

The "Computational Modeling in Biology" Network (COMBINE) is an initiative to coordinate the development of the various community standards and formats in systems biology and related fields. COMBINE 2016 will be a workshop-style event with oral presentations, posters, and breakout sessions. The five meeting days will include talks about the COMBINE standards and associated or related standardization efforts, as well as presentations of tools using these standards. Oral presentations will be selected from the submitted abstracts. In addition, poster sessions will allow people to inform each other about their software and other projects in a setting that fosters interaction and in-depth discussion.

# **KEYNOTE SPEAKERS**

- **Carole Goble** (Manchester)
- Michael Hucka (Caltech)
- **Dagmar Iber** (ETH Zurich)
- Andrew Millar (Edinburgh)
- Chris J. Myers (Utah)
- **Daryl P. Shanley** (Newcastle)
- Yujiang Wang (Newcastle)

#### **KEY DATES**

Abstract submission: 8 July 2016 **Scholarship application**: 8 July 2016 Notification: 15 July 2016

COMBINE: 19-23 September 2016

## TOPICS OF INTEREST

- **Alfonso Bueno-Orovio** (Oxford) Data exchange and model standards for systems biology
  - Graphical notation standards for systems biology
  - · Standards for sharing and analysing biological pathway data
  - Standards for computational biological models

# **LOCAL CHAIRS**

Paolo Zuliani & Anil Wipat

ICOS Group

School of Computing Science

**Newcastle University** 

COMBINE 2016 gratefully acknowledge funding from:

### TRAVEL SCHOLARSHIPS

PhD students and postdocs may apply for travel funds to attend COMBINE. More information on the COMBINE website.

### **COMBINE COORDINATORS**

Gary Bader (Toronto) Martin Golebiewski (Heidelberg) Michael Hucka (Caltech) Nicolas Le Novère (Babraham) Chris J. Myers (Utah) David Nickerson (Auckland) Falk Schreiber (Monash) Dagmar Waltemath (Rostock)

### **LOCAL ORGANISERS**

Keith Flanagan & Claire Smith







