



ComMet

Microbiomes and Metagenomes

Warwick Business School, The Shard, London

3rd-4th March

Committee Meeting 3rd March 2015

Present: Liz Wellington, Emma Travis, Rob Finn, Alan Walker, Carl Mayers, Adrian Smith, Mark Blight, Sharon Huws, Julian Marchesi, John Ward, Penny Hirsch, Phillip Poole

Apologies: Nick Loman, Joy Watts, Jason Snape

Welcome to new members: Carl Mayers (DSTL), Adrian Smith (Unilever), Mark Blight (Biocatalysis), Sharon Huws (Aberystwyth University), Phillip Poole (Oxford University), Joy Watts (University of Portsmouth), Brindha Lekshmisaran

Discussed other possible people to invite: Jens Maestrom , Eraina Branca (Syngenta through Penny Hirsch)

Website development- need to make it more interactive

- in bioinformatics meeting develop descriptions of what is comprised in EBI portal with examples

- more case studies

- decision tree - issues with branch points where people disagree on

approach

- issues with how to keep it up to date

Discussion on metadata and sequence data. RF commented that it is difficult to design a system that suits all. Data needs to be accessible eg MGRAST can't access other data. Noted that metadata varies by field and that for clinical samples it may not be possible to have much information. Include DNA extraction methodology, PCR primers and sequencing platform as key elements of metadata. To drive users to deposit detailed metadata it needs to be required for publication. Network members to approach journals with minimum acceptable standards. ISME?

Networking of members : Linked in group suggested, thought to be of particular use for postdocs and students to discuss technical issues and network. Action : ET / JW

Future meetings:

EBI 1st-3rd Dec - workshop for 30 people

-invite submissions to be viewed by committee

need own data or have identified existing relevant sample in portal to use

Additional meeting on analysis tools which is less data intensive and more about methodologies/ algorithms and what to link to. Also to include what hardware to use with capabilities of machines.

Brindha

DSTL running comparison of platforms to compare different analytical tools with different parameters using defined samples which could be shared to run through platforms? Need to blind test samples. Need to include Oxford Nanopore.