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| ***Session Title*** | ***Organizers*** | ***Session’s Abstract*** |
| *Tutorial on Tools of the Trade for Precision Medicine: Deep Data Analysis with Machine Learning and Process Modelling Techniques* | Edward Kim  *Department of Computing Sciences, Villanova University*  *edward.kim@villanova.edu* | Widespread adoption of HealthIT and eHealth systems has resulted in exponential growth of health related data that can be computationally processed and analyzed. Several healthcare organizations are utilizing data mining, machine learning and related approaches to analyze healthcare data and improve quality of care. For example, deep data analysis can give insights into drug interactions and contraindications. In addition to data analysis, we also need to focus on understanding the underlying processes to effect changes. For example, modeling signaling pathways can give insights into various biological triggers by running what-if scenarios on the process model. |
| Vijay Gehlot  *Department of Computing Sciences, Villanova University*  *vijay.gehlot@villanova.edu* |
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| *Implementing an IBM Watson Instance for University Research and Education* | Elliot Sloane  *Center for Healthcare Information Research*  *and Policy*  *Osprey, USA*  *ebsloane@gmail.com* | IBM’s Watson software is an advanced artificial intelligence system that provides unique learning and discovery capabilities. IBM offers qualified University researchers the opportunity to create their own, local instance of IBM Watson to support research and education. This Workshop will show how to install and configure Watson, and will allow attendees to begin learning by hands-on exercises. |
|  | Matthias Reumann  *Sustainable, Resilient Health Systems Research IBM Research*  *mre@zurich.ibm.com* |
| *Computational Histopathology: Tissue Slides to Personalized Medicine* | Chukka Srinivas  *Roche Tissue Diagnostics*  [*Chukka.srinivas@roche.com*](mailto:Chukka.srinivas@roche.com) | Today, multiple cancer tissue repositories and drug development clinical cohorts exist for different tissue types, along with associated clinical, patient survival and outcome data.  Digital pathology and image analysis have not only transformed cancer tissue diagnostics from a manual process of subjective, semi-quantitative interpretation of glass slides under analog microscopes to a precise and reproducible quantification of digitized H&E and immunohistochemistry (IHC) whole slides, but also enable systematic extraction and mining of exhaustive set of varied and rich amount of image features at multiple scales. Similarly, molecular and sequence analyses result in equally rich and complementary tissue information. Computational histopathology refers to the development of novel machine learning method and informatics workflows to correlate the exhaustive set of tissue features (image,molecular and genomic) against patient outcome data to construct prognostic and predictive models and discover the prominent features. Given several cohorts and varied biological applications, there is an strong medical need for the development of robust computational pathology toolset for use in cancer diagnostics, biomarkers and drug development.  This topic stands at the scientific intersection of multiple evolving fields - cancer biology, digital pathology, integration of image/molecular/genomic analyses, machine learning, big data handling and pipelines. It fits in very well with the “Informatics for smart, precision and preventive medicine” theme of the conference. |
| Bahram Parvin  *University of Nevada, Reno*  [*bparvin@unr.edu*](mailto:bparvin@unr.edu) |
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