CCM
THE CENTER FOR COMPUTATIONAL MEDICINE NEWSLETTER
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Welcome!

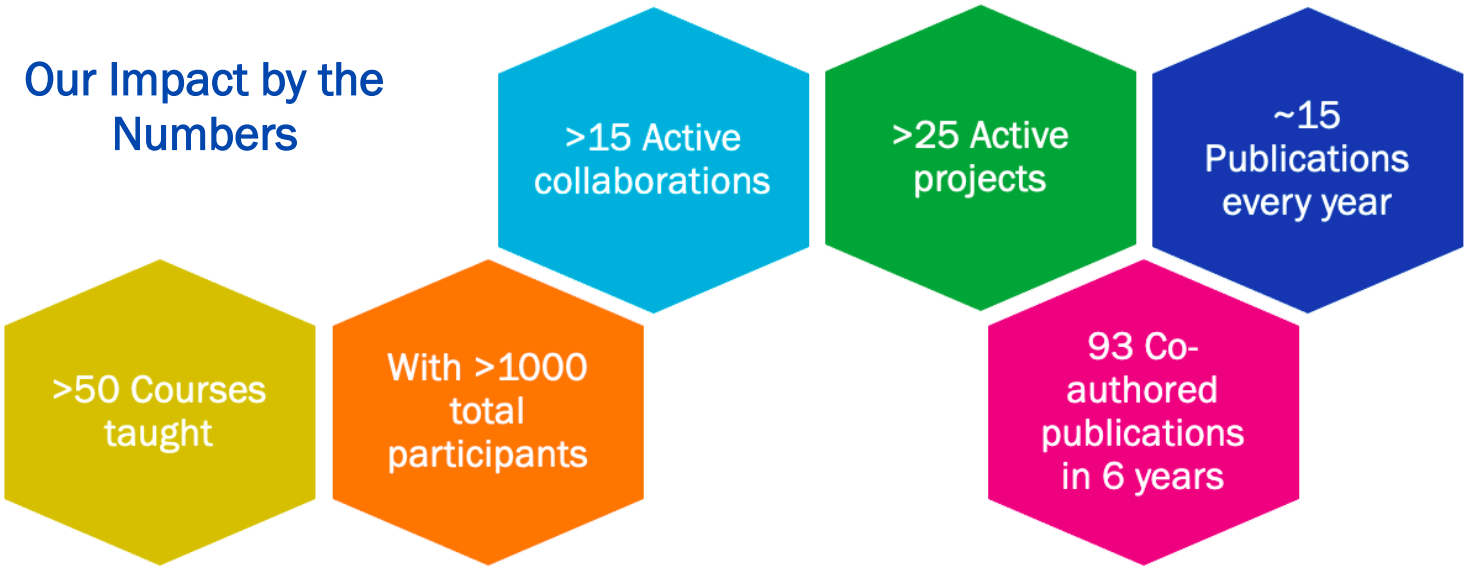
Welcome to the first edition of the *Centre for Computational Medicine (CCM) Newsletter*! CCM is a core facility in The Hospital for Sick Children (SickKids) Research Institute. We specialize in bioinformatics pipelines, software development, web portals, RNAseq, DNA-seq, WES, WGS, scRNA-seq, variant calling, epigenetics, multi-omics, machine learning, and image analysis. Our newsletter will give you highlights about key works from CCM as well as how we may be of use to you.

Who we are

CCM provides scientists and clinicians at SickKids and throughout Canada with computational expertise, high performance computing resources, bioinformatics analysis consulting, software development and much more. We work with you to prepare your data for analysis, examine it using statistical and software tools, and finalize the results for journal publications. We also create novel web portals and analysis pipelines to benefit the biomedical community and provide learning opportunities for bioinformaticians of any skill level.

In this issue:

Our Impact by the Numbers



Data Analysis Pipelines

Our team develops pipelines and applications for RNAseq, whole genome and whole exome sequencing (WGS and WES), single-cell RNAseq, methylation and other data types generated by our collaborators. As an example, we recently applied our expertise in WES to help identify rare genetic variants in Inflammatory Bowel Disease (IBD) by analyzing a cohort of over 1000 pediatric samples. This large-scale collaborative study was led by Dr. Aleixo Muise's team with bioinformatics support provided by CCM. The results were recently published in the prestigious journal *Gastroenterology* (PMID: 32084423).

Web Portals and Tools

Part of our work involves the development of new web portals for data visualization and analysis representing our research projects. One such resource is EpigenCentral (http://epigen.ccm.sickkids.ca/), a web portal for epigenomic data analysis developed in collaboration with Dr. Rosanna Weksberg's lab. We built a web interface to machine learning models and analysis tools to help users search for disease patterns in DNA methylation (DNAm) samples or classify genetic sequence variants. EpigenCentral uses results from several epigenetic studies led by the Weksberg lab and makes data analysis accessible to researchers of all bioinformatics skill levels (PMID: 32623772).

Customized Data Analysis

CCM also provides analytical services for a variety of studies and research initiatives that require customized analysis. Recently, we have worked with Dr. Thomas Eiwegger's lab on the study of allergen sensitivity detection methods. Multi-plex allergen testing platforms, which assess patient sensitivity to many allergens at the same time, often rely on different techniques and measurement units, making it difficult to compare them. We demonstrated how statistical models can bridge the gap between multi-plex allergen testing methods and laid the groundwork for the development of conversion models that can be applied in the clinic (PMID: 32738829).

High-performance Computing

The CCM bioinformatics team works closely with the SickKids Research IT High-Performance Computing (HPC) team, which provides the infrastructure to run data-intensive applications securely, efficiently, and reliably. The HPC service offers enhanced data processing capability using powerful compute processing, large-capacity storage and a high-speed network infrastructure. Together we develop optimal ways to utilize the HPC resources for various bioinformatics applications, which can be used by all SickKids researchers and clinicians. Contact us to learn more.

Other services

CCM is part of many collaborative efforts with scientists at SickKids and beyond. Take a look below to see some of the other services we provide and how they may be of use to you.

Grant Writing and Computational Support

The CCM team is happy to help you with your grant writing in a number of ways. We can provide the computational expertise, an extensive suite of data analysis software, and a state-of-the-art high-performance computing infrastructure to support your project. We can make sure that the computational needs of your grant application are well-covered, by either serving as co-applicants or by providing a letter of support for your application while also contributing to the grant writing as needed.

Bioinformatics Training

> *"I learned and incorporated several techniques in my current work within days of being exposed to it in your workshops. Very topical, very well presented!"*
>
> - *Anonymous Workshop Participant*

We host a range of bioinformatics training workshops and tutorials for clinicians and researchers with different levels of bioinformatics experience. In 2020 we offered hands-on bootcamps on R programming and AI, and a tutorial series on data visualization, next generation sequencing data analysis, machine learning and more. For more information on our training sessions please visit us at http://ccm.sickkids.ca/bioinformatics-training/.

Coming soon!

Stay tuned for a special announcement about an exciting new initiative for Bioinformatics Rounds hosted by CCM!

Careers at CCM

We are always looking for new talent to join the CCM team! Currently, we are looking for an Administrative Coordinator to help us operate efficiently and meet our business and strategic needs. For more information, please visit our careers page at https://ccm.sickkids.ca/jobs/.

Your project is the perfect fit for us!

Some of our collaborations are short fee-for-service projects lasting only several days or weeks, while other collaborations span several years and result in multiple joint publications, novel methodologies and new software tools or web resources. Find out more about us on our website (http://ccm.sickkids.ca), Twitter (@CompMedicine), or by contacting us at ccm.contact@sickkids.ca.