

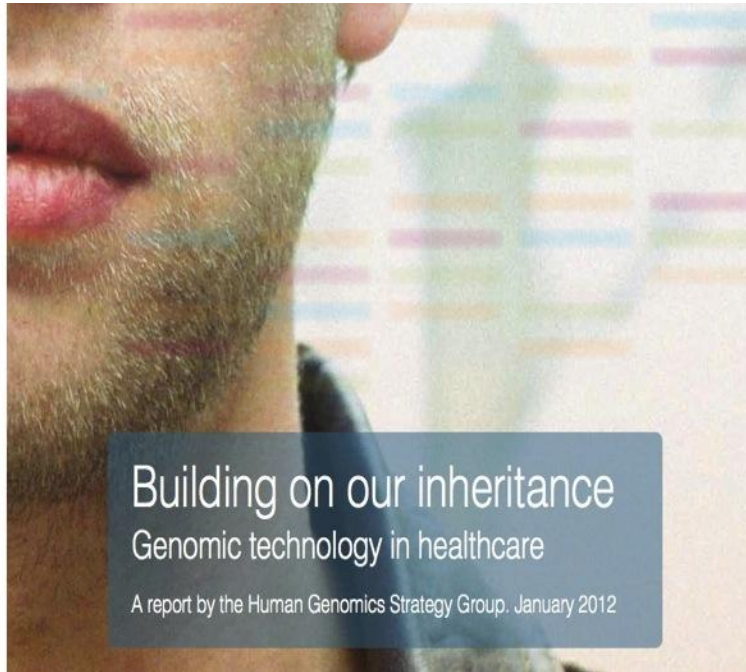
New Technologies: Diagnosis of Infections and Advances in Epidemiology

Professor Eric Bolton
President of the BSMT
Honorary Professor
University of Liverpool

31st Annual Scientific Meeting of the BSMT
20th May 2016

Copyright of author

Genomics in Healthcare: Cracking the Enigma Code!!



Genomics: application of specific technologies to analyse wider sets of genetic information e.g the entire genome.

Genomic medicine covers a wide spectrum of disciplines and potential applications.

These are linked by the use of the same underlying technologies

Next Generation Sequencing (**NGS**) is the technology that is used to determine the whole genomes of animals, plants and microorganisms

Is Genomics the Future of Clinical and Public Health Microbiology??



- Next Generation Sequencing
- Whole genome sequencing
- Meta-genomics – sequencing directly from clinical specimens

Next Generation Sequencing (NGS)

NGS was introduced into research in 2007



NEW HiSeq 2500



MiSeq

Application of Next Generation Sequencing (NGS) in Microbiology

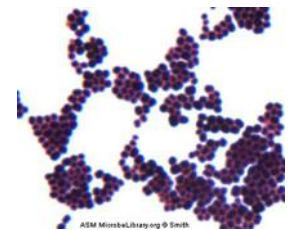
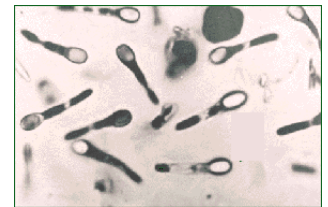
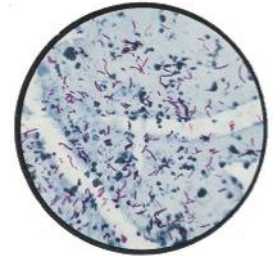
- For identification and fingerprinting of microorganisms
- Simultaneous detection of pathogenicity, virulence and antimicrobial resistance genes
- Within a few years the cost of sequencing a bacterial genome will approach that of current routine laboratory tests for identification.

Application of Next Generation Sequencing (NGS) in Microbiology

NGS is already yielding results in understanding transmission of:

- *Mycobacterium tuberculosis*
- *Clostridium difficile*
- *Staphylococcus aureus*

- It has proved particularly valuable in tracking hospital acquired infections and managing episodes in hospital settings.



Next Generation Sequencing: Meta-genomics

- Ability to sequence directly from microbial environments e.g. clinical specimens
- A widely used method for studying phylogeny and taxonomy.
- This method has been used to evaluate bacterial diversity in many environments, allowing researchers to characterize microbiomes from samples that are otherwise difficult or impossible to study.
- **NGS with its ability to sequence thousands of organisms in parallel is uniquely suited to this application.**

Fully integrated, real-time detection, diagnosis and control of community diarrhoeal disease clusters and outbreaks

Professor Sarah J O' Brien

Department of Epidemiology and
Population Health

University of Liverpool



17 million cases of IID per year in the UK (around 1 in 4 of the population)
Costs the UK economy > £2 billion/year

Health Innovation Challenge Fund
Wellcome Trust and Department of Health

What is the Vision?

- To create a new, one-health paradigm for detecting and investigating clusters and outbreaks of diarrhoea and vomiting in the community
 - New approach to population sampling
 - New approach to cluster detection
 - **Modern Microbiology**
 - Rapid Molecular Diagnostics
 - Microbial genomics
 - Integration with human and veterinary surveillance systems

Modern Microbiology: Genomics

The Centre for Genomic Research (**CGR**) University of Liverpool is using Next Generation Sequencing in a targeted fashion:

1. Sequencing of Isolates of Enteric Pathogens

For typing and monitoring the evolution of pathogens i.e. detecting changes in virulence and antimicrobial resistance markers.

2. Investigation of Clusters of Cases

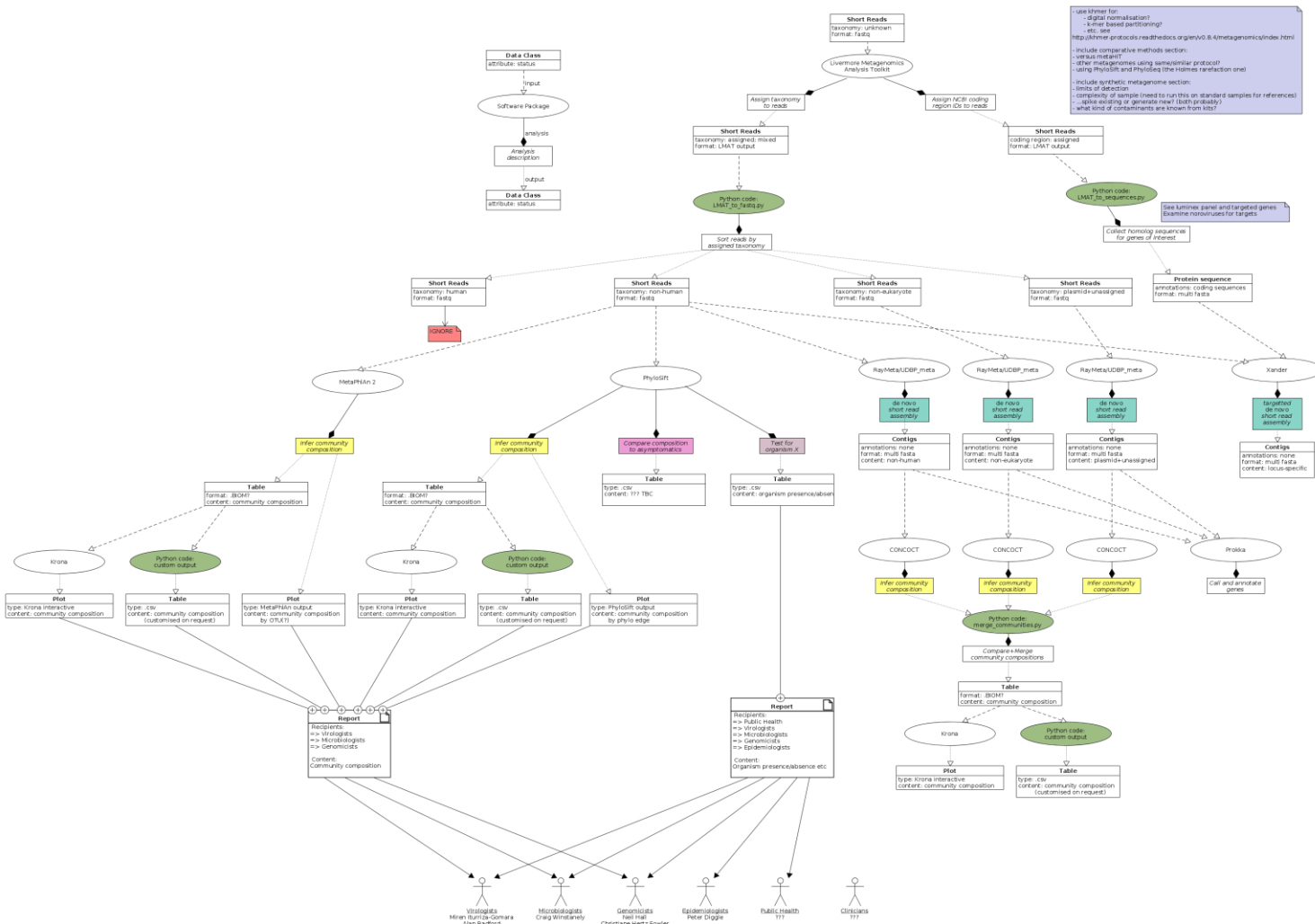
3. Meta-genomics:



Meta-genomic Sequencing Studies: Aims

1. Detect the presence/absence of all of the major GI Pathogens directly in faecal samples.
2. Attempt to discover “new” or slightly different pathogens
3. Learn about pathogen community composition in symptomatic patients i.e. mixed infections
4. Ability to characterise pathogens directly in faecal samples to aid rapid epidemiological investigations.

Sequencing Studies: Developing the pipeline!



Meta-genomics: Future Challenges

1. Selecting the optimum bio-informatics tools
2. Reproducibility: aspire to the precision of a clinical test:
 - Setting the thresholds: when is something present
 - When is a positive clinically significant?
3. Ability to detect Clusters
4. Scalability: 100s+ samples
5. Information transfer: clinicians, scientists, epidemiologists
6. Reusability: life after development and roll out