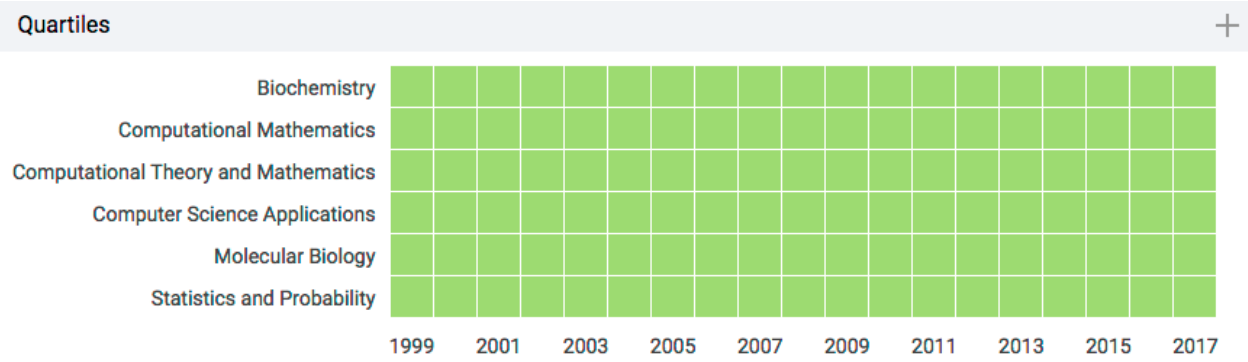
Данные о журнале

Журнал ***Bioinformatics***, издается Oxford University Press (с 1985 под названием Computer Applications in the Biosciences, с 1998 под текущим названием).

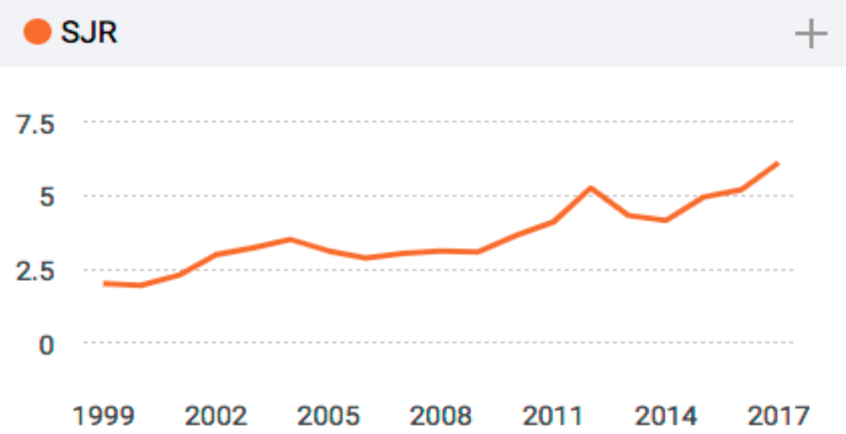
По данным Clarivate Analytics (*на текущий год / на год публикации представленных на конкурс работ*)
https://academic.oup.com/bioinformatics/pages/About
импакт-фактор 5.481 / 7.307
место по направлению Mathematical & Computational Biology: 3 / 2 из 59 / 57 журналов
место по направлению Biochemical Research Methods: 6 / 4 из 78 / 77 журналов
место по направлению Biotechnology & Applied Microbiology: 17 / 11 из 160 / 158 журналов

По данным SJR
https://www.scimagojr.com/journalsearch.php?q=17945&tip=sid&clean=0

Квартиль (зеленый -- Q1)

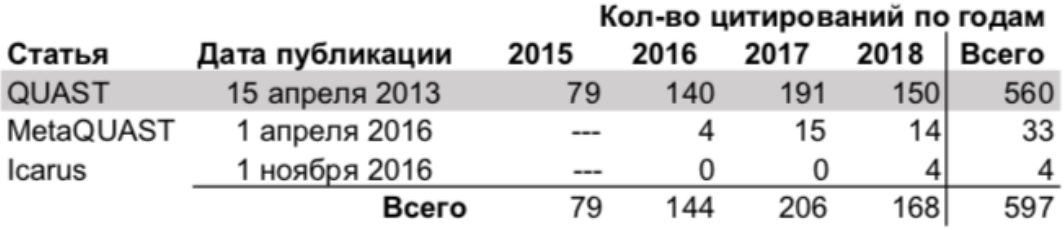


SJR индекс (6.14 за 2017 год)



Данные о цитировании

По данным Web of Science Core Collection на 1 октября 2018 года (общее число цитирований работ о пакете программ QUAST: 597)

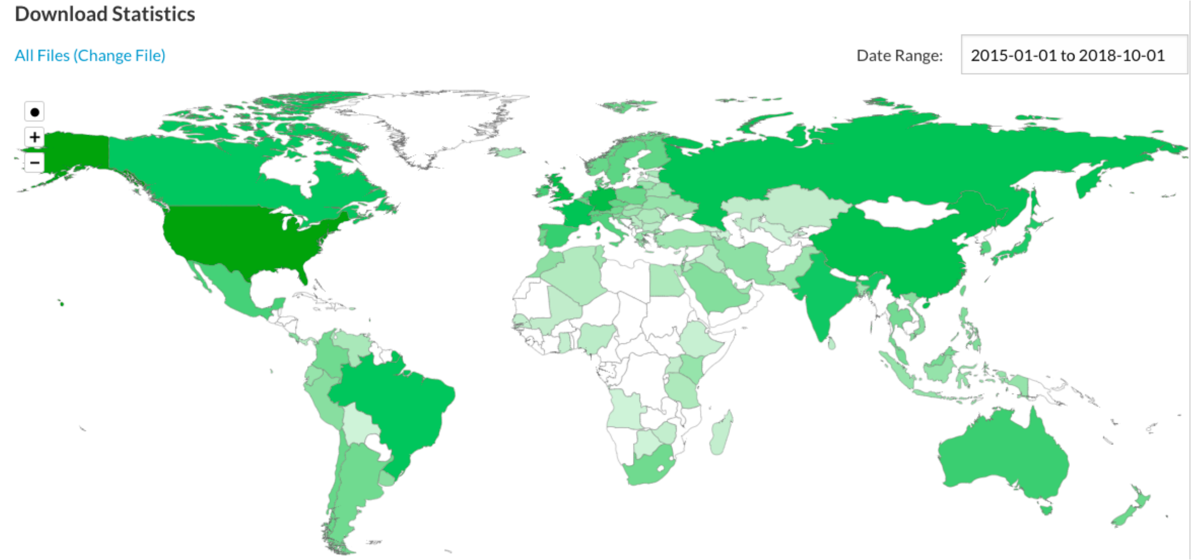


		Кол-во цитирований по годам				
Статья	**Дата публикации**	**2015**	**2016**	**2017**	**2018**	**Всего**
QUAST	15 апреля 2013	79	140	191	150	560
MetaQUAST	1 апреля 2016	---	4	15	14	33
Icarus	1 ноября 2016	---	0	0	4	4
	Всего	79	144	206	168	597

Примечание: статья про QUAST (Gurevich et al., 2013) не выдвигается на конкурс (выполнена не в СПбГУ), но указаны цитаты на нее начиная с 2015 года, т.к. она используется при цитировании всего пакета программ QUAST (выдвинут на конкурс). В 2015 году Гуревичем А.А. и Михеенко А.А. была начата работа над пакетом QUAST в СПбГУ, что вылилось в значительный рост количества цитирований данного программного продукта (с 2016 в Реестре программ для ЭВМ, правообладатель: СПбГУ).

Данные об использовании

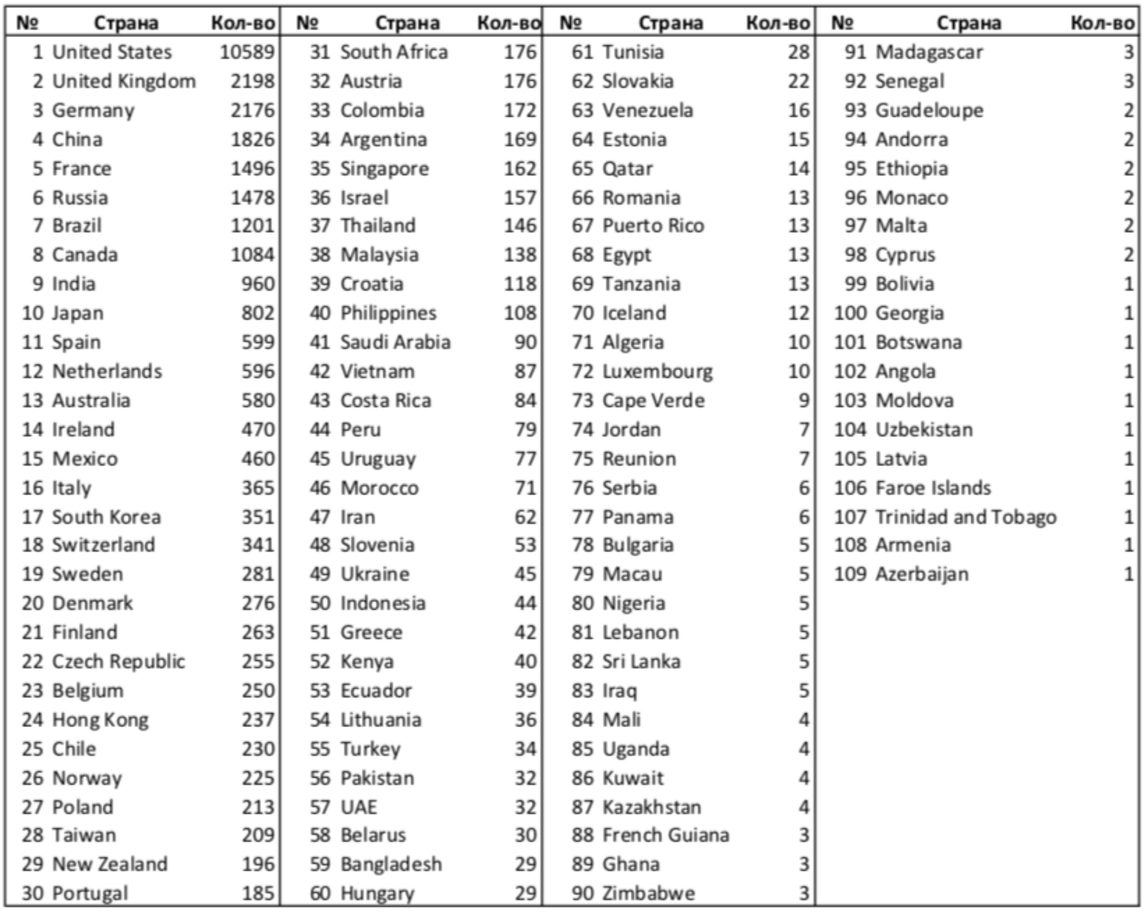
По данным платформы Sourceforge с 1 января 2015 по 1 октября 2018 (общее число загрузок с учетом случаев, когда страна загрузки не определена: 33 290)
https://sourceforge.net/projects/quast/files/stats/map?dates=2015-01-01+to+2018-10-01



Download Statistics

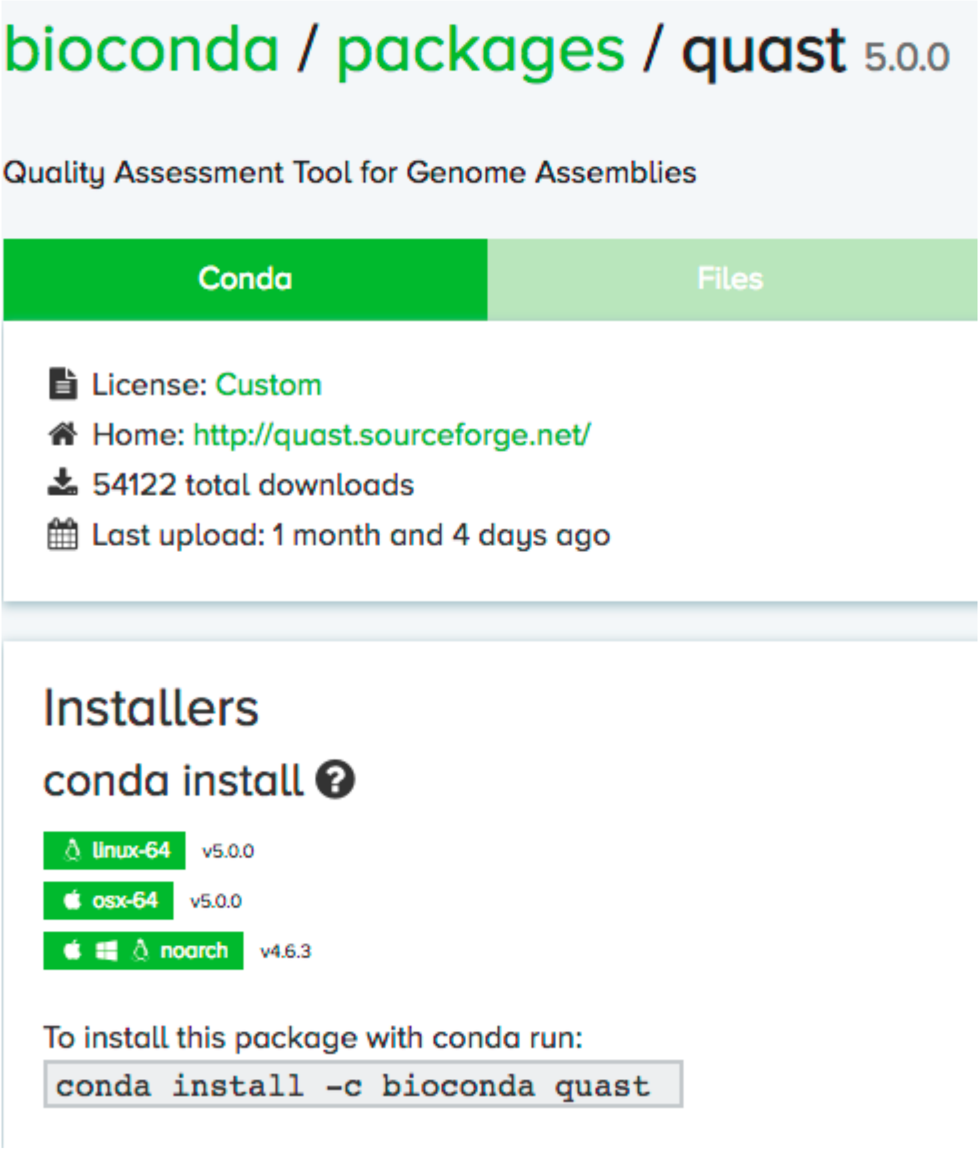
All Files (Change File)

Date Range: 2015-01-01 to 2018-10-01



№	Страна	Кол-во	№	Страна	Кол-во	№	Страна	Кол-во	№	Страна	Кол-во
1	United States	10589	31	South Africa	176	61	Tunisia	28	91	Madagascar	3
2	United Kingdom	2198	32	Austria	176	62	Slovakia	22	92	Senegal	3
3	Germany	2176	33	Colombia	172	63	Venezuela	16	93	Guadeloupe	2
4	China	1826	34	Argentina	169	64	Estonia	15	94	Andorra	2
5	France	1496	35	Singapore	162	65	Qatar	14	95	Ethiopia	2
6	Russia	1478	36	Israel	157	66	Romania	13	96	Monaco	2
7	Brazil	1201	37	Thailand	146	67	Puerto Rico	13	97	Malta	2
8	Canada	1084	38	Malaysia	138	68	Egypt	13	98	Cyprus	2
9	India	960	39	Croatia	118	69	Tanzania	13	99	Bolivia	1
10	Japan	802	40	Philippines	108	70	Iceland	12	100	Georgia	1
11	Spain	599	41	Saudi Arabia	90	71	Algeria	10	101	Botswana	1
12	Netherlands	596	42	Vietnam	87	72	Luxembourg	10	102	Angola	1
13	Australia	580	43	Costa Rica	84	73	Cape Verde	9	103	Moldova	1
14	Ireland	470	44	Peru	79	74	Jordan	7	104	Uzbekistan	1
15	Mexico	460	45	Uruguay	77	75	Reunion	7	105	Latvia	1
16	Italy	365	46	Morocco	71	76	Serbia	6	106	Faroe Islands	1
17	South Korea	351	47	Iran	62	77	Panama	6	107	Trinidad and Tobago	1
18	Switzerland	341	48	Slovenia	53	78	Bulgaria	5	108	Armenia	1
19	Sweden	281	49	Ukraine	45	79	Macau	5	109	Azerbaijan	1
20	Denmark	276	50	Indonesia	44	80	Nigeria	5			
21	Finland	263	51	Greece	42	81	Lebanon	5			
22	Czech Republic	255	52	Kenya	40	82	Sri Lanka	5			
23	Belgium	250	53	Ecuador	39	83	Iraq	5			
24	Hong Kong	237	54	Lithuania	36	84	Mali	4			
25	Chile	230	55	Turkey	34	85	Uganda	4			
26	Norway	225	56	Pakistan	32	86	Kuwait	4			
27	Poland	213	57	UAE	32	87	Kazakhstan	4			
28	Taiwan	209	58	Belarus	30	88	French Guiana	3			
29	New Zealand	196	59	Bangladesh	29	89	Ghana	3			
30	Portugal	185	60	Hungary	29	90	Zimbabwe	3			

По данным системы управления пакетами биоинформатических программ bioconda с 1 января 2015 по 1 октября 2018 (общее число загрузок: 54 122)
https://anaconda.org/bioconda/quast



bioconda / packages / quast 5.0.0

Quality Assessment Tool for Genome Assemblies

License: Custom
Home: http://quast.sourceforge.net/
54122 total downloads
Last upload: 1 month and 4 days ago

Installers

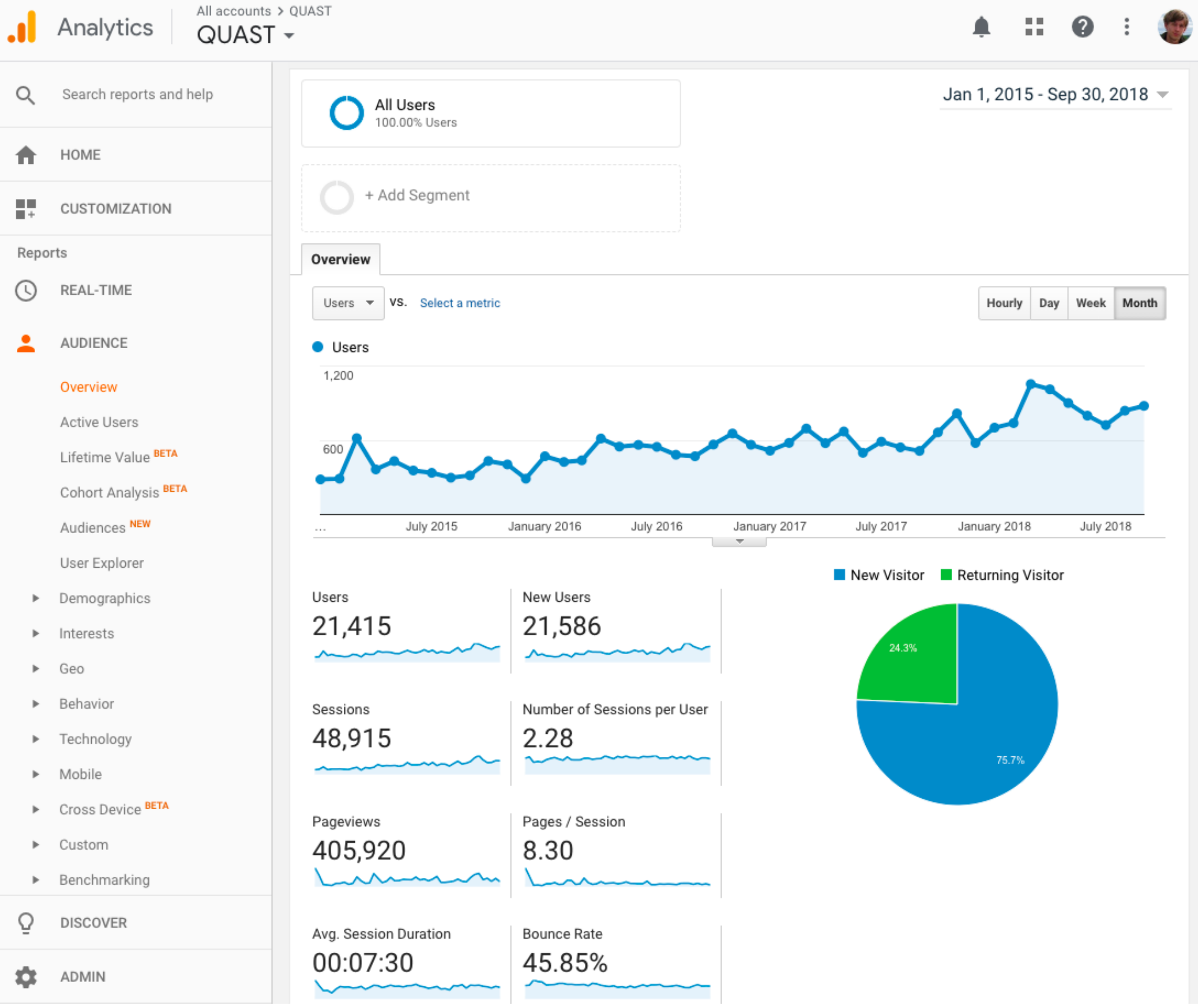
conda install

linux-64 v5.0.0
osx-64 v5.0.0
noarch v4.6.3

To install this package with conda run:

```
conda install -c bioconda quast
```

По данным Google Analytics с 1 января 2015 по 30 сентября 2018 (общее количество посетителей веб-сервиса QUAST http://quast.sf.net/wi 21 415 пользователей)



Jan 1, 2015 - Sep 30, 2018

Users
21,415

New Users
21,586

Sessions
48,915

Number of Sessions per User
2.28

Pageviews
405,920

Pages / Session
8.30

Avg. Session Duration
00:07:30

Bounce Rate
45.85%

Рецензии/обзоры в журналах Scopus/Web of Science

Florian P. Breitwieser Jennifer Lu Steven L. Salzberg. (2017). A review of methods and databases for metagenomic classification and assembly. *Briefings in Bioinformatics*, bbx120. https://doi.org/10.1093/bib/bbx120

Фрагмент из статьи:

> Validation of the assembly and binning is an important step in metagenomic genome reconstruction. **MetaQUAST** [128] computes genome statistics of metagenomics assemblies, and, by aligning against reference genomes, can report the number of misassemblies and mismatches.

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Blawid, R. , Silva, J. and Nagata, T. (2017). Discovering and sequencing new plant viral genomes by next-generation sequencing: description of a practical pipeline. *Annals of Applied Biology*, 170: 301-314. https://doi.org/10.1111/aab.12345

Фрагменты из статьи:

> With a variety of pipelines, tools and even parameters of tools, many assembly outcomes are possible, and the improvement of the analysis is of great interest. NGS metrics might be useful for assessing the assembly quality, although it is not a straightforward task. The **QUAST** (Gurevich et al., 2013) and **MetaQUAST** (Mikheenko et al., 2015) programmes are options to assess and compare the quality of our assemblies. Contig size is one of the metrics that can be evaluated for de novo assembly with or without a reference genome.
>
> …
>
> **MetaQUAST** also generates other valuable metrics as the NA50 and NGA50. These metrics are obtained by breaking the contigs mapped to a reference into aligned blocks and calculating the N50 and NG50 using only these blocks. SPAdes also often gives the highest value of NG50 and NGA50, as shown for our case study with all segments of ZLCV (Table 5).
>
> **MetaQUAST** supports more than one reference sequence and calculates the reference-based statistics separately for each sequence.

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Sebastian Jünemannac et al. (2017). Bioinformatics for NGS-based metagenomics and the application to biogas research. *Journal of Biotechnology*, 261: 10-23. https://doi.org/10.1016/j.jbiotec.2017.08.012

Фрагмент из статьи:

> A dedicated software that calculates various metrics to evaluate metagenome assemblies is **MetaQUAST** (Mikheenko et al., 2016), a modification of the genome assembly evaluation tool **QUAST** (Gurevich et al., 2013). Besides common metrics (e.g. N50), it provides a reference based evaluation to identify mis-assemblies by mapping contigs to references and reporting statistics for each reference separately. If, as usual, the references are not known a priori, a de novo evaluation can be performed, where appropriate references are identified on the basis of BLASTn hits of contigs against 16S rRNA gene references of the SILVA database and thereafter downloaded from NCBI.

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Nathan D. Olson, Todd J. Treangen, Christopher M. Hill, Victoria Cepeda-Espinoza, Jay Ghurye, Sergey Koren, Mihai Pop. (2017). Metagenomic assembly through the lens of validation: recent advances in assessing and improving the quality of genomes assembled from metagenomes, *Briefings in Bioinformatics*, bbx098. https://doi.org/10.1093/bib/bbx098

Фрагмент из статьи:

> MetaQuast. **MetaQUAST** [11] is a reference-based method that identifies mis-assemblies and structural variants in an assembly relative to reference genomes. **MetaQUAST** is a modification of **QUAST** [86], an isolate genome assembly validation tool that computes alignments of assembled contigs to a single reference genome. For data sets with known reference genomes, **metaQUAST** uses the user-provided reference sequences to evaluate the assembly. For the data sets where genomes in the sample are not known, metaQUAST identifies appropriate reference sequences using a 16 S ribosomal RNA database. Additionally, **metaQUAST** applies a structural variant finding algorithm to distinguish between structural variants and true assembly errors.

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Roumpeka Despoina D., Wallace R. John, Escalettes Frank, Fotheringham Ian, Watson Mick. (2017). A Review of Bioinformatics Tools for Bio-Prospecting from Metagenomic Sequence Data. *Frontiers in Genetics*, 8. https://doi.org/10.3389/fgene.2017.00023

Фрагмент из статьи:

> There are some standard statistical measures for evaluating the performance of assembly tools. These often refer to the number of scaffolds, their length, cover rate (the proportion of the genome covered by assembled scaffolds) and gene prediction/completeness (using gene predictors in later stage). One of the most useful assembly measures is the N50 size, defined as the scaffold length value such that 50% of the assembled sequences are equal or longer (Mäkinen et al., 2012). Contig and scaffold lengths are particularly important metrics for bio-prospecting as these need to be longer than gene-length to enable full length recovery of the gene sequence. **MetaQUAST** (Mikheenko et al., 2016) is a tool specifically designed for the quality assessment of metagenomics assemblies. Amongst other things, **MetaQUAST** uses alignment of the original reads to the assembled data to enable detection of putative structural variants and mis-assemblies.