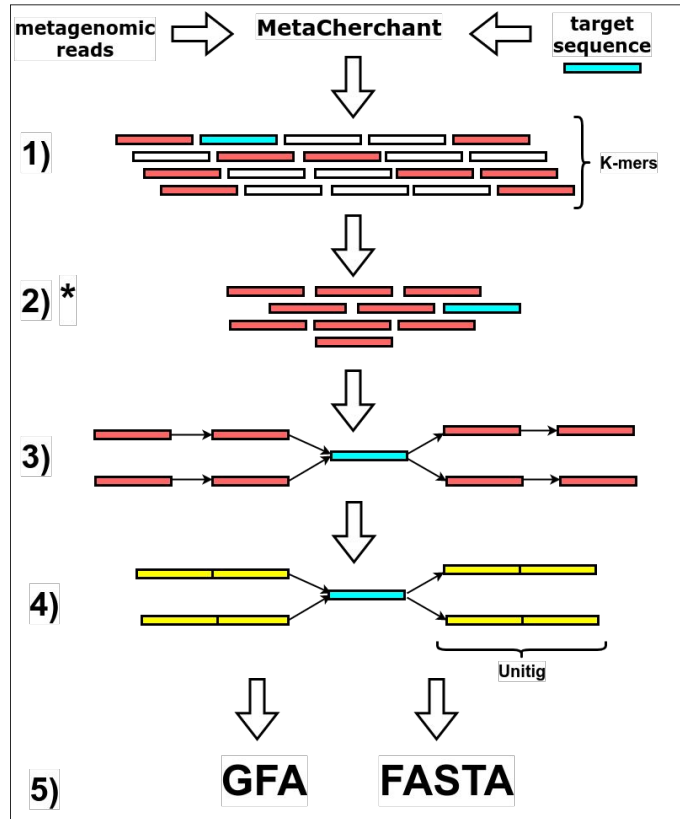


Граф геномной сборки
Enterococcus faecium в программе
SPAdes



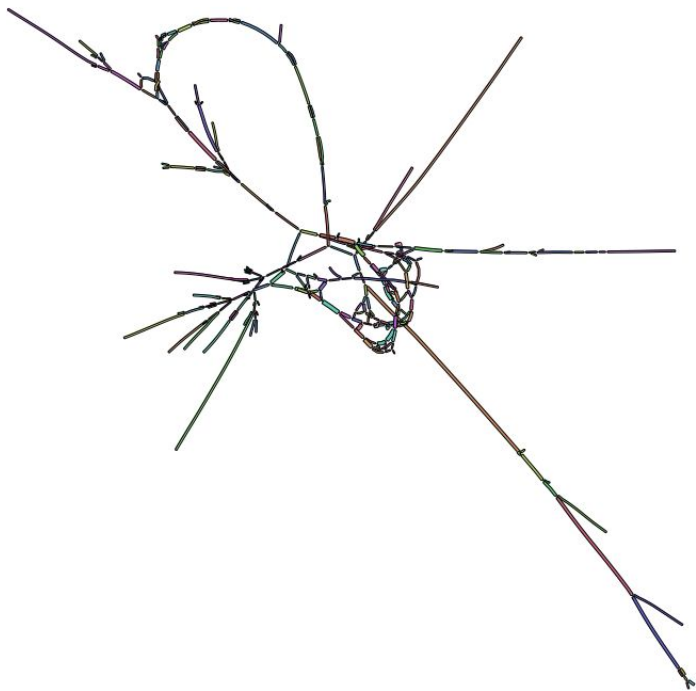
Часть графа метагеномной сборки в
программе SPAdes

Basic MetaCherchant workflow (environment-finder tool)

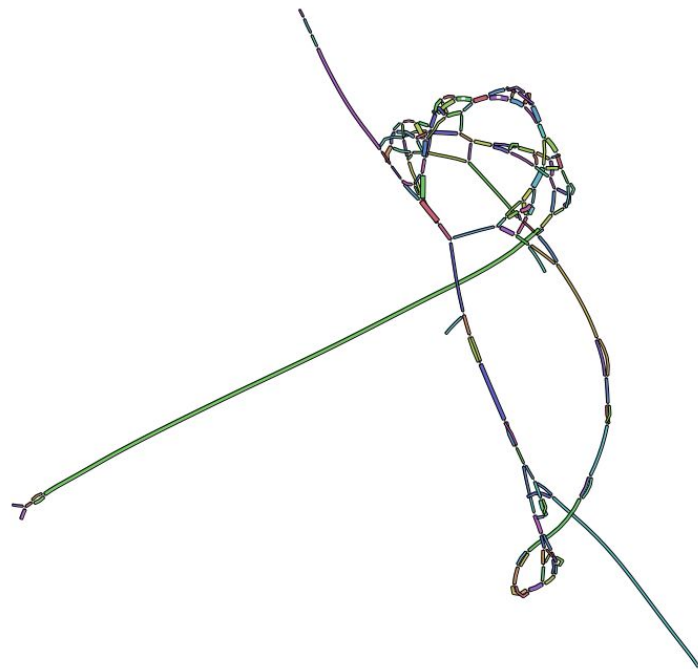


<https://github.com/ctlab/metacherchant>

--trim function

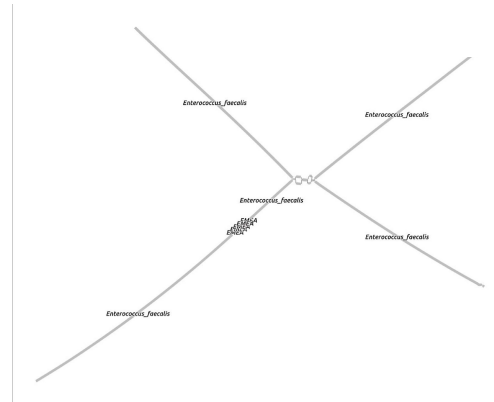
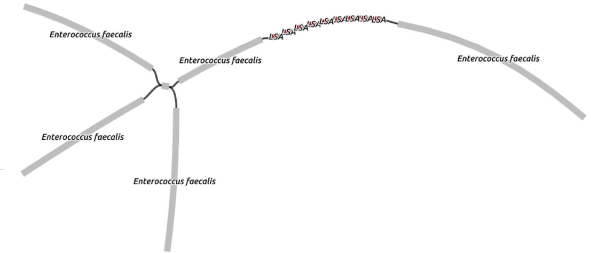
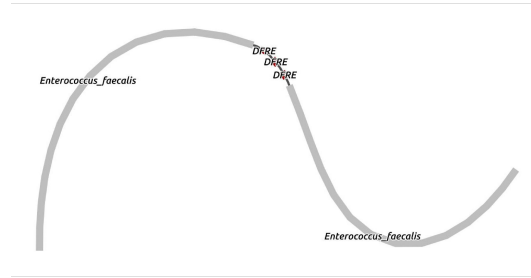
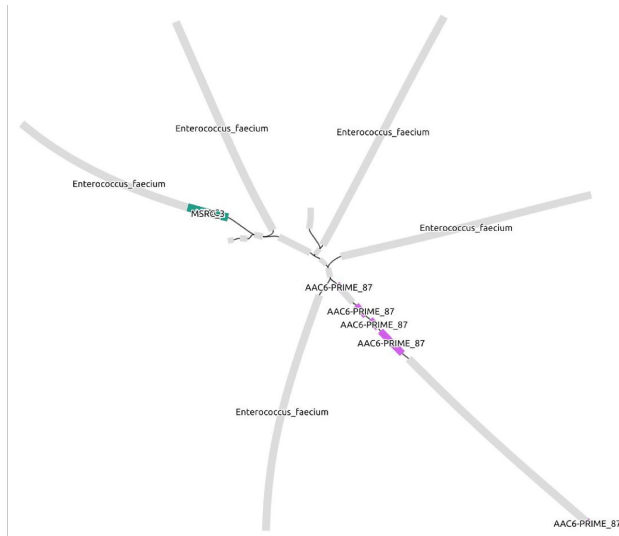


ДО

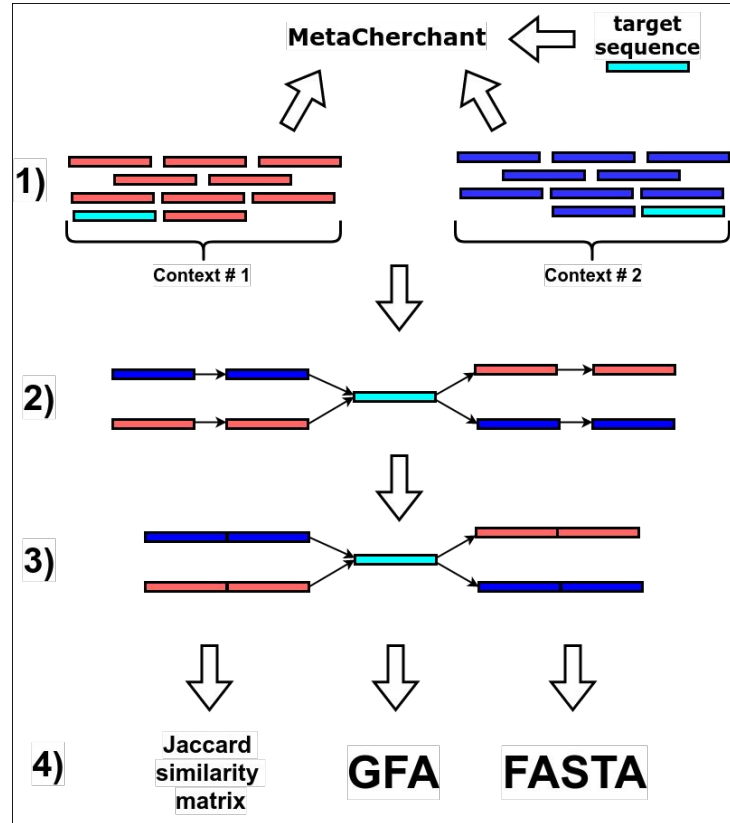


ПОСЛЕ

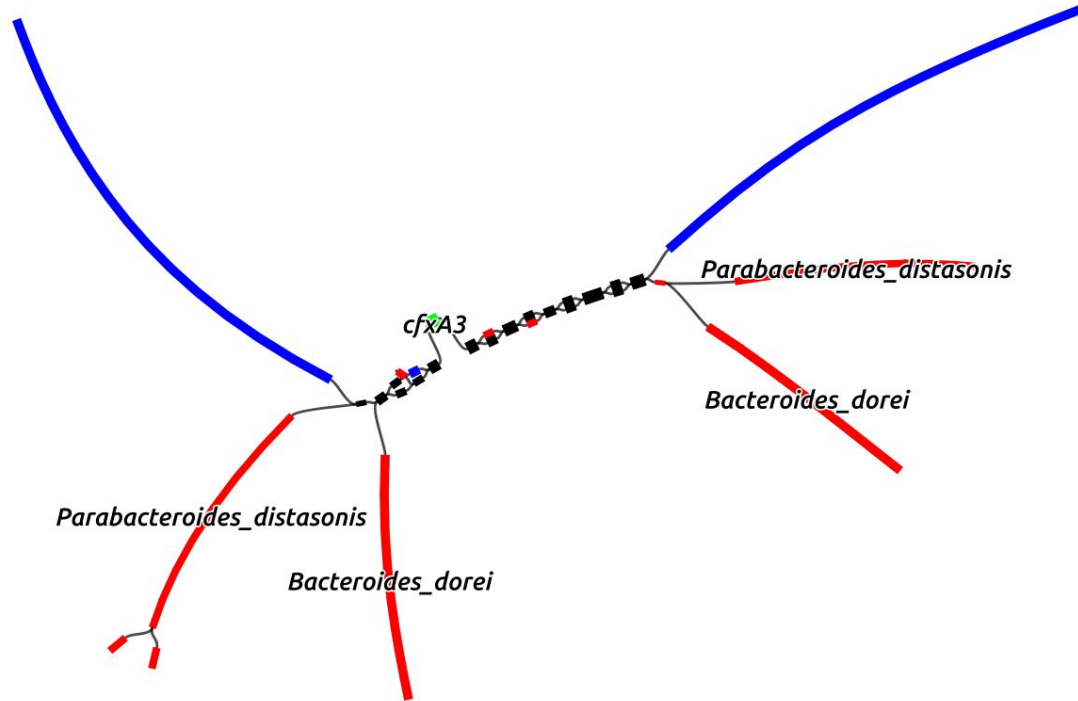
Анализ окружения генов резистентности к антибиотикам



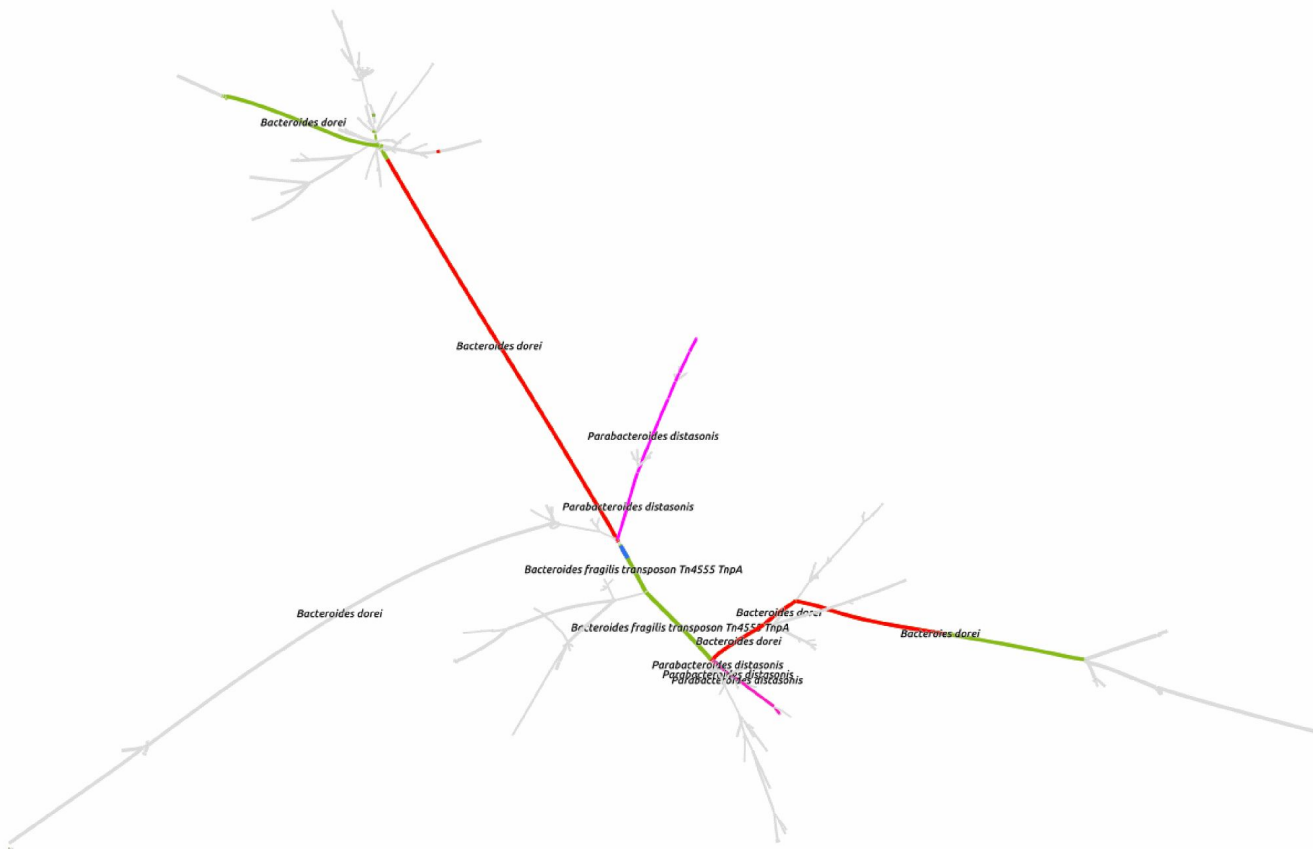
environment-finder multi tool



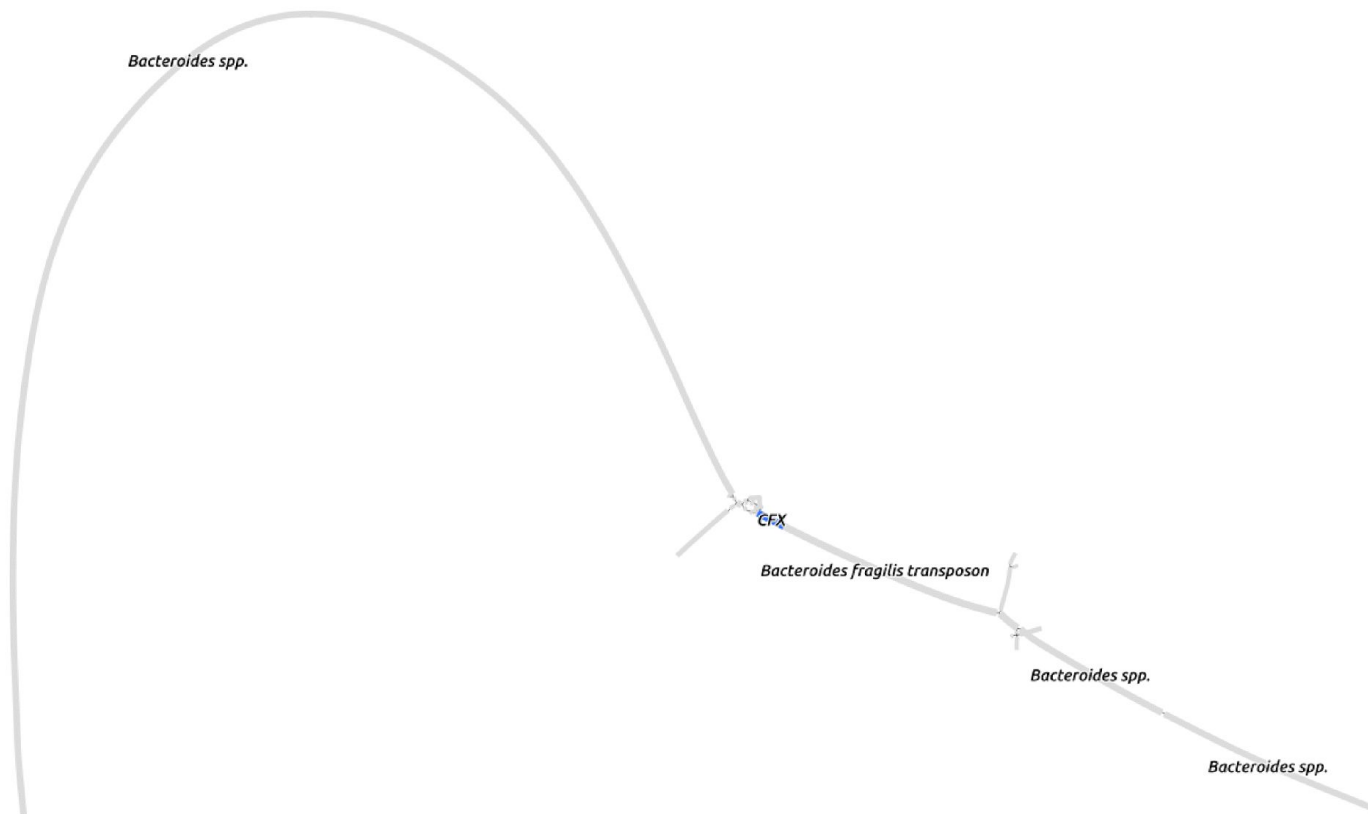
Гипотетический горизонтальный перенос транспозона с геном *cfxA3* между представителями *Bacteroides* spp.



Сравнение со SPAdes v.1

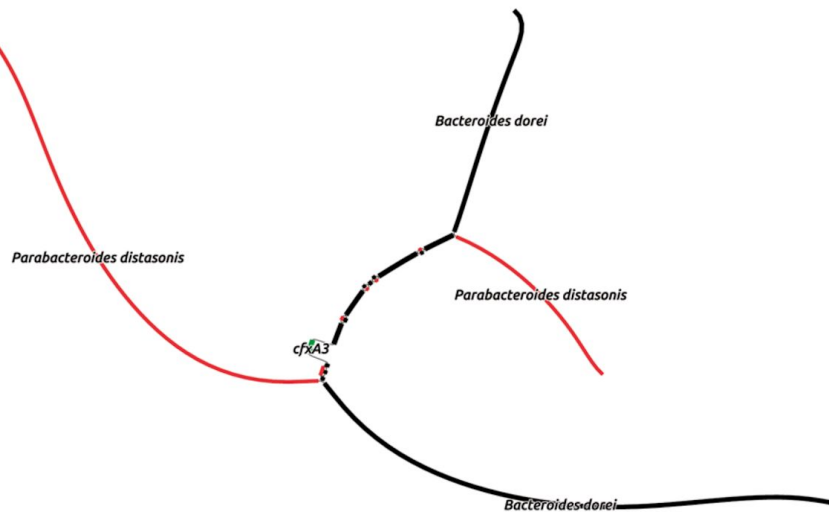


Сравнение со SPAdes v.2

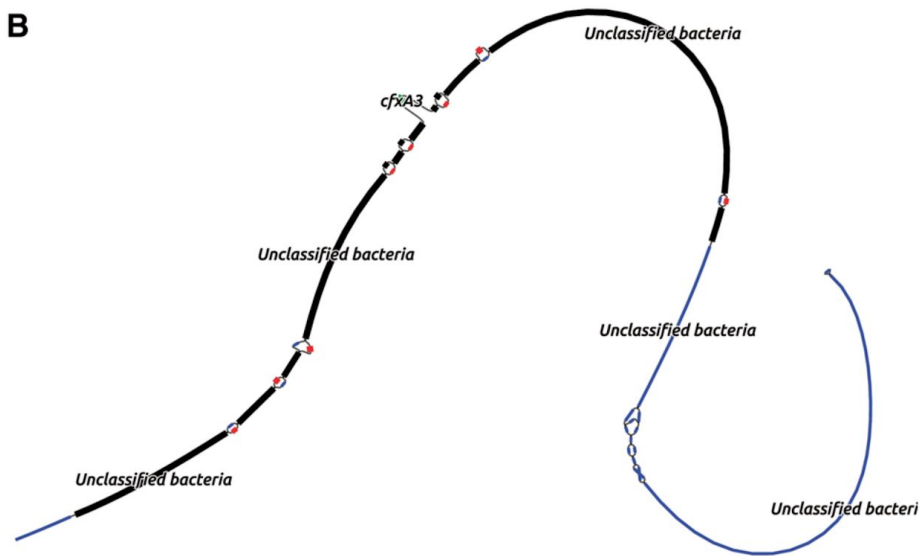


Сравнение со SPAdes v.3

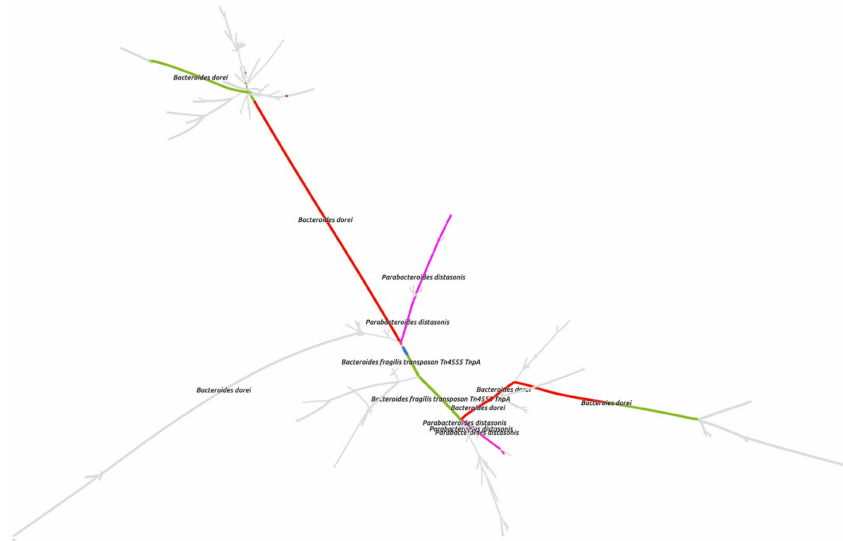
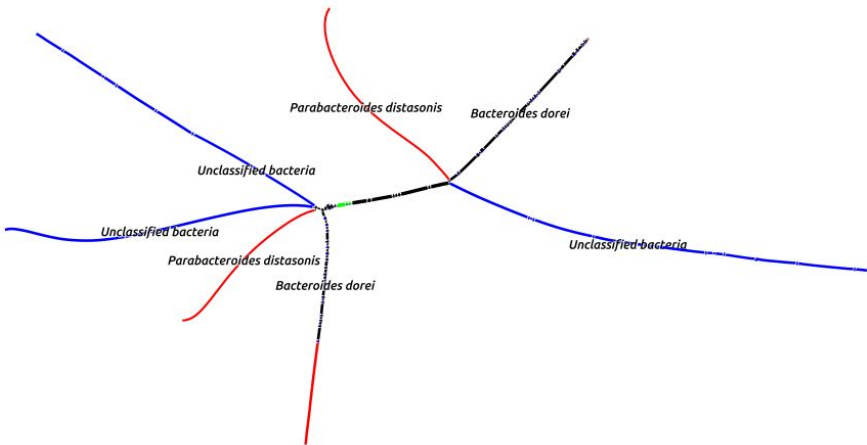
A

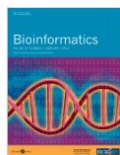


B



Если подпилить настройки





Volume 34, Issue 3

01 February 2018

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Acknowledgement

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Supplementary data

Comments (0)

MetaCherchant: analyzing genomic context of antibiotic resistance genes in gut microbiota

Evgenii I Olekhovich, Artem T Vasilyev, Vladimir I Ulyantsev ✉, Elena S Kostryukova, Alexander V Tyakht [Author Notes](#)

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<https://doi.org/10.1093/bioinformatics/btx681>

Published: 28 October 2017 [Article history ▼](#)

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Abstract

Motivation

Antibiotic resistance is an important global public health problem. Human gut microbiota is an accumulator of resistance genes potentially providing them to pathogens. It is important to develop tools for identifying the mechanisms of how resistance is transmitted between gut microbial species and pathogens.

Results

We developed MetaCherchant—an algorithm for extracting the genomic environment of antibiotic resistance genes from metagenomic data in the form of a graph. The algorithm was validated on a number of simulated and published datasets, as well as applied to new ‘shotgun’ metagenomes of gut microbiota from patients with *Helicobacter pylori* who underwent antibiotic therapy. Genomic context was reconstructed for several major resistance genes.



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P-VALUE < 0.05?



DATA ANALYSIS COMPLETE!

memegenerator.net

Dissimilarity of k -mer frequency spectra between multiple metagenomic datasets calculated for two genes- CFX (A) and APH3-Prime (B) (Jaccard metric, non-metric MDS).

