Preface

Welcome to the BioCreative VI workshop which is being held in Bethesda MD, USA on October 18-20, 2017. On behalf of the Organizing Committee, we would like to thank you for your participation and hope you enjoy the workshop.

The BioCreative (Critical Assessment of Information Extraction systems in Biology) challenge evaluation consists of a community-wide effort for evaluating text mining and information extraction systems applied to the biological domain (http://www.biocreative.org/). Its aim is to promote the development of text mining and text processing tools which are useful to the communities of researchers, publishers, and database curators in the biological sciences. The main emphasis is on the comparison of methods and the community assessment of scientific progress, rather than on the purely competitive aspects.

The first BioCreative was held in 2004, and since then each challenge has ensure the active involvement of the text mining user community in the design of the tracks, preparation of corpus and the testing of interactive systems. BioCreative VI consists of five tracks:

Track 1: Interactive Bio-ID Assignment for innovations in Biomedical Digital Curation. Organizers: Lynette Hirschman, Cecilia Arighi, Thomas Lemberger, Robin Liechti and Cathy Wu. The Bio-ID track explores the ID assignment to selected bioentities both at the pre- and post-publication , using the SourceData framework as a real world use case.

Track 2: Text-mining services for Kinome Curation. Organizers: Julien Gobeill, Patrick Ruch and Pascale Gaudet. This track focuses on literature triage (selection of relevant articles for curation), a basic task performed by virtually all curated molecular biology databases. More specifically on triage for both Protein-Disease and Protein-GO annotations related to human kinases.

Track 3: Extraction of causal network information using the Biological Expression Language (BEL). Organizers: Juliane Fluck, Sumit Madan and Justyna Szostak. BEL track focuses on automatic extraction of biological network information, one of the most desired and most complex tasks in biological and medical text mining, represented in Biological Expression Language (BEL).

Track 4: Mining protein interactions and mutations for precision medicine. Organizers: Rezarta Islamaj Dogan, Andrew Chatr-aryamontri, Sun Kim, Donald C. Comeau, Zhiyong Lu. This track aims to bring together the biomedical text mining community in a new challenge for precision medicine, focusing on identifying and extracting protein-protein interactions affected by mutations described in the biomedical literature.

Track 5: Text mining chemical-protein interactions. Organizers: Martin Krallinger, Alfonso Valencia, Analia Lourenço. This track focuses on chemical-protein interactions that might be of relevance for precision medicine as well as for drug discovery and basic biomedical research.

We would like to thank all participating teams, panelists, all the chairs, sponsors and committee members.

Organizing Chairs
Cecilia Arighi, University of Delaware, USA
Cathy Wu, University of Delaware and Georgetown University, USA