



Microbiomes and Metagenomes

Warwick Business School, The Shard, London

3rd-4th March

1st breakout meeting Shard

To discuss:

- What can ComMet do for us?
- Are we being driven too much by structure rather than function?
- Tools for functionality
- how to manage data handling/ funding opportunities/connectivity and networking

Networking

- Collaborative network for emerging scientists
- Link to other networks (Biocat / synthetic biology)- a network of networks
- Communicate between disciplines – how to learn from others and not reinvent the wheel
- A LinkedIn group as a practical self support group
- Join existing groups
- It is a large field and a mine field to approach and get started.

Funding

- Concept funding
- Need to innovate funding opportunities

Data handling

- Only ever as good as reference databases – how to feed information back into cycle of knowledge?
- Bioinformatics – need to be easier to get into for non-specialists
- How do we annotate to make sense of the unknowns? Link genes and function – this is a problem across all microbe systems.
- Should there be an agreed assignment of function?
- Statistical analysis – what is needed?
- Need a database of unknowns and the metadata to allow linking of unknowns with ecosystem
- Need to get microbial physiologists and chemists talking
- Scaling and informatics
- Knowledge transfer – need to feed back to pfam
- Ease of submission vs metadata amount (for portals)
- Difficult to compare data taken in different time frames – what to do with old 454 data?

- Looking at bacteriophage – phage database would be very useful – difficult to tell difference between phage and remnant in metagenomics
- Difficult to put the information from artificial environments into real life.
- Analysis systems very important to outcome – have to reanalyse data from raw data – platform dependent.