**Background information on the seven BC-based projects awarded funding through Genome Canada & CIHR Bioinformatics and Computational Biology Competition:**

**Project Title:** Next generation bioinformatics for clinical genomics: using de novo assembly in personalized medicine
**Project Leaders:** Drs. Inanc Birol, Steven Jones and Aly Karsan
**Lead Institution:** Michael Smith Genome Sciences Centre, BC Cancer Agency

Genomics technologies that detect variations and mutations in DNA and RNA can advance cancer care and reduce health care costs by improving preventive care, diagnosis and treatment. Advanced high throughput DNA and RNA sequencing technologies can help realize this vision by generating large amounts of sequence data rapidly and at low cost.

However, solid analysis of the generated data is essential to reach its full potential and will provide the backbone to application. Drs. Inanc Birol, Steven Jones, Aly Karsan and team are developing an analytical approach to detect variations and mutations in DNA and RNA related to cancer diagnosis and care. This approach could lead to more efficient and effective clinical testing for various types of cancers across Canada.

**Project Title:** A federated bioinformatics platform for public health microbial genomics
**Project Leaders:** Drs. Fiona Brinkman, Gary Van Domselaar and William Hsiao
**Institutions:** Simon Fraser University, Public Health Agency of Canada, BC Public Health Microbiology & Reference Laboratory

Despite recent advances in medical, sanitary and public health practices, diseases communicable via bacteria still remain a serious threat. Whole genome sequencing of disease-causing bacteria can provide comprehensive data to identify and track these organisms. However, the current complexity of analytic tools makes it difficult for public health investigators to use and share genomics information in a timely and effective manner.

Drs. Fiona Brinkman, Gary Van Domselaar, William Hsiao () and team aim to address these gaps by providing public health workers with easy-to-use bioinformatics and genomics analytic tools to allow them to better manage communicable diseases and provide quicker responses to infectious disease outbreaks.

**Project Title:** Computational interpretation of cancer genomes: defining mutational landscapes for translational genomics
**Project Leaders:** Drs. Sohrab Shah and Paul C. Butros
**Institutions:** BC Cancer Agency & University of British Columbia

Tumours develop through the accumulation of mutations in DNA. Recent advances in high-throughput (next-generation) DNA sequencing allow researchers rapid identification of mutations in a genome. This has increased understanding of the biology of cancer cells, and has led to more effective drugs and better predictions of patient outcomes.

However, maximizing the clinical use of next-generation sequencing data requires sophisticated software to improve the analysis of genomes and identification of mutant sequences related to tumours.

Drs. Sohrab Shah, Paul C. Boutros and team are developing innovative software that will improve patient care by identifying and analyzing the mutations involved in cancer progression.

**Project Title:** Applied bioinformatics of Cis-regulation for disease exploration (ABC4DE)
**Project Leader:** Dr. Wyeth Wasserman
**Lead Institution:** UBC Centre for Molecular Medicine & Therapeutics

The goal of personalized medicine is to treat patients in the manner that is most appropriate for each individual. Before this can happen, doctors will need software that can perform detailed high-speed and low-cost analyses of patients' specific genetic mutations.

Dr. Wyeth Wasserman and team are developing software that will understand and categorize the pieces of DNA that help turn genes on or off. These small sequences of DNA are spread throughout the human genome and serve a critical role in controlling when and where genes are turned on. Mutations in these on/off switches can cause birth defects, disease risk and adverse drug reactions.

The software will help physicians analyze patients' genetic mutations and pave the way for personalized medicine.

**Project Title:** Tool for proteome-wide identification of regulatory switches
**Project Leader:** Dr. Joerg Gsponer
**Lead Institution:** University of British Columbia

Despite significant progress in diagnosis and treatment, cancer remains Canada's leading cause of death. Although scientists have made major efforts in identifying mutations in some cancers, it is still not known how these mutations cause cancer. Cancer is often related to the disruption of regulatory mechanisms in the cell, including auto-inhibition, a process that allows proteins to switch their functions on and off. Mutations can alter these protein switches, which can lead to changes in cell behaviour and ultimately cancer.

However, there is no easy way to determine when cancer-causing mutations affect auto-inhibitory switches. Dr. Joerg Gsponer and team are developing a new method to identify auto-inhibitory switches through the use of genomic and proteomic information.

**Project Title:** A compressed sensing framework for identifying differentially expressed isoforms and transcriptomic aberrations in cancer samples
**Project Leaders:** Drs. Cenk Sahinalp and Colin Collins
**Lead Institution:** Simon Fraser University

New technology provides fast and accurate ways to analyze RNAs (which act as messengers carrying instructions from DNA) that code protein in a tissue. While there are many potential RNA products in a gene, it is believed that it is only necessary to identify and quantify a small number of RNA products in order to get information about a sample's RNA content.

Drs. Cenk Sahinalp, Colin Collins and team are using a computing technique called *compressed sensing* to find the smallest possible number of RNA products from each gene. Their approach will also help pinpoint the essential differences between samples of RNA products from the same gene. Sahinalp and Collins will also use *compressed sensing* to identify tissues from prostate cancer patients that develop into more aggressive forms of the disease.

**Project Title:** Measuring and modeling tumour evolution from next generation sequencing data: enabling clinical study of clonal diversity in cancer patients
**Project Leader:** Dr. Sohrab Shah
**Lead Institution:** BC Cancer Agency

Breast and ovarian cancers are significant causes of disease and death among North American women. Tumours in these cancers can acquire different mutations, resulting in cells that may respond differently to therapy. However, this genetic diversity within tumours is rarely considered when it comes to treatment, even though it is believed to contribute to drug resistance and disease progression.

While new sequencing technologies have provided some insight into the nature of tumour evolution, it is still unclear how evolutionary processes contribute to cancer.

Dr. Sohrab Shah and team are using sequencing data gathered from breast and ovarian cancer patient samples to create software that will improve understanding of tumour evolution and help predict clinical results.