Description of the Bioinformatics Option

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The goal of this document is to provide an overview of the graduate option in Bioinformatics. General information regarding Bioinformatics at McGill is accessible at http://www.mcb.mcgill.ca.

Bioinformatics, which is the application of computer science, mathematical, statistical and engineering techniques to problems in the medical and biological sciences, extends in many directions: instrumentation and real-time control for data acquisition, the construction of large-scale software and databases for organizing and extracting meaning from the data, the design and analysis of algorithms for interpreting biological data, and the modeling and identification of cellular and subcellular functions. The rapid development of this field has been fueled by large-scale, international and inter-disciplinary projects in genomics, proteomics, and other areas of medical and pharmacological research. In turn, developments in Bioinformatics have accelerated these projects and opened up broad new paradigm shifts in biology and medicine. The shift to *in silico* research (i.e. computer-based analyses and modelling) offers enormous opportunities both intellectually and financially. Nationally and provincially, Bioinformatics has been singled out as one of the most important growth areas (see for example "La Bio-informatique au Québec: un levier essentiel du développement des bio-industries"; Conseil de la science et de la technologie, Québec), in part to produce the highly qualified personnel needed by industry and to develop the area as a focus of academic research excellence.

The intention of the Bioinformatics Option is to train graduate students to become researchers in the area, by helping them develop the necessary skills including the following:

1. strategies for experimental design (e.g., how microarray studies should be performed from initial setup to the analysis of particular datasets),

2. tools to analyze datasets (e.g., the development of software to analyze conserved sequences between species),

3. modeling techniques (e.g., using dynamical systems for protein expression),

4. tools to acquire, manage, and make accessible datasets (e.g., data generated by high-throughput genomics, proteomics, and meta(1.gbEc biom)chnol(ughg(t g(re,),)TjETEMC /P AMCID 21 3BDC BT/TT1 1 Tf0 Tc 10.80 0 10.8

6. algorithms and statistics (e.g., the construction of