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xcelris NEWSBYTES

Volume-IV, December-2015

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About Xcelris

Xcelris Labs Limited is a life sciences based innovative research organization delivering solutions across domains such as Agriculture, Environmental Genetics, Animal science, Nutrition and Human health. We operate through two key divisions i.e Genomics and Medical Genetics. At Xcelris Genomics Division, we partner with more than 1000 research institutions across India and world to provide key services like Sanger Sequencing, Next Generation Sequencing, Molecular Biology kits and Oligo synthesis. In a span of 10 years, we have completed 15,000+ sequencing projects and 1000+ Next Generation Sequencing projects. Through our Xcelris Medical Genetics (XMDx) division we offer genetic testing service based on Sequencing for cancer diagnosis and therapy selection, infectious diseases and inherited genetic disorders in humans.

Key People

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Chandan Badapanda
Sr. Scientist, Bioinformatics

"Metagenomics: Tools for Analyzing NGS data derived from Biodiversity studies"

by Mr. Chandan Badapanda

What is Metagenomics?

Metagenomics refers to the study of genomic DNA obtained from microorganisms that cannot be cultured in the laboratory.

Significance of Metagenomics study:

The challenge that has frustrated microbiologists for decades is how to access the microorganisms that cannot be cultured in the laboratory and Metagenomics provides an additional set of tools to study uncultured species. Cracking the secrets of some of Earth's countless microbial communities will reveal ways to meet myriad challenges in biomedicine, agriculture, and environmental stewardship.

Method of Sequencing:

Metagenomics entails extraction of DNA from a community so that all the genomes of organisms in the community are pooled. These genomes are usually fragmented and cloned in to an organism that can be cultured to create 'Metagenomic libraries', and these libraries are then subjected to analysis based on DNA sequence or on functions on DNA sequence on the surrogate host by the metagenomic DNA. Two commonly used NGS technologies utilized to date are the 454 Life Sciences and the Illumina systems, with the ratio of usage shifting in favor of the latter recently. In Xcelris, we have Illumina platform for the sequencing of Metagenomic libraries.

Bioinformatics analysis:

(I) Metagenome analysis: De novo assembly of high quality PE reads can be accomplished using CLC Genomics Workbench/MetaVelvet/SOAPdenovo to generate contigs. From these contigs, rRNA is predicted through WebMGA (http://weizhonglab.ucsd.edu/metagenomic-analysis/server/)using hmm_rRNA algorithm or through RNAmmer, and those contigs which do not contain rRNA is subjected for ORFs(Open Reading Frames) predictions through Prodigal (v2.6.1). In the end the predicted rRNA containing contigs along with ORFs is uploaded into MGRAST web server for functional annotations. In addition to this, the predicted ORFs are subjected to Blastx annotation against NCBI 'nr' database and later on parsed into MEGAN (MEtaGENOME Analyzer).

(ii) 16S rRNA based analysis: The high quality PE data is stitched and the stiched 16S reads are submitted to MGRAST Web server for taxonomic assignments process. We have also QIIME (Quantitative Insights Into Microbial Ecology; http://qiime.org/), a standalone software for analysis of 16S sequencing data. QIIME is comprehensive software comprising of tools and algorithms (Caporaso et al., 2010) such as blast for picking out OTU's and assigning taxonomy (Altschul et al, 1990); pynast for aligning sequences (Caporaso et al, 2010); and greengenes database of 16S rRNA sequences was used as reference for the assignment of taxonomic data (DeSantis et al, 2006).

Bioinformatics Analysis

Workflow of Metagenomics

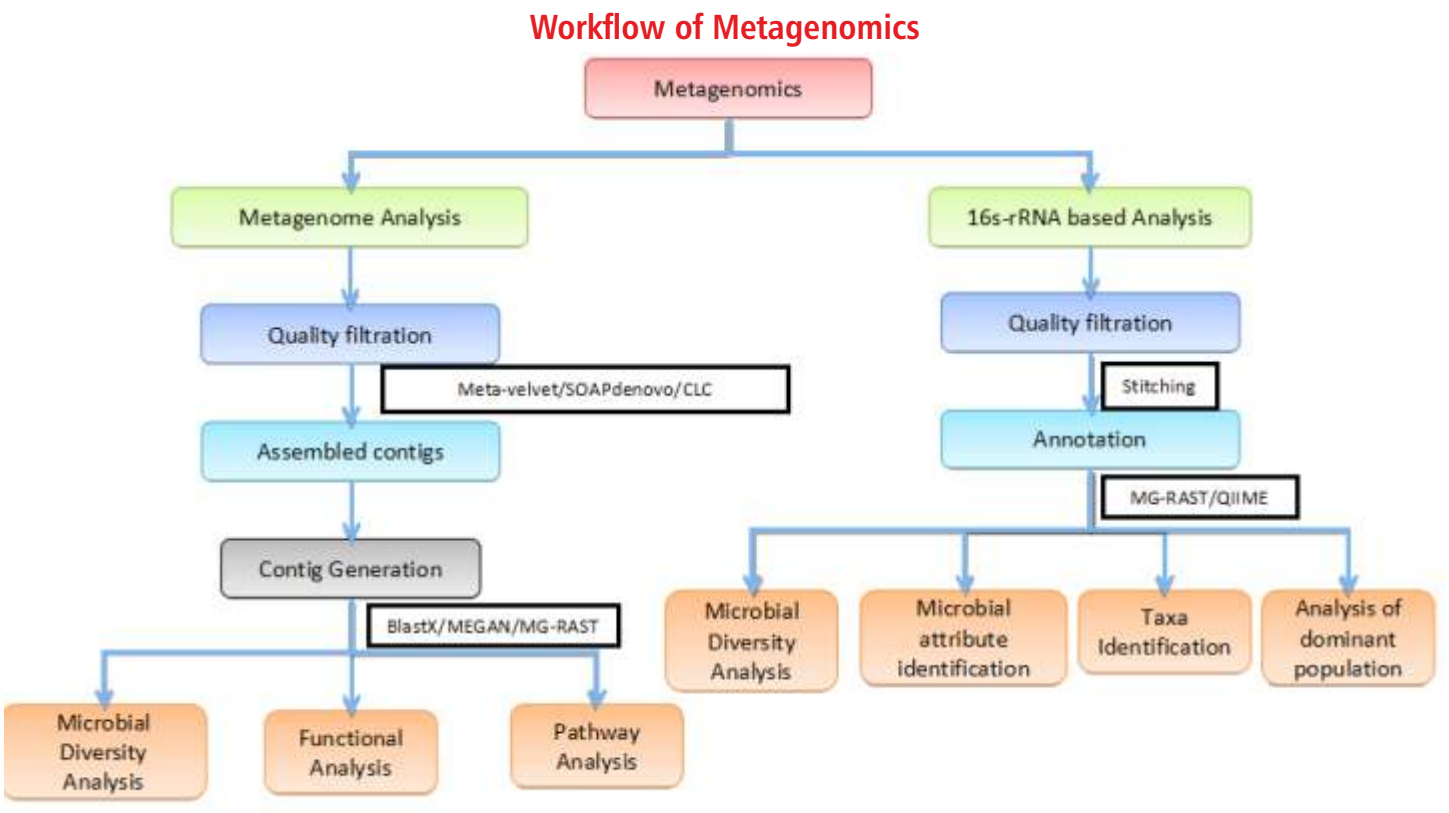

Table 1- Comparison between MGRAST and QIIME for 16s data analysis.

	Availability	Analysis time	16S detection method	Diversity analysis	Ease of Use	Taxonomic assignment
MGRAST	Web based	Min.2weeks per sample	Alignment with BLAT	Only alpha diversity	Very simple GUI	
QIIME	Standalone	2hrs per sample	OTU picking	Alpha and beta diversity	Requires skill	Up to genus level

Chandan Badapanda (Sr. Scientist, Bioinformatics)

Mr. Chandan heads the Bioinformatics Dept. at Xcelris Labs. He has more than 11 years of research and industrial experiences both at National and International level on Next Generation Sequence (NGS) data analysis, Immunoinformatics study for vaccine design, Biological database development, Biodiversity-informatics, statistical data analysis, Agricultural Bioinformatics, patent filing etc. He also has an expertise in Bioinformatics, IT-Architecture, Cloud platforms and recently he has published one book chapter on "Natural Antibiotics and its therapeutic potential for biotechnology industry".

Next article

Dr. Prashanth Bagali

Emerging technologies in the management and understanding of complex hereditary diseases.

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