Bioinformatics up to Date

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About us

The Bioinformatics Infrastructure Facility (BIF) at Biotechnology division, CSIR NEIST, Jorhat runs under the Biotechnology Information System Network (BTISnet) programme of DBT, Ministry of Science & Technology, and Government of India. The Centre was established on 2nd February, 2008 to promote innovation in Biological research and education through Bioinformatics accomplishment. The main goal is to facilitate and expose students and researchers from different academic institutions of North East India in Bioinformatics. The center conduct training and workshops for enlightening the use of bioinformatics applications in biological research and development. The Centre has access to global information through 24 hour high speed internet facility, and also e-journal facilities with DeLCON, Science Direct etc. To date the Centre has profoundly extended support in R & D work with a great intensity to different biological discipline including medicinal chemistry, computer aided drug design, genomics and proteomic data analysis etc.

Analyzing gut microbiota and host biomarkers

Now a days, there is a urgency for large-scale, longitudinal studies to determine the mechanisms by which the gut microbiome and its cooperation with the host affect human health and disease. Current procedure for profiling the microbiome commonly handle the NGS approach that are expensive, slow performance and complicated. Melissa K. Takahashi et al., present a fabricated biology platform for low-cost, economical, on-demand and simple analysis of microbiome samples using RNA toehold switch sensors in paper-based, cell-free reactions. Researchers were indicated that species-specific detection of mRNAs from 10 different bacteria that affect human health.
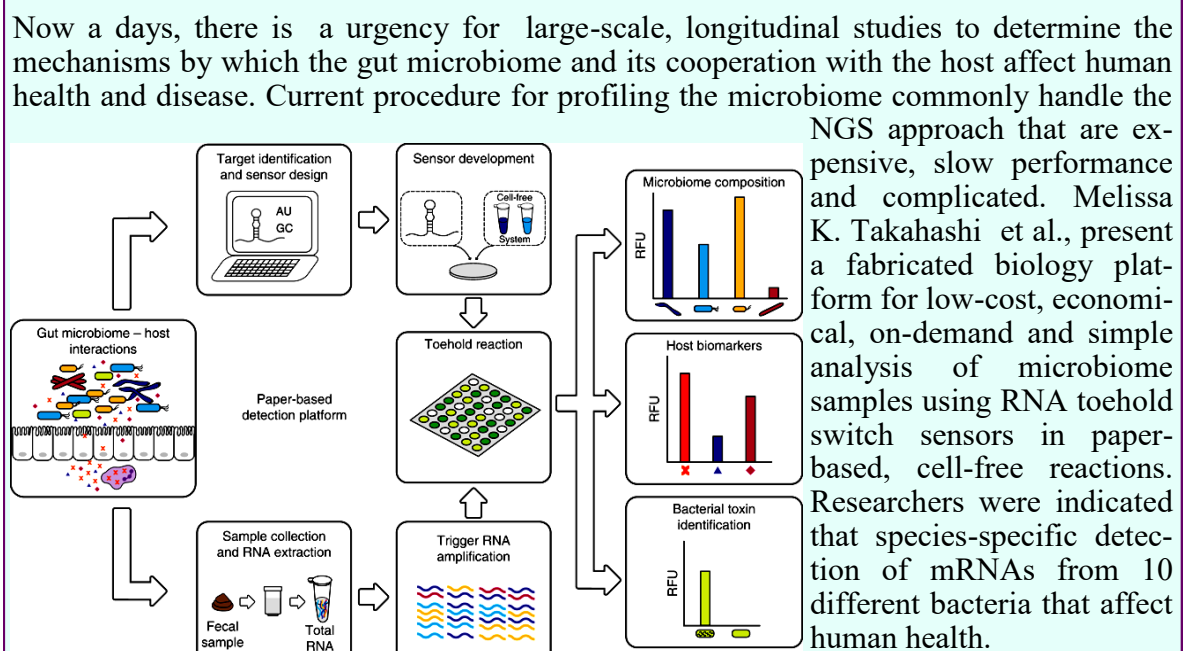

Figure: Workflow for analysis of gut microbiota from healthy & disease samples.

Also four clinically relevant host biomarkers were determined. They develop a method to quantify mRNA using our toehold sensors and validate our platform on clinical stool samples by comparison to RT-qPCR. Further they focus on the potential clinical utility of the platform by showing that it can be used to rapidly and reasonably detect toxin mRNA in the diagnosis of *Clostridium difficile* infections.

Source: Melissa K. Takahashi *et al., Nature* (2018)

AncestryView: a visualization tool

Data visualization is a general term that describes any effort to help people understand the significance of data by placing it in a visual context. It is a important tool for data investigation, analysis and explanation. In some study, researchers developed a new software tool, called AncestryView to visualize the ancestry data. They demonstrate its functionality with the data from admixed individuals.

Fig:An example of AncestryView output (plot_genome) of whole-genome ancestry map
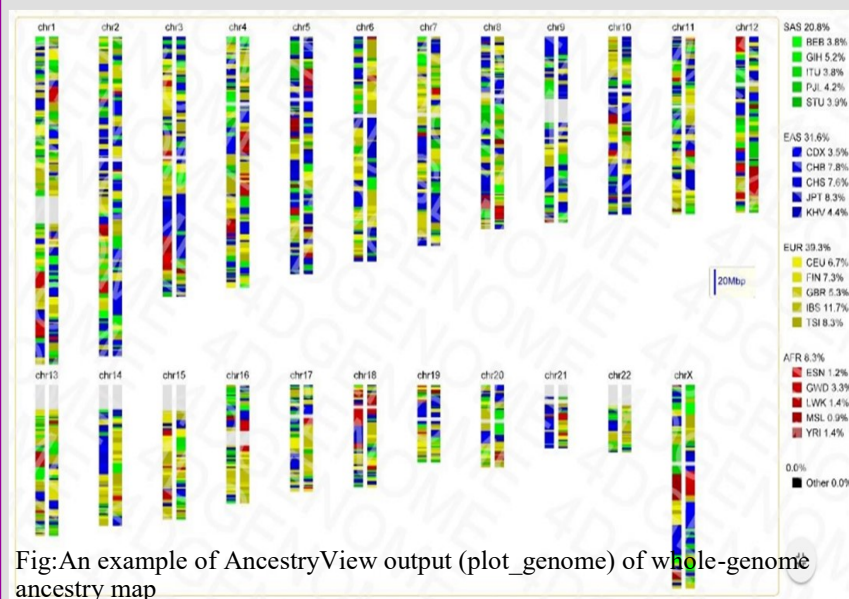
The script of AncestryView software is written in Scala programming language. It takes the aMAP data as the input, and then output an image using the Java graphical interface. This software first using command line parameters and then generates a color scheme; then it extracts the sample IDs from the input files and allocates the required resources for each sample in the second step; thirdly, it up-takes the digital ancestral data from aMAP or other ancestry inference software tools and draws the genome or chromosome map of local ancestry; last, it summarizes the statistics of the aMAP results of local ancestry and generates the legends. The tool is available on https://f001.backblazeb2.com/file/4DGenome/AncestryView.zip.

MOLGENIS Advanced bioinformatics data package

MOLGENIS Research, is a web application for the biomedical field to work with multi-omics data sets without being dependent on bioinformaticians. MOLGENIS Research authorize more well organized collection, manage, analyze, visualize and share data, and support to make data FAIR in a flexible and safe way. MOLGENIS Research offers all the advantages of a true database system with detailed data management and access control options, while at the same time being able to grow 'organically' by allowing data to be dynamically shaped based on what is needed in practice, and adding custom extensions such as visualizations and algorithms into a running system without downtime.
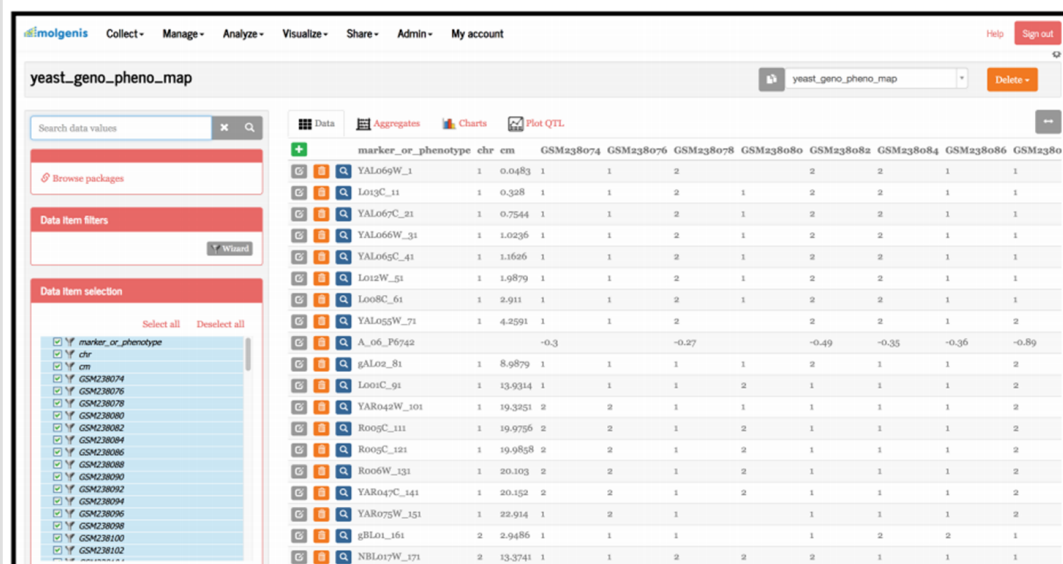

Fig: Snapshot of the MOLGENIS Research graphical user interface

It can be used as a project database from day one as there is no need to design a data model upfront. The tool is available on http://github.com/molgenis.
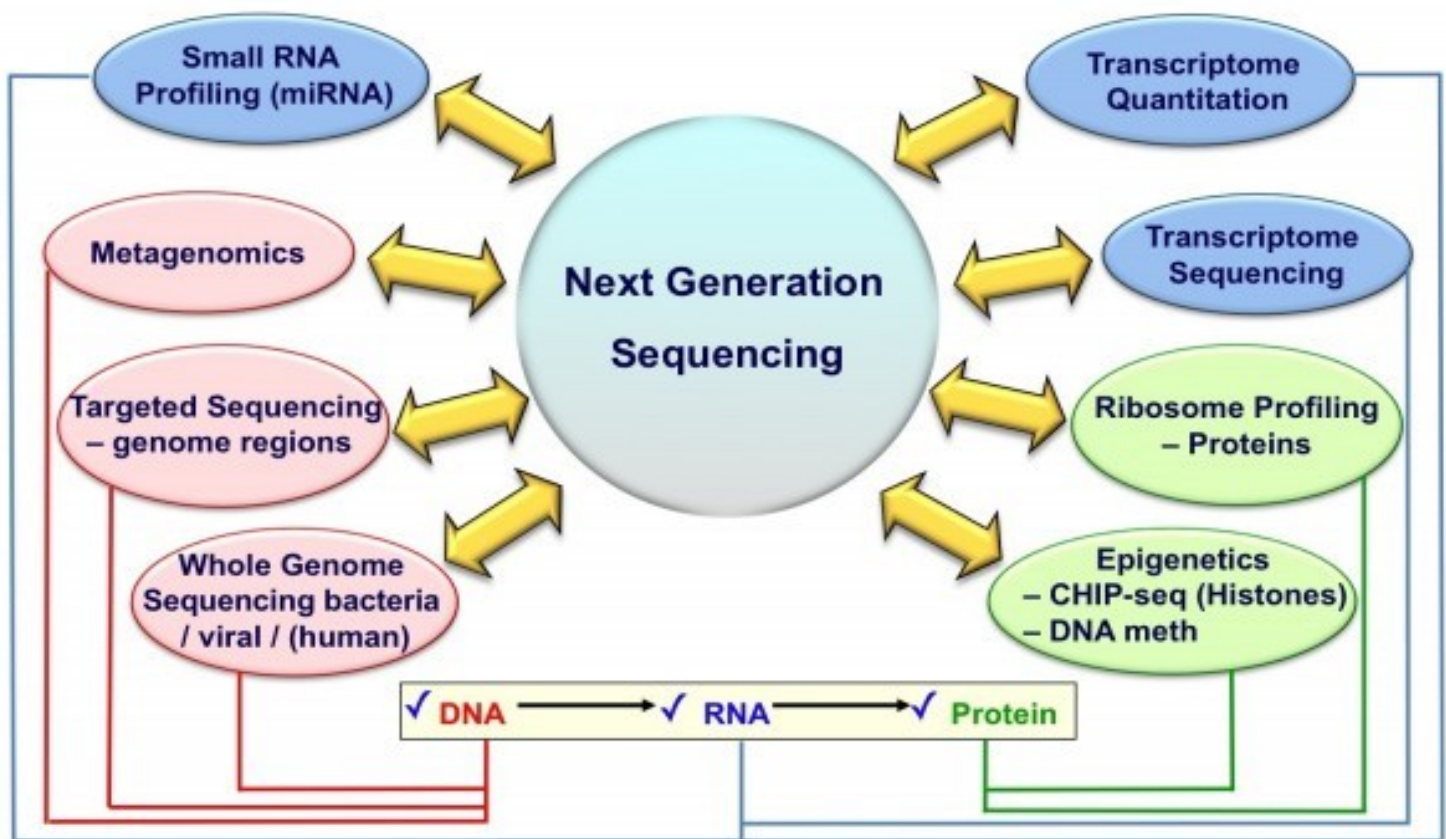
Fig: Application of NGS technologies

Upcoming event

2018NGBT — NEXTGEN GENOMICS, BIOLOGY, BIOINFORMATICS AND TECHNOLOGIES (NGBT).

30 Sep 2018 - 02 Oct 2018 • Jaipur, India

Contact: Phone: [+91- 9591 506 568];   Email: ngbt2018@sgrf.org

Topics: genomics conference, bioinformatics, computational biology, CRiSPER, CaS9, Biotechnology, Genetics, Personalized Genomics, Preventive medicine, clinical genomics

10TH ANNUAL NEXT GENERATION SEQUENCING & CLINICAL DIAGNOSTICS CONGRESS

08 Nov 2018 - 09 Nov 2018 • London, United Kingdom

Contact: Phone: [1865248455];   Email: d.dalby@oxfordglobal.co.uk

Topics: NGS Technologies, NGS data analysis, clinical application, diagnostics of NGS, DNA Sequencing, biomarker development, genome biology, population genetics, whole genome sequencing, clinical genomics in immunotherapy, oncology, infectious and hereditary diseases, pre-natal genetic testing

Event listing ID: 1068897

Event website: https://www.oxfordglobal.co.uk/nextgenerationsequencing-congress/

1.https://www.conference-service.com/conferences/in/bioinformatics.html
2. https://www.conference-service.com/conferences/gb/bioinformatics.html

Phytase

Phytase is a phytate-degrading enzymes, most useful in agriculture to mobilize indigestible phosphate compounds in livestock feed. Availabilities of Phosphorus are known to reduce the competitive ecological communities, and provide living organisms to establish their ways to interact among themselves. We
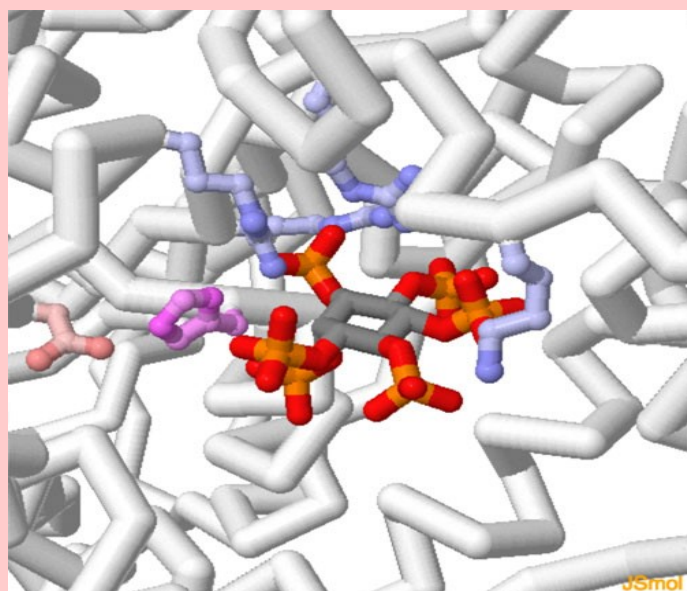

phytic acid
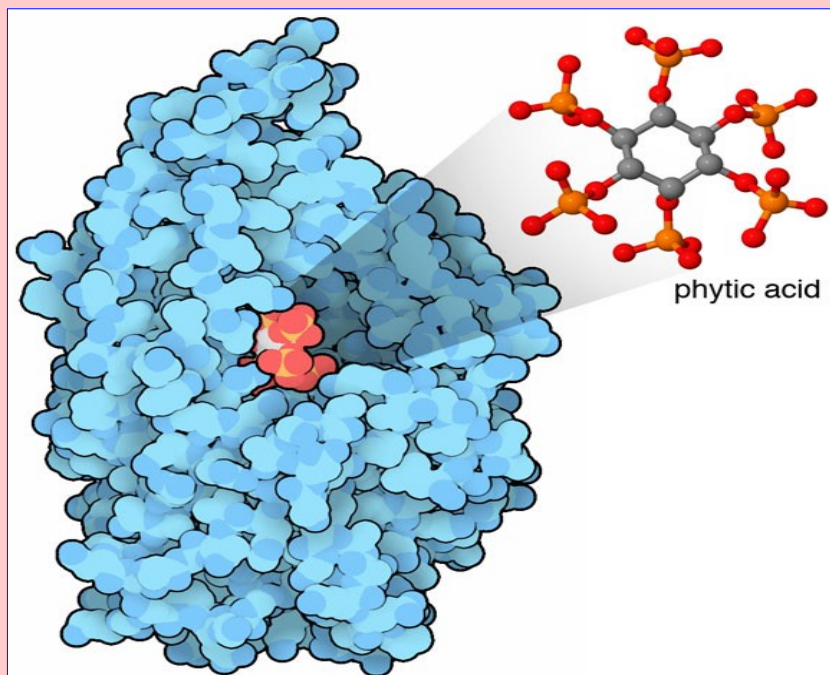
get phosphorus in the foods that we eat along with useful molecules such as nucleotides and phosphate ions. Plants create their own resources that circulate to them, and they often hoard the phosphorus they find in an unusual molecule called phytic acid (or more technically, inositol hexakisphosphate). It is stable and almost indigestible, unless you have the proper enzymes to break it into useful pieces, which causes special problems in agriculture. Phytases are small, acid-stable enzymes that progressively break off the phosphate groups from phytic acid. Two similar types are commonly used as feed supplements: one from bacteria, shown here from PDB entry 1dkq, and one from mold, as seen in PDB entry 1ihp.

The biotechnology community has also worked diligently to engineer more heat stable and more active forms of phytases, making them better and better for large-scale agricultural use.

Forms of Phytase: It has been classified into four general categories based on their structures, namely i)Histidine acid phytases (HAPhy), ii) BPPhy, iii) PTPhy and iv) PAPhy.

Exploring the Structure of Phytase and Phytic Acid

The stick and bold models of phytase enzyme with phytic acid is shown in the figure. Unlike other phytase the phytase AppA derived from *Escherichia coli* utilized a histidine (magenta) in the reaction phytase AppA, which is operated by a neighboring aspartate (pink). Phytic acid, because of its many phosphate groups (in red and orange), carries a strong negative charge, so it is recognized and positioned by an array of positively-charged arginine and lysine amino acids (in blue).

Source: http://pdb101.rcsb.org/motm/225

Kindly send us your feedback to

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