

## **Developing a National Network for Increasing Accessibility to Bioinformatics Tools and Resources**

**Presented by** Benjamin King, Joel Graber, Ashok Ragavendran

**Description:** The goal of this bioinformatics workshop is to discuss our goal of creating a national network to increase accessibility of bioinformatics tools and resources among IDeA states. Delivering bioinformatics training is a major focus of the Maine INBRE Program as well as many other IDeA programs. During these workshops and courses, we provide servers where all analysis tools and required data resources are already installed. However, it can be challenging for participants from different institutions and IDeA states to access equivalent computing environments for their research at their home institutions. Operating system-level virtualization technologies, such as Docker, can be used to create server environments with sets of applications. We will describe Docker and bioflows (<https://compbiocore.github.io/bioflows>) as example technologies. Following brief presentations about these technologies, we will have a panel discussion about creating a national network to increase accessibility of bioinformatics tools and resources among IDeA states.

**Session theme or topic:** Bioinformatics

**Session format (Lecture, facilitated discussion, panel discussion, Q&A):** Lecture, Facilitated Discussion, Panel Discussion, Q&A

### **3 anticipated participant learning outcomes:**

By actively participating this workshop, participants will be able to:

- Describe the overall goal of creating a national network to increase accessibility of bioinformatics tools and resources among IDeA states.
- Describe the concept of operating system-level virtualization.
- Describe the feasibility of using virtualization products, such as Docker or bioflows, to create a server environment with many bioinformatics tools.

**Intended audience:** INBRE, COBRE, CTR, Students, Faculty, PI's, Administrators

### **Name, title, Institution/bio for each facilitator/presenter:**



**Benjamin King**  
Assistant Professor  
Maine INBRE Program & University of Maine

Benjamin King is an Assistant Professor of Bioinformatics in the Department of Molecular and Biomedical Sciences at the University of Maine. Dr. King is co-Director of the Maine INBRE Bioinformatics Core that supports biomedical research faculty and students across 12 institutions in Maine. Dr. King received his PhD from the Graduate School for Biomedical Science and Engineering at the University of Maine.



**Joel Graber**  
Sr. Staff Scientist  
Maine INBRE Program and MDI Biological Laboratory

Joel Graber is a Senior Staff Scientist and Director of the Computational Biology and Bioinformatics Core at the MDI Biological Laboratory. Dr. Graber is co-Director of the Maine INBRE Bioinformatics Core that supports biomedical research faculty and students across 12 institutions in Maine. Dr. Graber received his PhD from Cornell University and a post-doctoral fellowship with Temple Smith at Boston University.



**Ashok Ragavendran**  
Lead Data Scientist  
Center for Computational Biology of Human Disease COBRE & Brown University

Ashok Ragavendran is the Lead Data Scientist for the Computational Biology Core in the Center for Computational Biology of Human Disease at Brown University. Dr. Ragavendran and his colleagues developed the bioflows (<https://compbiocore.github.io/bioflows>) package for running several analysis pipelines for high-throughput DNA sequencing datasets. Dr. Ragavendran received his PhD from Michigan State University and a post-doctoral fellowship at Purdue University.

\*\*\*\*\*