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SupercomputingAsia 2020 (SCA20)

Hurry and Register now! Early Bird Registration ends on 27 Jan 20! Visit SCA20 website now to enjoy limited time early bird rates.

Happy New Year 2020!

NSCC wishes all our Users, Partners, Stakeholders and Friends a Happy New Year!



We look forward to working with all of you in developing a vibrant high performance computing ecosystem for Singapore research. Thinking about a new year's resolution? Here's a thought; what about...

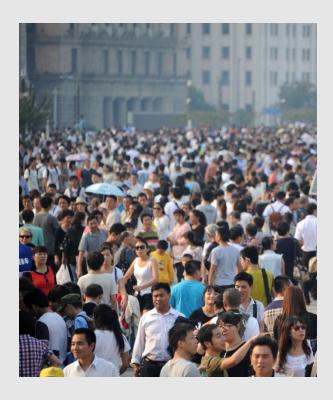
Think supercomputing,

think bigger and faster,

think supercharged research aspirations, think blue sky ambitions!

The Asian genome is one of the most diverse but least studied

With the help of supercomputing resources from NSCC, researchers from the GenomeAsia 100K project published the data in the Nature journal. The study also highlighted the research gap in the research of genetic information for the Asian population.



The Asian genome had at least 10 different ancestral groups or lineages whereas Europeans can be grouped into just one.



Though Asians make up more than a third of the world's population, genetic studies on the Asian genome only make up six percent of the genome sequences that have been deciphered worldwide. The disparity in research is compounded by a new genetic study which found that the Asian are much more genetically diverse. To put the discovery into context, the Asian genome had at least 10 different ancestral groups or lineages whereas Europeans can be grouped into just one.

The <u>GenomeAsia 100K</u> study, which was published in December 2019 in the <u>Nature</u> journal, analysed the genomes of more than 1,700 people, the widest coverage of genetic diversity in Asia to date. The huge amount of data was compiled and analysed by <u>Nanyang Technological University (NTU)</u> scientists, with the help of NSCC's compute resources and other international collaborators.

Why is the discovery important? Different people react differently to diseases and may also respond differently to the same drugs used to treat a disease. For instance, those with North Asian ancestries (eg. Japanese, Korean, Mongolian or Chinese) have a higher than usual risk of an adverse reaction to Warfarin, a drug used in the treatment of heart or cardiovascular diseases. Researchers could use the data from genetic analysis to identify such groups with a predisposition to a specific drug and begin screening for these populations. One of the benefits to put greater focus on deciphering the genetic variance of the Asian population is to help advance the customisation of therapies and medicines for healthcare.

GenomeAsia 100K is a non-profit global consortium which aims to better understand the genome diversity of Asians by sequencing 100,000 genomes of individuals in Asia. The project is hosted by Nanyang Technological University (NTU) and includes three companies; Macrogen (South Korea), Genentech (US) and MedGenome (India / US).

Read more about the research in the NTU media release, 'Asia-wide genome mapping project reveals insights into Asian ancestry and genetic diversity'.

Building an enzyme library and the tools to decipher their functions

The Enzyme Function Initiative (EFI) is a large-scale collaborative project looking at charting and compiling a database of enzymes functions. NUS' SINERGY is now part New enzymes are being discovered every day. of the initiative and is leveraging NSCC's compute power in its research.

Structure of a key enzyme for the biosynthesis of therapeutical compounds

Enzymes are important in sectors like food technology chemical engineering, pharmaceuticals, biotechnology, healthcare, genetic engineering and agriculture.

Enzymes are proteins that help accelerate biochemical reactions. These biocatalysts are important in a number of industrial and chemical processes. Enzymes are important in sectors like food technology chemical engineering, pharmaceuticals, biotechnology, healthcare, genetic engineering and agriculture.

However, the functions of a large number of these have not been ascertained, are unknown or incorrect. The EFI, funded by the US National Institute of General Medical Sciences, began as a project to develop and disseminate a robust strategy to determine enzyme function through integrated sequence-structure-based an approach. The EFI@Illinois, based at the US University of Illinois at Urbana-Champaign (UIUC), has a web resource with genomic enzymology tools that leverage protein, genome and metagenome databases to determine function and aid in the discovery of novel enzymes and metabolic pathways.

The Singapore Consortium for Synthetic Biology (SINERGY), supported by the National Research Foundation and based at the <u>National University of Singapore (NUS)</u>, aims to consolidate Singapore's capabilities in synthetic biology and harness synergies across industry sectors to create a vibrant and globally connected biobased economy in Singapore.

UIUC and NUS' SINERGY collaborated to establish the EFI@SINERGY on 1 Nov 2019. The EFI@SINERGY, with the support of computing power from NSCC, is a trans-global partnership to develop next generation genomic and synthetic enzymology tools.



The EFI team Illinois and SINERGY visited NSCC to find out more about the petascale ASPIRE 1 supercomputer and its capabilities.

Through its enzyme research, EFI@SINERGY aims to develop solutions in areas like sustainable and affordable medicine for common health problems associated with ageing, cancer, metabolic diseases and infectious diseases; upcycling of societal waste streams like organic food waste, electronic waste, plastic waste, etc.; sustainable and affordable supplements such as nutriceuticals for maintaining human health; and sustainable and affordable functional foods for maintaining and extending wellness and healthy living. Find out more about EFI and SINERGY.

SCA20 Highlights – Tutorials & User Group Workshops!

Looking for an introduction to Deep learning for Computer Vision? Or interested to learn, experience and share knowledge with your PBS peers? Sign up now for the limited availability paid tutorials and receive special rates for SCA20 conference registration!

Head on over to the <u>SupercomputingAsia 2020 (SCA20)</u> website for the latest updates on our programme, <u>Tutorials</u>, <u>User Groups</u> and more!

Get special rates for the SCA20 conference registration when you sign up now for an SCA20 Conference Pass! To do this register via the Standard Pass Registration link, include the Tutorial or User Group, and use the following promo code to enjoy a discounted rate on your conference pass!

Promo code: SCATUT<Only applicable for Standard Pass Registration>



Fundamentals of Deep Learning for Computer Vision

*Paid Tutorial. Limited slots available!

Date: 24 Feb 2020, Monday | Time: 9AM - 6PM



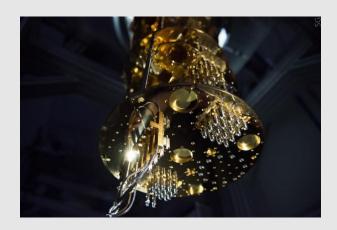
PBS Works User Group

*by Invitation only

Date: 24 Feb 2020, Monday | Time: 9AM - 12.30PM

The Last Byte...

Shared articles and news from the HPC world.



Russia Invests \$790M into its Quantum Future



Top 10 stories of 2019 from Science Node

by Kevin Jackson

Sky taxis, rewiring the human brain, weaponized AI, the end of traffic jams and why climate studies are both right and wrong. These are some of Science Node's most popular stories of 2019... Read the full articles on ScienceNode.org – Part 1 & Part 2.



Powering Innovation Supercomputing in Asia

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