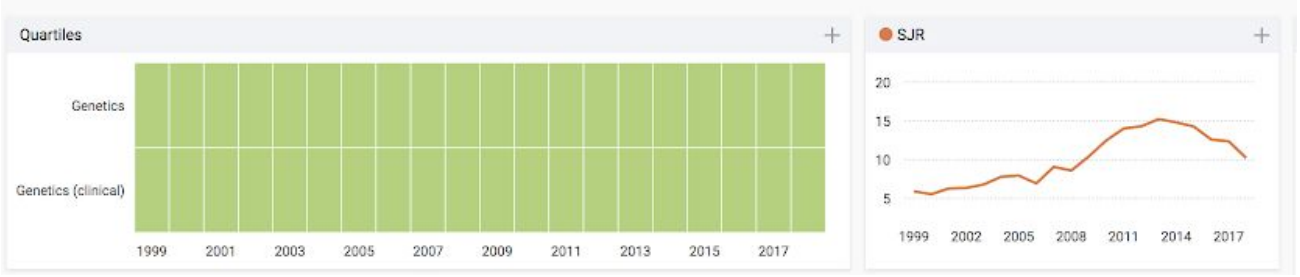
Данные о журнале

Журнал **Genome Research**, издается Cold Spring Harbor Laboratory Press (с 1991 под названием “PCR Methods and Applications”, с 1995 под текущим названием).

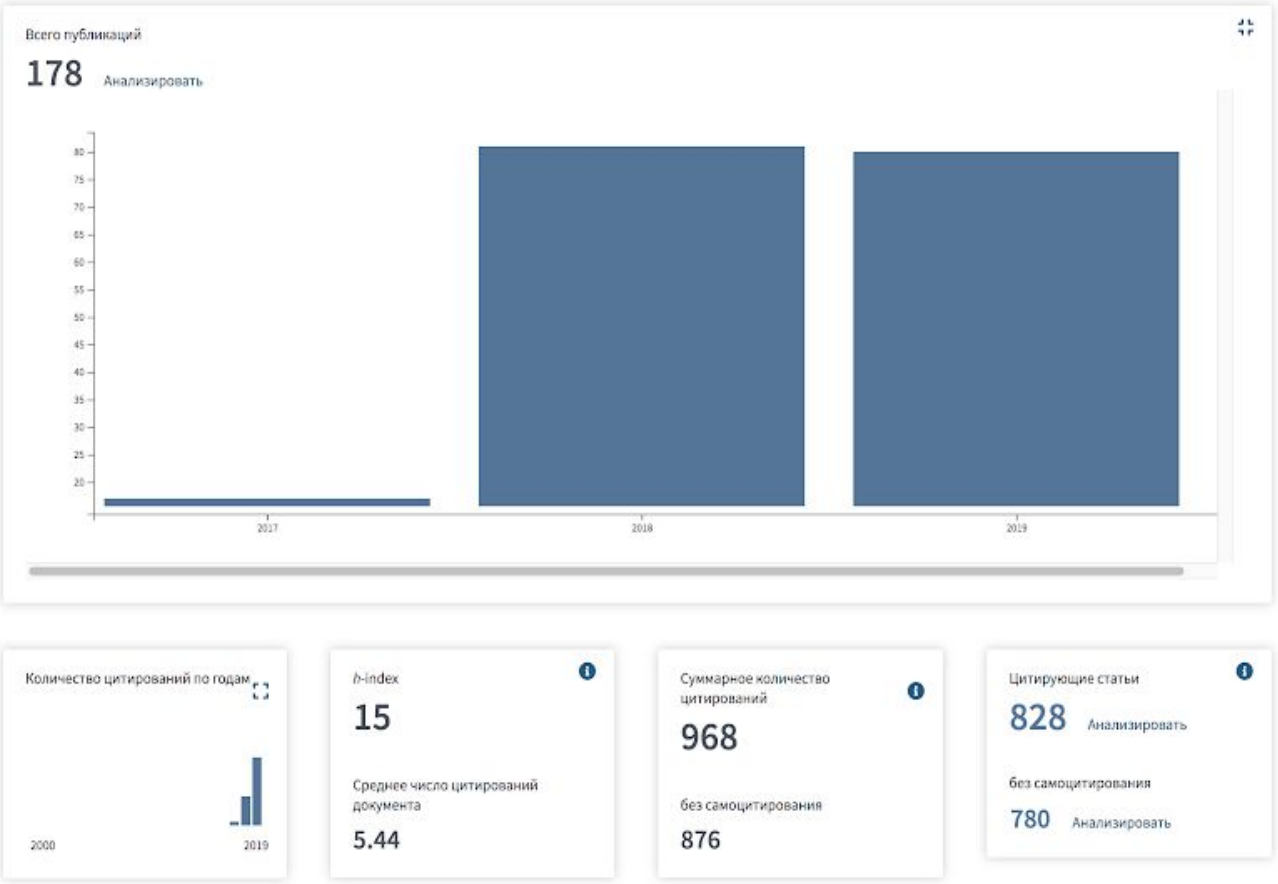
По данным SJR :
импакт-фактор 10.1 (2017 - год публикации)
место по направлению Genetics: 5 из 343 журналов
Квартиль (зеленый -- Q1)



SJR индекс (12.367 за 2017 год)

Данные о цитировании

По данным Web of Science Core Collection на 1 сентября 2019 года - 178.



Рецензии/обзоры в журналах Scopus/Web of Science

Forouzan E, Shariati P, Maleki MS, Karkhane AA, Yakhchali B. Practical evaluation of 11 de novo assemblers in metagenome assembly. Journal of microbiological methods. 2018 Aug 1;151:99-105.

Next Generation Sequencing (NGS) technologies are revolutionizing the field of biology and metagenomic-based research. Since the volume of metagenomic data is typically very large, *De novo* metagenomic assembly can be effectively used to reduce the total amount of data and enhance quality of downstream analysis, such as annotation and binning. Although, there are many freely available assemblers, but selecting one suitable for a specific goal can be highly challenging. In this study, the performance of 11 well-known assemblers was evaluated in the assembly of three different metagenomes. **The results obtained show that metaSPAdes is the best assembler** and Megahit is a good choice for conservative assembly strategy. In addition, this research provides useful information regarding the pros and cons of each assembler and the effect of read length on assembly, thereby helping scholars to select the optimal assembler based on their objectives.

Quince C, Walker AW, Simpson JT, Loman NJ, Segata N. Shotgun metagenomics, from sampling to analysis. Nature biotechnology. 2017 Sep;35(9):833.

The CAMI challenge reported that MEGAHIT was in the top three metagenomics assemblers across their benchmark data sets (C.Q.) and, together with **metaSPAdes (not evaluated in CAMI), is probably the best current choice.** Whatever assembler is used, the result will not be genomes but rather potentially millions of contigs, and this motivates the need for binners to link the contigs back to the genomes they derived from.

Greenwald WW, Klitgord N, Seguritan V, Yooseph S, Venter JC, Garner C, Nelson KE, Li W. Utilization of defined microbial communities enables effective evaluation of meta-genomic assemblies. BMC genomics. 2017 Dec;18(1):296.

We tested five metagenomic assemblers: Omega, metaSPAdes, IDBA-UD, metaVelvet and MEGAHIT on known and synthetic metagenomic data sets. **MetaSPAdes excelled in diverse sets**, IDBA-UD performed well all around, metaVelvet had high accuracy in high abundance organisms, and MEGAHIT was able to accurately differentiate similar organisms within a community. **At the ORF level, metaSPAdes and MEGAHIT had the least number of missing ORFs within diverse and similar communities respectively.**