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Using genomics cloud platform and machine learning for genome variant analysis

Next Generation Sequencing (NGS) allows performing massively parallelised DNA sequencing and is currently revolutionizing biological studies. Instead of sequencing a specific set of genes solely, NGS allows to sequence a wider portion of the genome (even a whole genome), which opens the door for a wider analysis of biological pathways within an individual. Researchers have never before accessed such a wealth of genomic data which holds the promise of unveiling the secrets of the most daunting diseases of the century such as cancer. It also comes with its own set of challenges for the management and analysis of Big Data to extract meaningful and actionable insights. Cloud computing and machine learning do have the capacity to solve this challenge. In this talk we will show how Cloud based Genomics platform allows to manage petabytes of genomic data as well as foster fast and agile Secondary Analysis. We'll also use genomics specific machine learning packages to perform Tertiary Analysis on gene variants data and visualization tools to expose and share the results with the scientific community. We will begin the talk with introduction to the genomics field and the commonly used genomic analysis process and will present practical applications of the above services and analysis.

Biography

Tilila is currently a Data Scientists and a Technical Evangelist for data and AI working at Microsoft. She accompanies partners in architecting and building their cloud based, AI powered solutions. She was previously a Technology Strategist for enterprise accounts including Education and healthcare industry. She's also a Fulbright scholar who earned, in 2012, a master in Computer Science and Business from San Francisco State university where her focus was on Bioinformatics including Genomics and Biomedical Image Analysis.

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