CB2 McGill: Computational Biology and Bioinformatics group at Macdonald Campus of McGill University

Dear all,

As science becomes increasingly interdisciplinary, we are expected to acquire both breadth of knowledge and depth of expertise and in bioinformatics this is especially true. Keeping up to date with the major techniques across multiple specializations it is difficult and you cannot face it alone.

In our campus, there is a lack of bioinformatics group and this does not give us the opportunity to exchange ideas, discuss and keep up to date with new technologies, new data analysis pipelines etc. Therefore, **we have created a Computational Biology and Bioinformatics users group at Macdonald campus**, which will give us the opportunity to discuss several topics, such as **Bioinformatics, Genomics, Statistics, Mathematics, Algorithms, Computational Biology, Systems Biology, Metabolomics, Metagenomics, Machine Learning, Biology**, etc.

Our regular meetings will take place in the summer semester on **every Thursday at 10 am, starting from 1st of June 2017** in room: TBD and we would like to invite everyone who is interested. We are going to talk about various topics that people would be interested to discuss in the future and listen to new ideas. We will create a GitHub account and a website through it (very soon). We have a **Slack group** which you can join only by a McGill email id, link: https://cb2mcgill.slack.com

There would be few **introductory lectures** (most of the slides would be from courses offered at Macdonald campus):

1. Bioinformatics and Genomics
2. An introduction to R programming
3. An introduction to Bash scripting and Python programming
4. NGS data analysis, Git, reproducible research and bioinformatics project structure

From July onwards, we will have regular meetings and Journal clubs on alternate weeks.

Who should attend?
Anyone who is interested in Bioinformatics should attend; people who already have more, or little or even not any Bioinformatics experience.

If you are (or will be) working with NGS (or other: maybe proteomics) data and you are not very familiar with the topic and you need more guidance or feedback about the pipeline/procedure you will follow, then please prepare a presentation for a meeting in which you:
1. Introduce: topic, background, problem, hypotheses, objectives, data, your approach and expected results.

2. Based on that, we will initiate a discussion in which all the members members would be able to give feedbacks and help. This will also introduce other members to new topics and experimental/analysis procedures. It will improve the way way deliver ideas and explain various topics. Finally, it will give the chance to people who have already the experience to exchange opinions and ideas and of course, it will help you in your experimental decisions!

From the introductory meeting we had on the 19th of May, 2017; we received very important (from researchers who have attended) feedbacks and we would like to highlight a few things here:

1. **This is not a course, this is a group!** No one teaches in a group, we exchange ideas. There are basic bioinformatics courses (all at Macdonald campus): BTEC 501 (Fall), BINF 511 (Winter), BINF 531 (Winter). These are very basic courses and we know many people, who did not have any background in Bioinformatics and have taken these courses.
   a. People with more experience can recommend books, articles, online tutorials on certain topics. For people who are new in Bioinformatics, we can help you with what it is more important to start with and in which areas to emphasize as a guidance.
2. If you have a computational problem in a field (i.e. microarray analysis), please write some code, try to do something and discuss it in the meetings, wherever you have problems. Additionally, do not forget that **Google is your best friend** for the difficult times!
3. Do not forget that **this group is based on <u>discussion</u>!** We will be talking about our research, our scientific interests; based on the experience of knowledge of all the members of the group; but also, what we want to learn. As our group is characterized by a special diversity of scientific fields; it will be a better idea for each one to study the problem we are struggling with and find possible solutions, make a presentation/discussion to the other members of the group, get feedback and then continue accordingly. This is a better approach than another person of the group starts from the beginning on studying a novel topic and trying to train other people on the specific analysis as we have already mention: this is not a course. Additionally, the person who is interested in a specific topic will get more knowledge by reading/studying it from scratch.
4. If you would be presenting in a conference etc, please feel free to practice in our meetings to get feedback and let the rest of the people to know what are you working on.

You will get more information about our first talk soon! Please do not hesitate to contact us if you have more comments or suggestions!

Best regards,

Maria (maria.kyriakidou@mail.mcgill.ca)
Deepak (deepak.tanwar@mail.mcgill.ca)