NETTAB 2018
Preliminary announcement

Paolo Romano
Ospedale Policlinico San Martino, Genoa, Italy
Scope and history

- **Innovative technologies and tools for bioinformatics**
- **From 2001, original focus themes each year:**
  - 2001 CORBA and XML
  - 2002 Software Agents
  - 2003 Microarrays analysis
  - 2004 From Biology to Bioinformatics
  - 2005 Bioinformatics Workflows
  - 2006 Web Services and GRID Infrastructures
  - 2007 Semantic Web for biomedicine
  - 2008 Biomedical Complex Systems
  - 2009 Collaborative / Social Research
  - 2010 Biological Wikis
  - 2011 Clinical Bioinformatics
  - 2012 Integrated Bio-Search
  - 2013 Semantic, Social, Mobile Tools
  - 2014 Structural Bioinformatics & Integrative Systems Biology
  - 2015 Bioinformatics for ncRNA
  - 2016 Reproducibility, Standards and SOP
  - 2017 Methods & Tools in Precision Medicine

- **Two main topic streams: data integration and data analysis**
NETTAB 2018 Preliminary Announcement

2001
CORBA and XML:
towards a bioinformatics integrated network environment,
Genoa

2005
Workflows management:
new abilities for the biological information overflow,
Napoli

2007
A Semantic Web for Bioinformatics:
Goals, Tools, Systems, Applications,
Pisa

2007
Semantic Web Applications and Tools
for Life Sciences workshop series

2016
Reproducibility, standards and SOP
in Bioinformatics,
Roma

2016
EMBnet

2016
GOBLET

2016
CHARMME

2016
myGrid

2016
SWAT4LS

2016
Taverna Workbench
We have:

- defined integration methods,
- developed standards,
- created technologies, software and tools.

We now have tools, what next in data integration?

We need to provide:

- targets for developers,
- targets for data producers,
- metrics to assess their achievement.

Hence, our data need to be FAIR:

Findable, Accessible, Interoperable and Re-usable!
The FAIR Guiding Principles

To be Findable:

F1. (meta)data are assigned a globally unique and persistent identifier
F2. data are described with rich metadata (defined by R1 below)
F3. metadata clearly and explicitly include the identifier of the data it describes
F4. (meta)data are registered or indexed in a searchable resource

To be Accessible:

A1. (meta)data are retrievable by their identifier using a standardized communications protocol
A1.1 the protocol is open, free, and universally implementable
A1.2 the protocol allows for an authentication and authorization procedure, where necessary
A2. metadata are accessible, even when the data are no longer available

To be Interoperable:

I1. (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.
I2. (meta)data use vocabularies that follow FAIR principles
I3. (meta)data include qualified references to other (meta)data

To be Reusable:

R1. meta(data) are richly described with a plurality of accurate and relevant attributes
R1.1. (meta)data are released with a clear and accessible data usage license
R1.2. (meta)data are associated with detailed provenance
R1.3. (meta)data meet domain-relevant community standards
Great interest at the decision level

- European Council adopted Open Science and the reusability of research data as a priority - European Open Science Cloud (EOSC)
  - FAIR principles are a core component of the EOSC Declaration
- The Directorate General for Research and Innovation of the European Commission started the FAIR Data EG Consultation
- Launch of the Big Data to Knowledge (BD2K) initiative of the National Institutes of Health
- Science Europe has adopted FAIR principles as the basis for sharing administrative data on funding

- ELIXIR Research Infrastructure statement on FAIR Principles
- IMI Call for FAIRification of EFPIA datasets
NETTAB 2018
Building a FAIR Bioinformatics environment

Many questions to answer
• What is FAIRness?
• How to make FAIR data a reality?
• How to facilitate the translation to FAIR data?
• How to measure it?

Many on-going projects
• EOSCpilot
• FAIRmetrics
• FAIRsharing
• GO-FAIR
NETTAB 2018
Building a FAIR Bioinformatics environment

Topics (explicative list)

• FAIR concept
  – Specification and revision of components, conceptual issues.

• FAIR development tools
  – FAIR Web Services, metadata for FAIR tools, revision of standard formats.

• FAIRness evaluation
  – FAIRness validation and correction tools.

• FAIR metrics
  – Levels of FAIRness, FAIRness scores, FAIRness minimal levels.

• FAIR environment
  – Integration and interoperation of FAIR data and systems.
NETTAB 2018

Building a FAIR Bioinformatics environment

Workshop Chairs

Carole Goble
University of Manchester, United Kingdom

Paolo Romano
Ospedale Policlinico San Martino, Genoa, Italy

Mauro Giacomini
University of Genoa, Italy
**NETTAB 2018**

**Building a FAIR Bioinformatics environment**

**Invited speakers (confirmed only)**

**Michel Dumontier**

Professor of Data Sciences, University of Maastricht, The Netherlands. Previously professor at the Stanford Center for Biomedical Informatics Research at Stanford University and of Bioinformatics at Carleton University.

Expert in computational methods for knowledge discovery, internationally recognized for his contributions in bioinformatics, biomedical informatics and semantic technologies.

Member of the Dutch TechCenter for Life Sciences (DTL), and participant in the Dutch node of Elixir, Elixir-NL. Scientific director for Bio2RDF, an open source project to generate Linked Data for the Life Sciences.
NETTAB 2018
Building a FAIR Bioinformatics environment

In collaboration with:

• University of Genoa, Italy
• Ospedale Policlinico San Martino, Genoa

• BITS Bioinformatics Italian Society
• ELIXIR-UK
• ELIXIR-IIB Istituto Italiano di Bioinformatica
• GO-FAIR
• FAIRsharing

• CHARME COST Action
NETTAB 2018
Building a FAIR Bioinformatics environment

Programme Outline (Provisional Scheduling)

• Tutorial & Hackathon
  – Monday October 22, 2018, morning
  – Wednesday October 24, 2018, afternoon

• Opening
  – Monday October 22, 2018, 2.30 PM

• Closure
  – Wednesday October 24, 2018, 1.00 PM

• Social activities
  – Guided Tour, Tuesday October 23, 2018, 5.30 – 8.00 PM
  – Social Dinner, Tuesday October 23, 2018, 8.30 – 11.00 PM
NETTAB 2018
Building a FAIR Bioinformatics environment

Key dates (Provisional Scheduling)

- November 2017: Invited Speakers defined
- January 2018: Tutorials defined
- **February 2018: Web site available**
- March 2018: Call for abstracts launched
- **May 2018: Oral communication submission deadline**
- **September 2018: Poster submission deadline**
- September 2018: Early registration deadline
- **October 22-24, 2018: Workshop**
How to reach Genoa

Genoa is on the sea in the North-Western part of Italy, near to the French border (165 Km).


By train from main Italian Northern cities, incl. Milan and Turin, and from Nice.
Location

Villa Cambiaso, Polytechnic School, University of Genoa

Located in one of the greenest areas of the town, Albaro hill.

Public transport from main railway station (15’) and city centre.

Designed in 1485 by Galeazzo Alessi.
NETTAB 2018
Building a FAIR Bioinformatics environment

Genoa is...
Building a FAIR Bioinformatics environment

Genoa is...
We are looking forward to meeting you at

NETTAB 2018 in Genoa

Email: nettab.workshops@gmail.com
NETTAB 2018
Building a FAIR Bioinformatics environment
October 22-24, 2018, Genoa, Italy