

A new way to research into human gut microbiome

Bin Hu, PhD

**BGI
(Beijing Genomics Institute)
Shenzhen, China**

**Vancouver, Canada
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Metagenomics

(Environmental Genomics, Ecogenomics or Community Genomics)

Tradition

Cultivation-based methods
Individual species



Modern



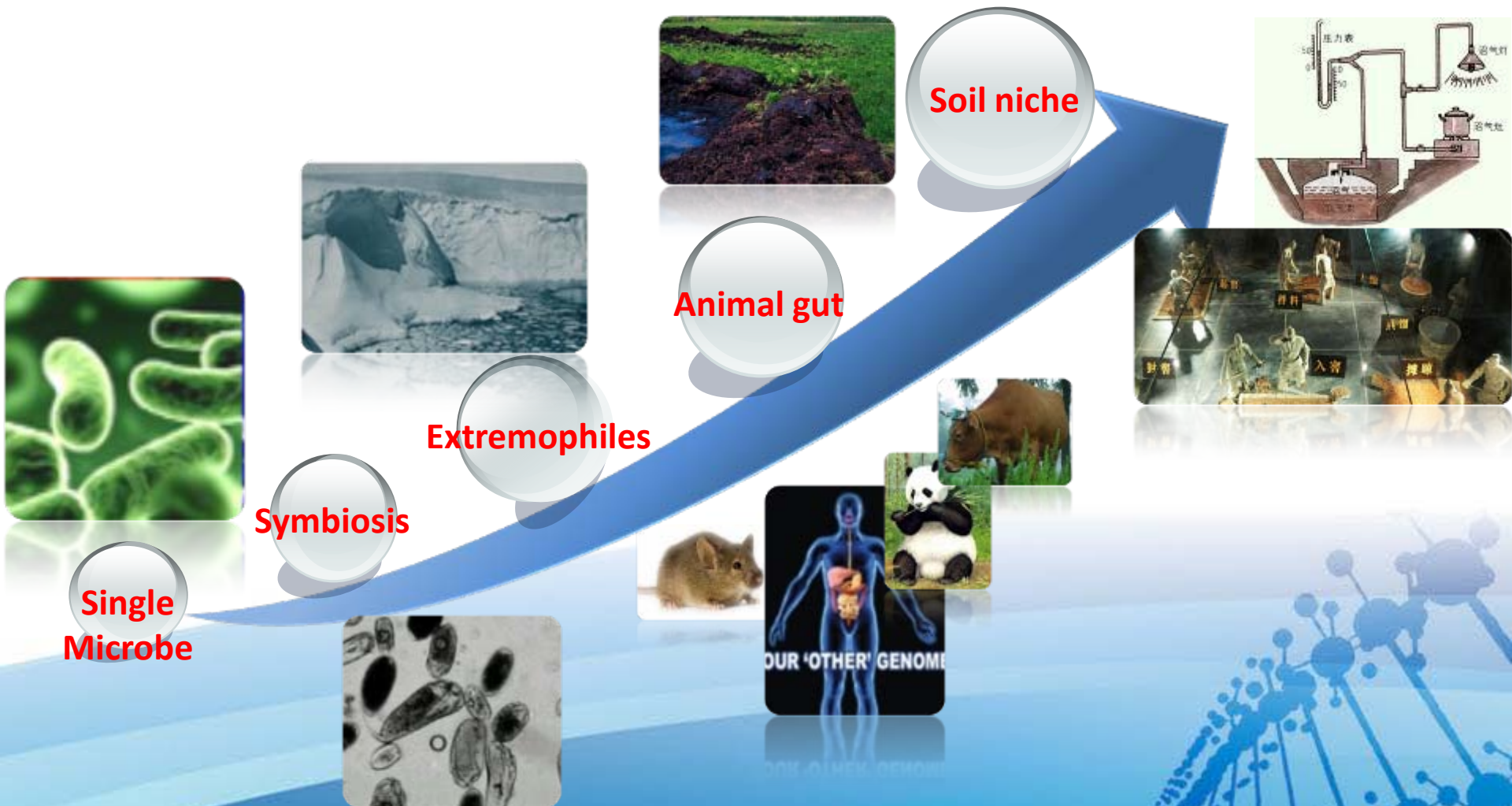
Diversity

>99% uncultured

Unbiased

Study the complex microbial world as one community

The complex of Environmental Microbiome



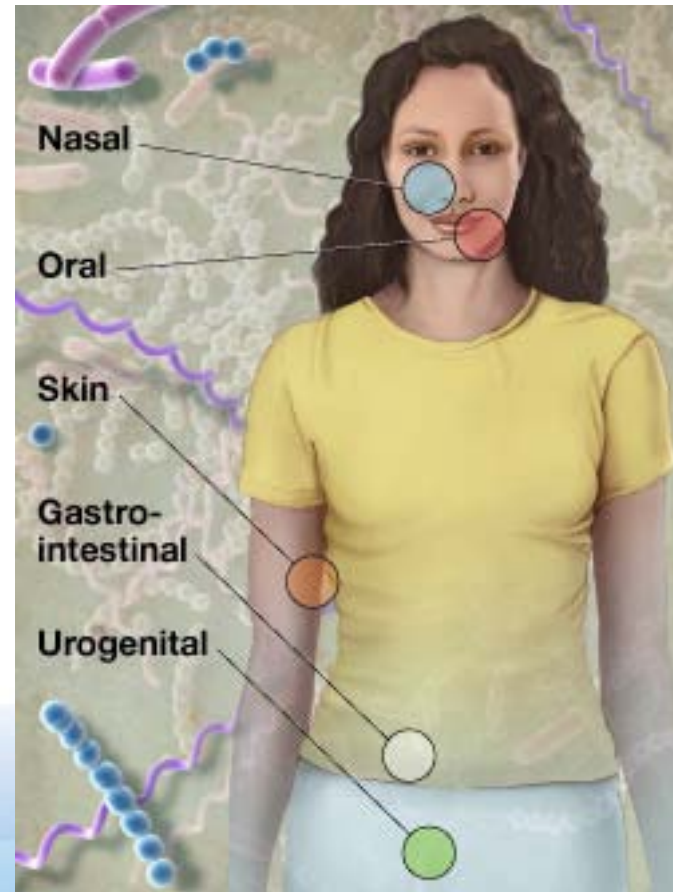
● *PLoS ONE*. 4, e4219(2009).

● *Journal of Microbiological Methods*.
79, 266-271(2009).

● *Genome Research*. 18, 1043–1050(2008).

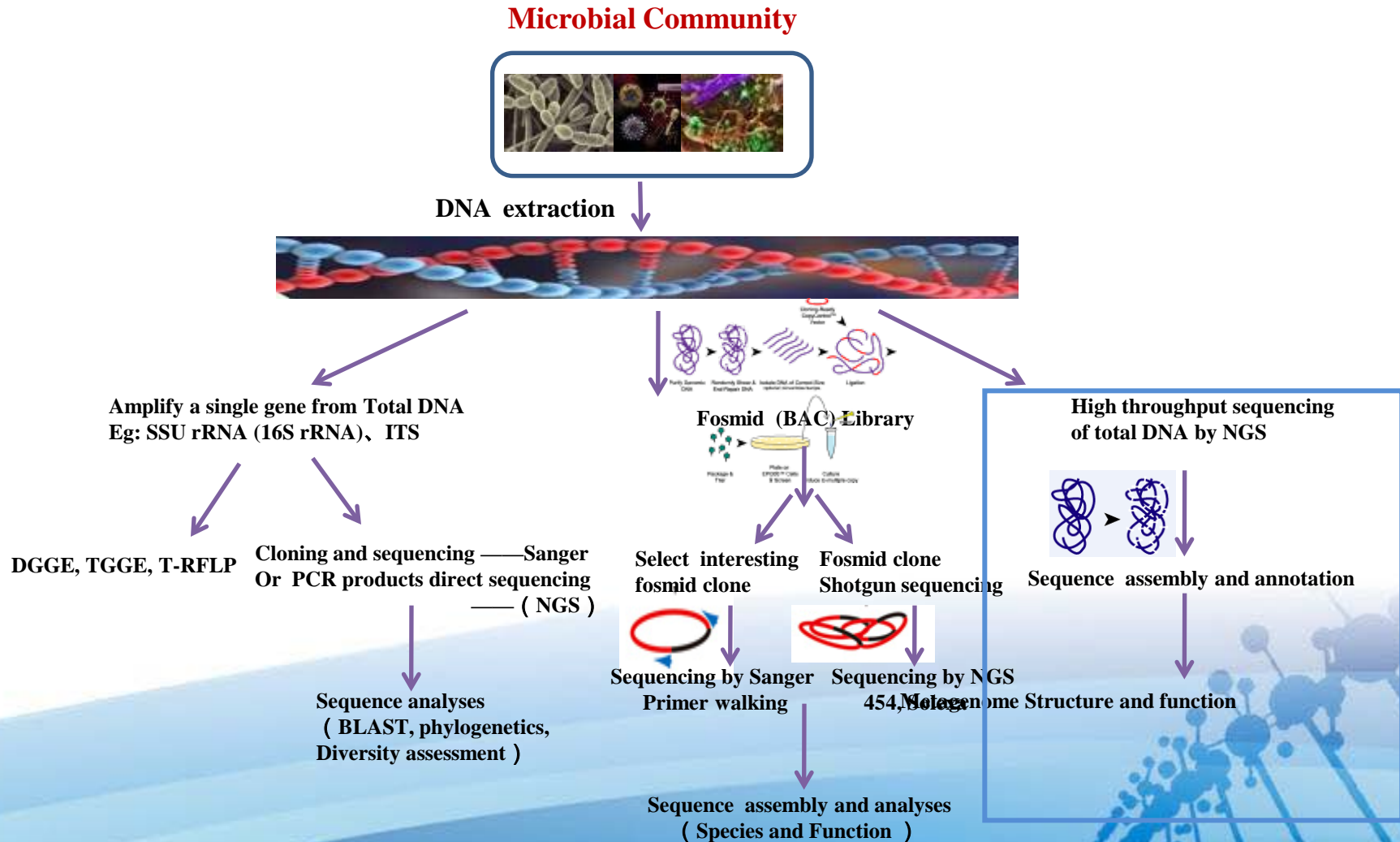
○ *Nature*. 464, 59-65(2010).

● *Andrologia*. 40, 66–71(2008).



From: <http://commonfund.nih.gov/hmp/>

A Framework for metagenomics



insert size

140bp, 180bp, 350bp, 500bp, 2k, ... , 10kb

reads length

(2×)90bp, (2×)100bp ...



16S rDNA

Metagenome

Metatranscriptome



Tens of millions of reads per lane, still increasing



137 Illumina HiSeq sequencers



27 SOLiD™ 4 systems sequencers



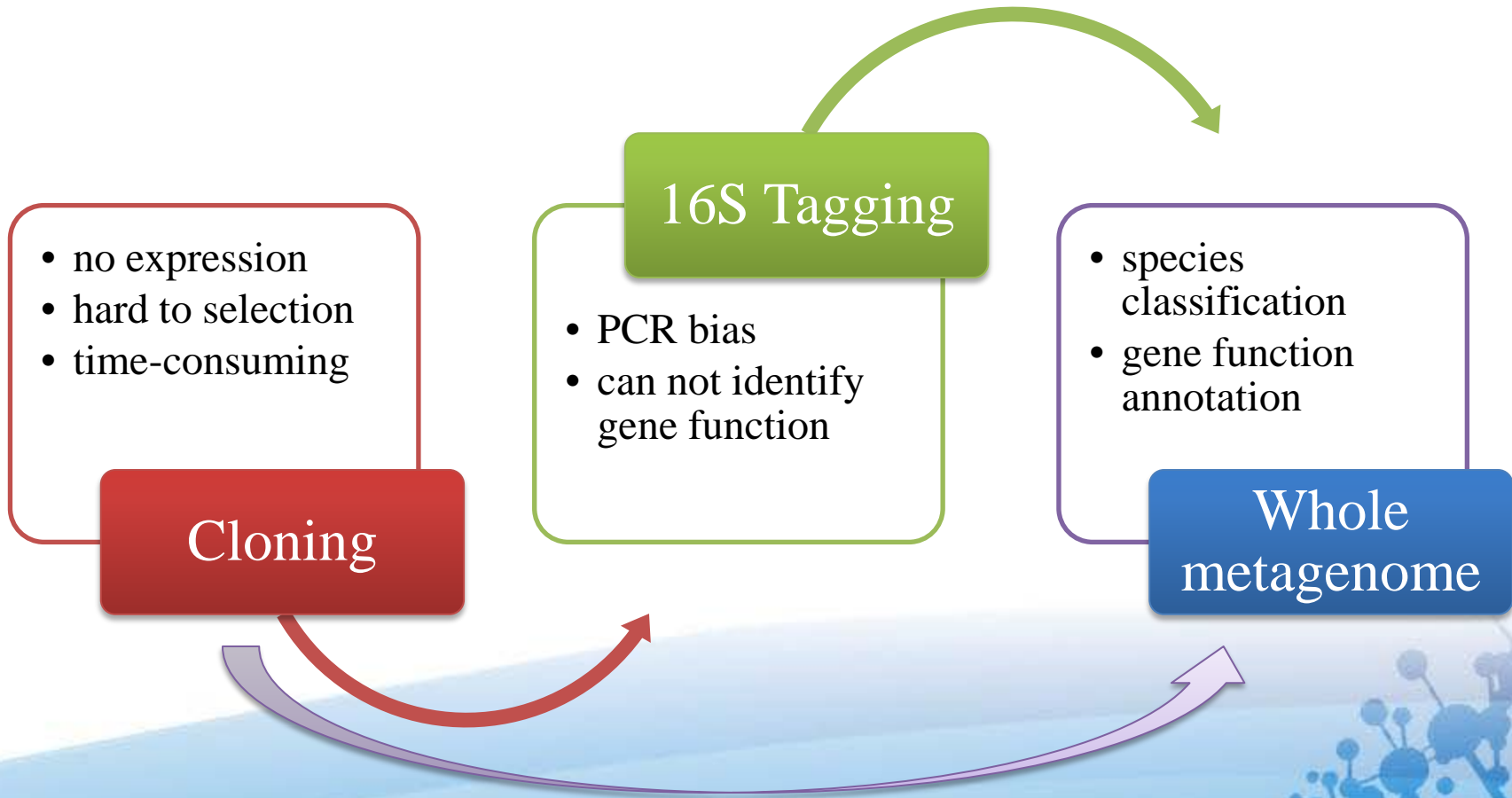
Hard disk storage is more than **10 TB**

CPU speed is more than **102 TFLOPS**

Have bioinformatics staff of **1000**

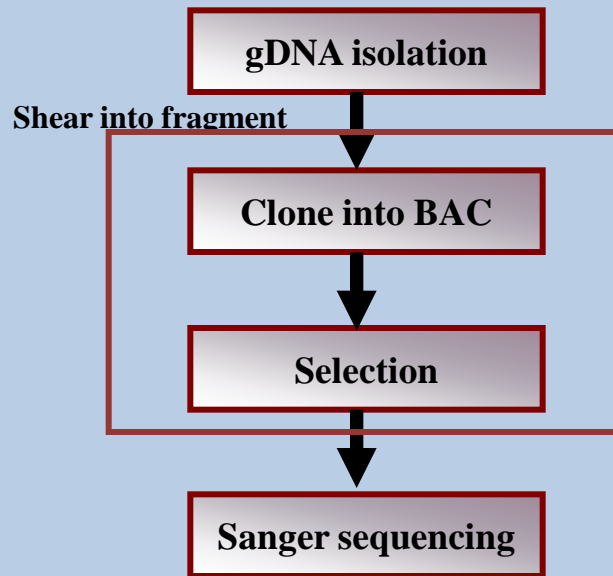


Comparisons of strategies



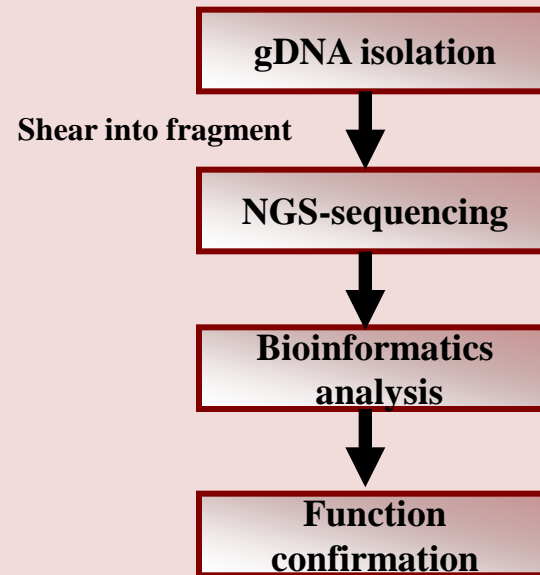
Comparisons of two method

Sanger method



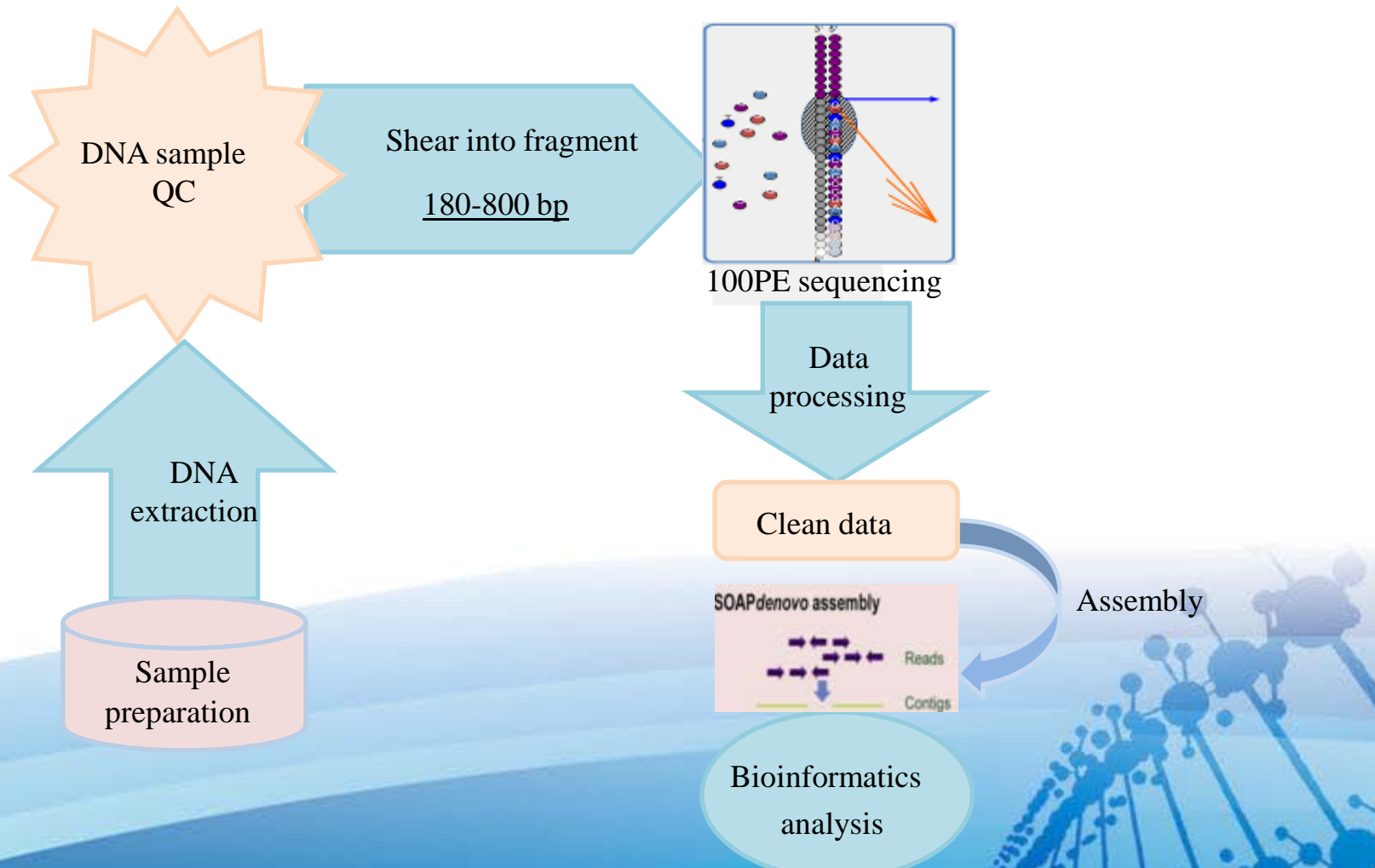
Hundreds of gene

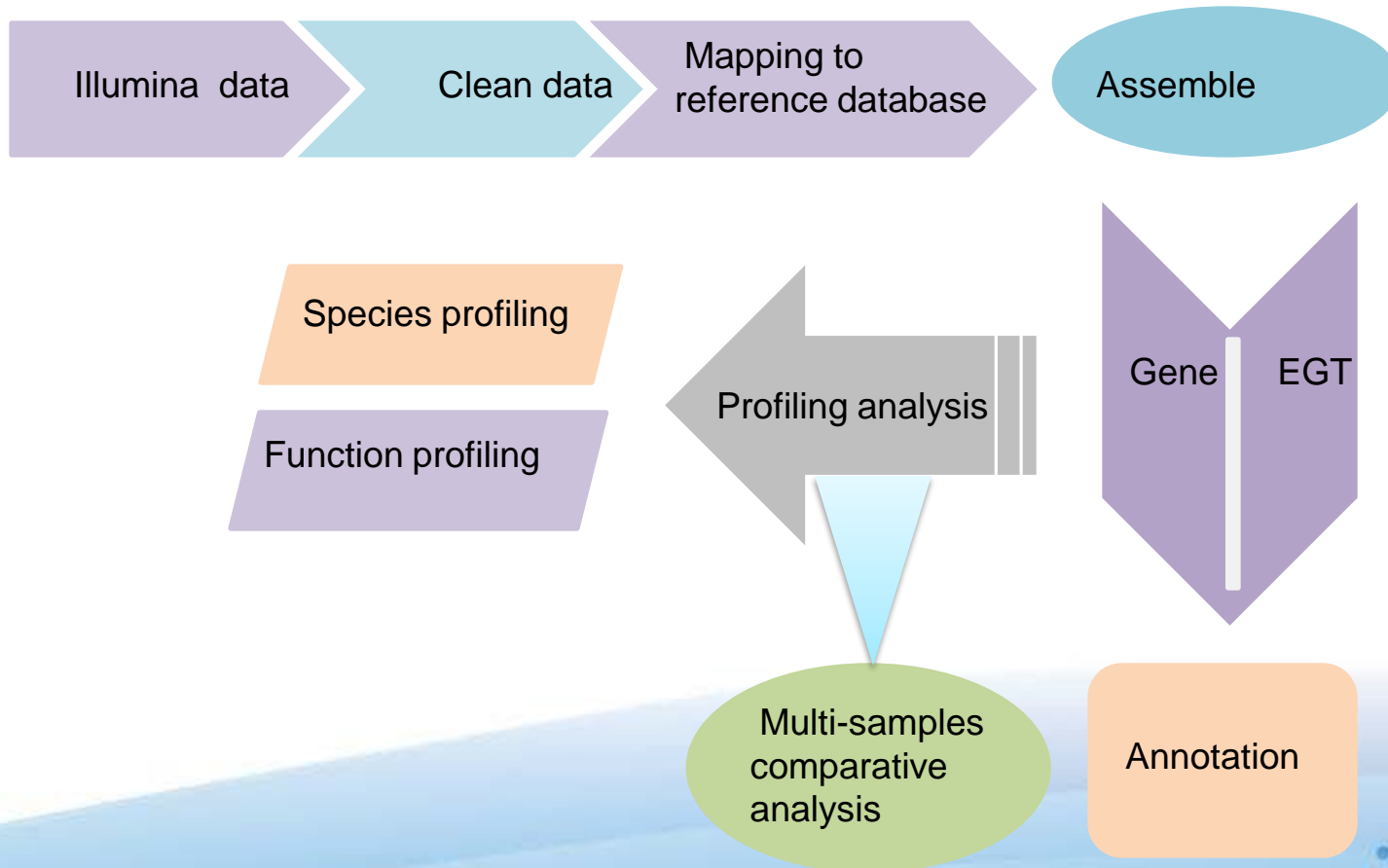
NGS method



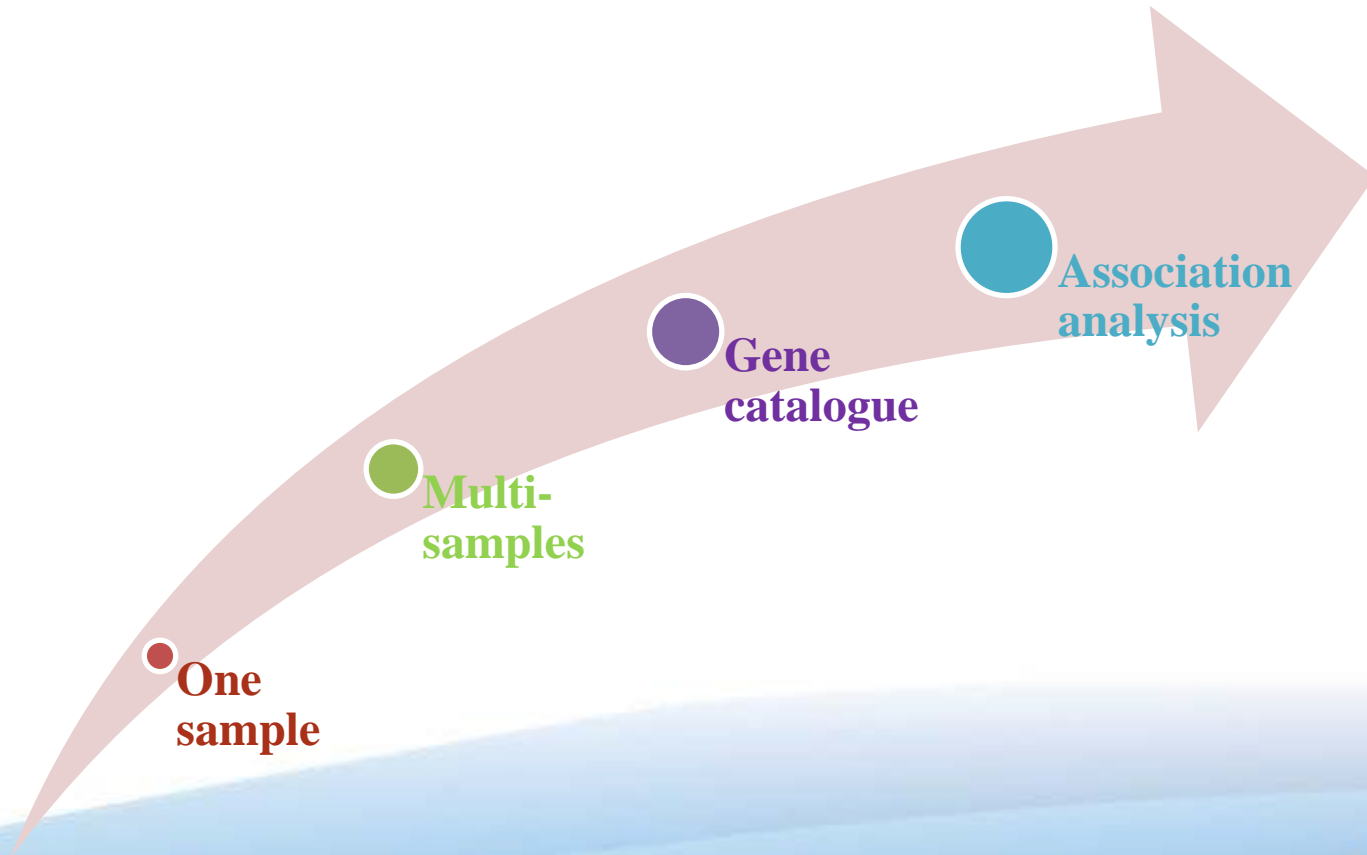
Millions of gene

Overview of Work Flow





What can metagenomics project proceed?



Reference Genomes

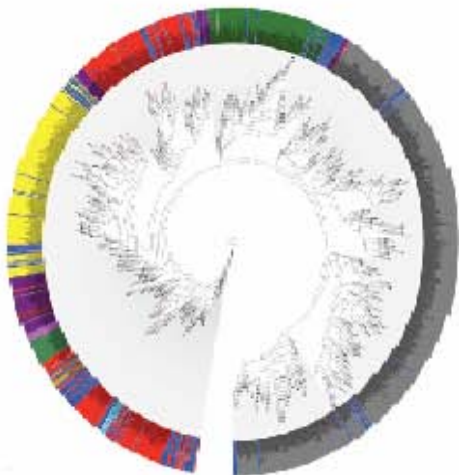
178 Bacterial genome sequence

Nelson, K. E. et al. *Science* 328, 994–999 (2010).

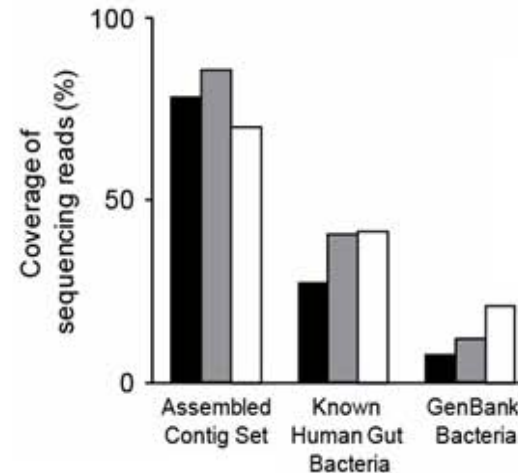
Reference gene catalogue

3.3 million gene data

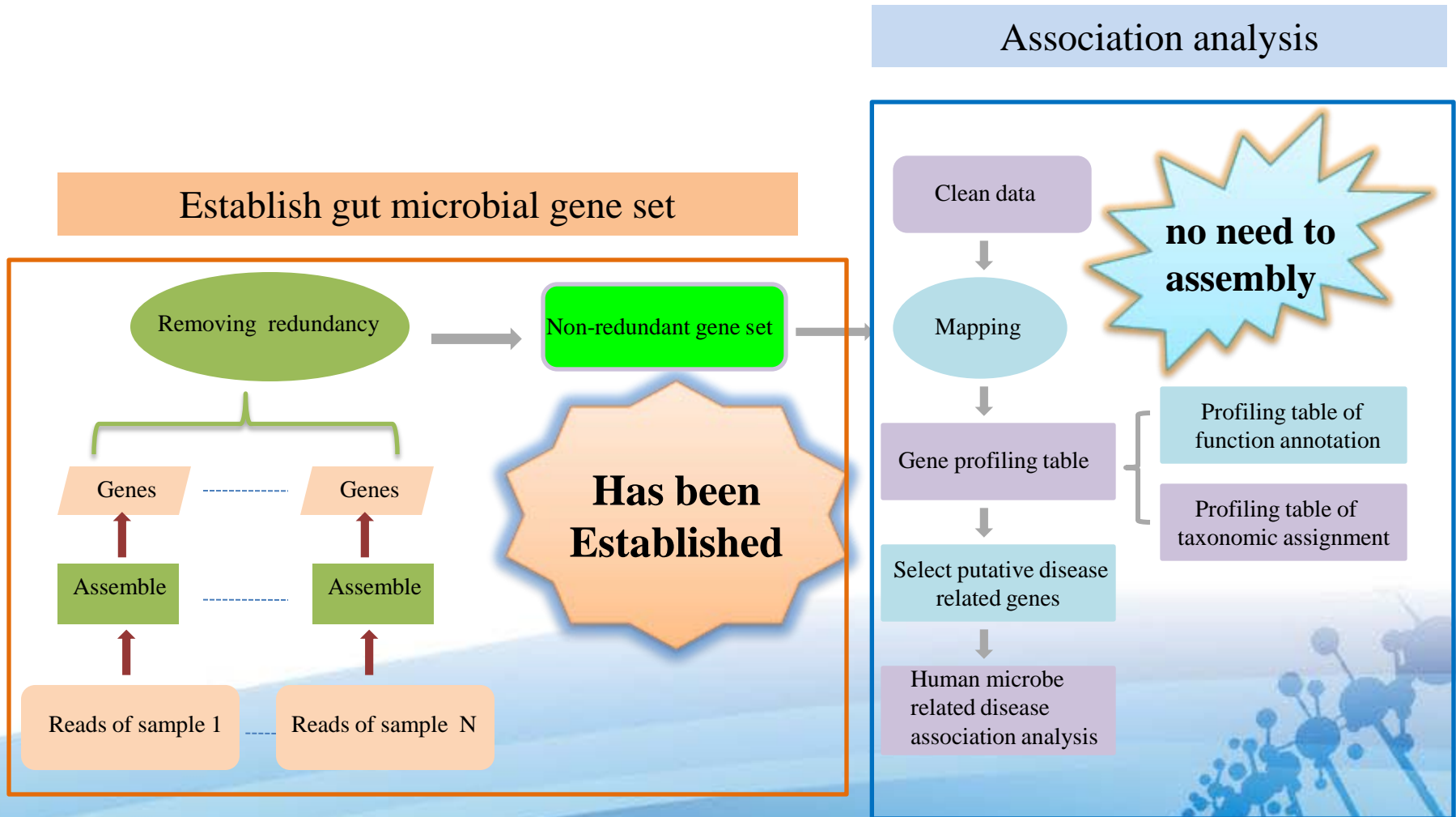
Qin, J. et al. *Nature* 464, 59–65 (2010).



NIH

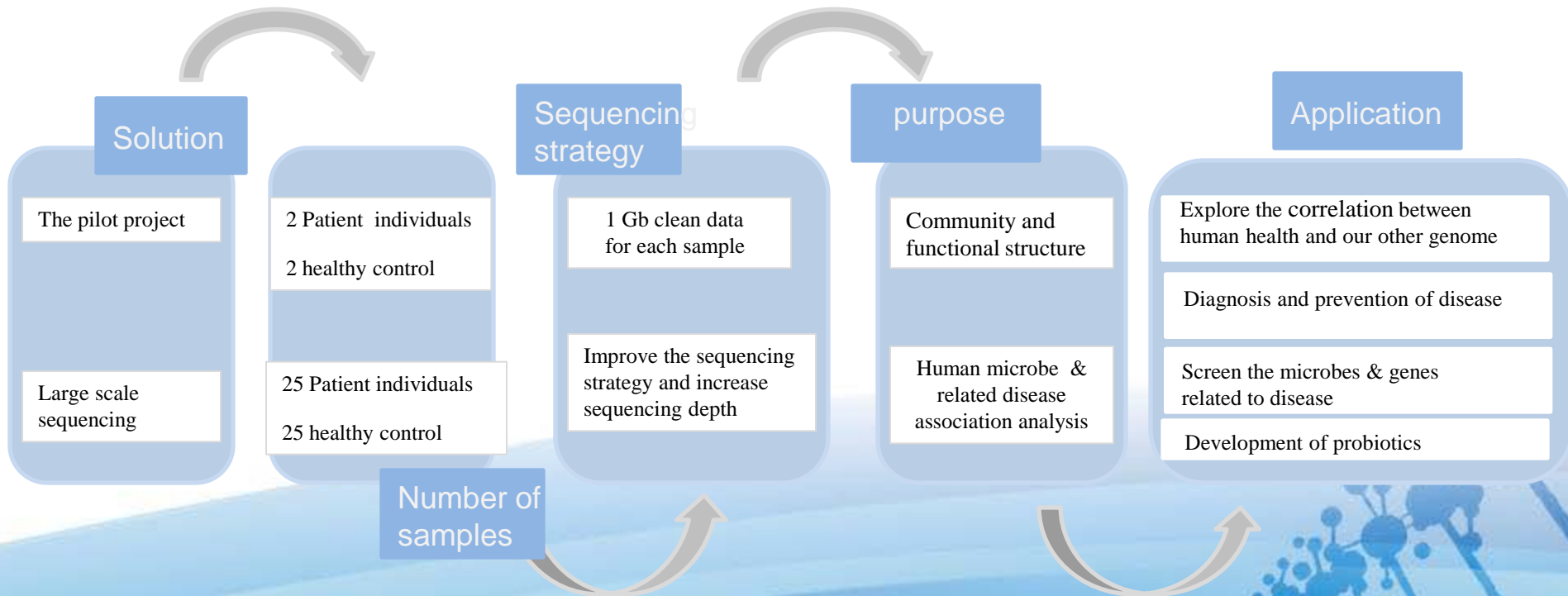


Association analysis: Based on reference gene set



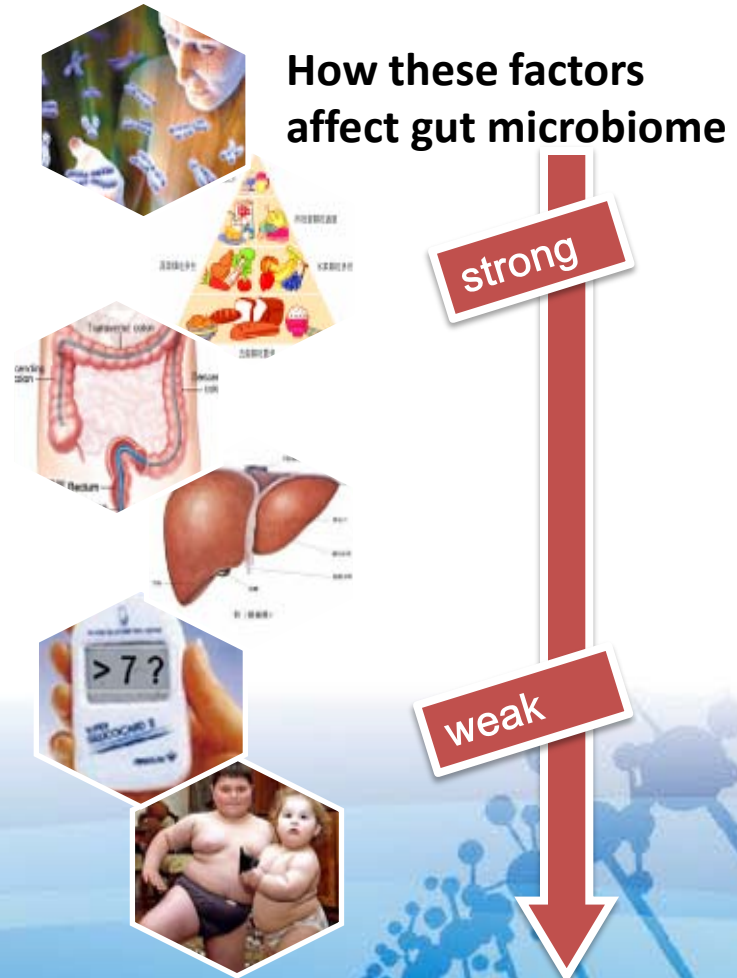
Association analysis: microbial genome & human disease

Package solution

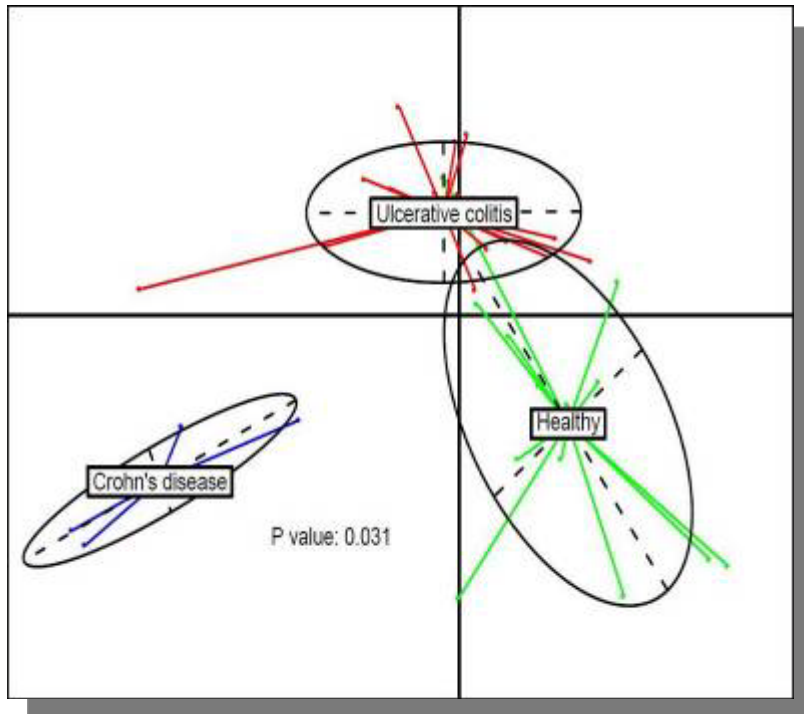


Association analysis: Project under process in BGI

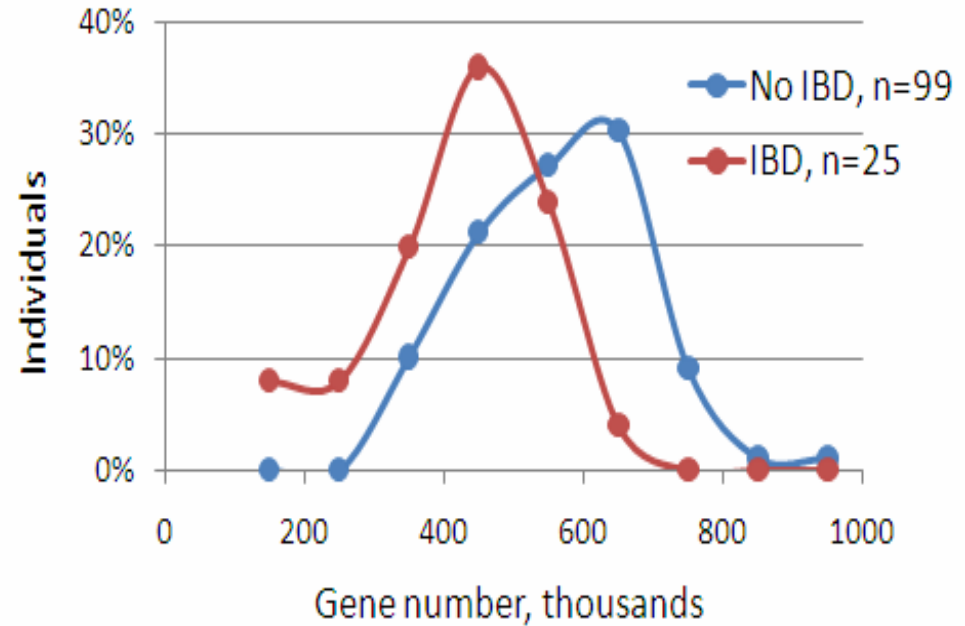
Focus	Sample number	Data (G)
Human health & food	24	43
Obesity	177	858
IBD	143	665
Type 2 Diabetes	73	171
HBV patient	8	32
Virus of human tissue	119	511
Total	425	1800



Demo case 1



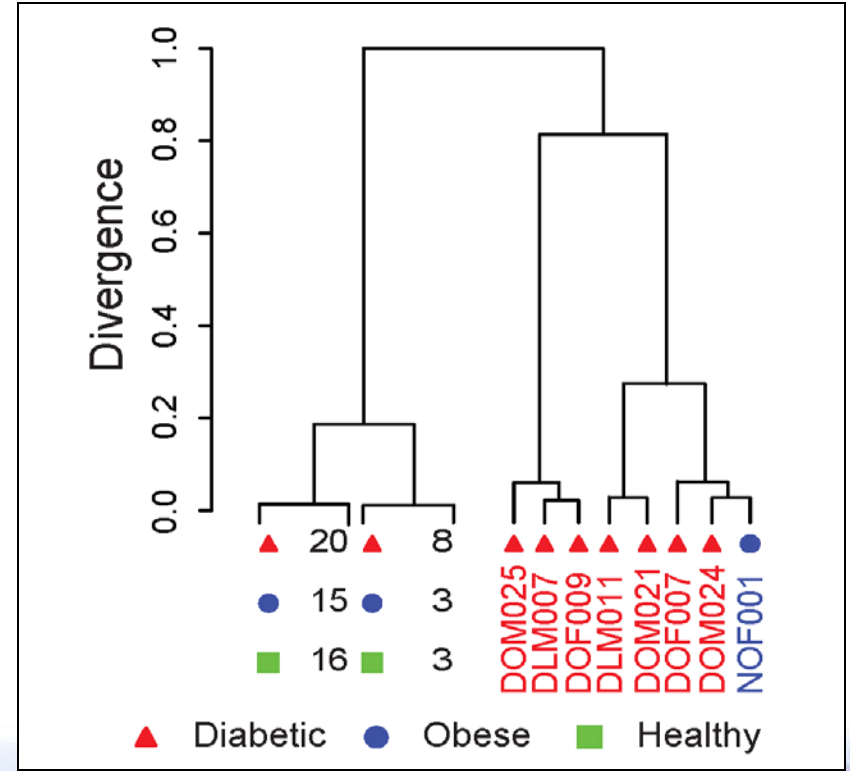
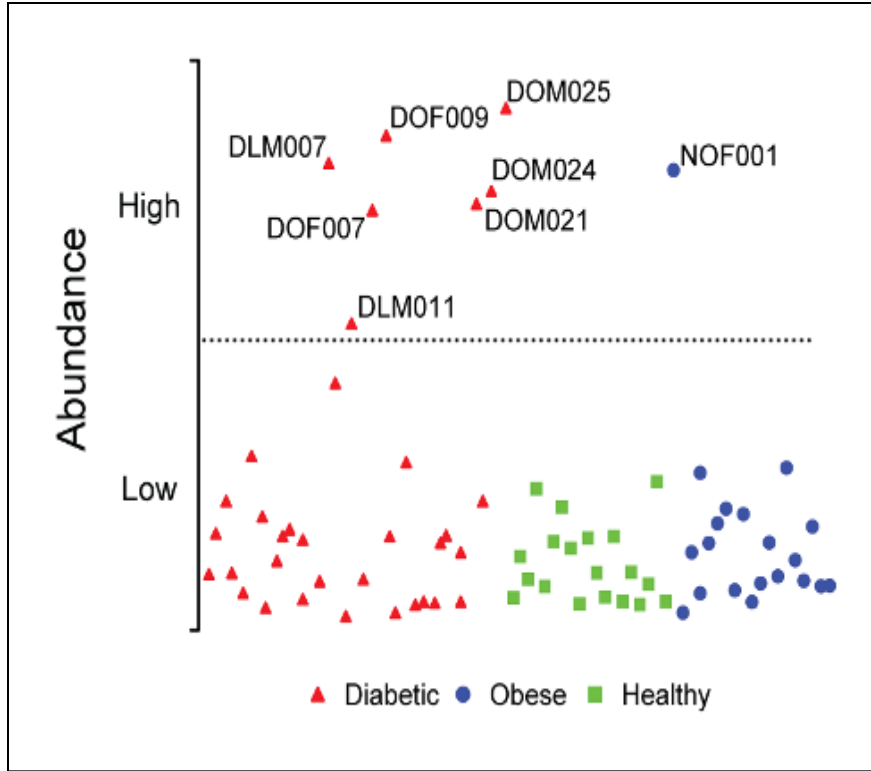
Bacterial species abundance differentiates IBD patients and healthy individuals



Distribution of nonredundant bacterial genes in IBD patients and healthy controls

Junjie Qin, et al.(2010).“A human gut microbial gene catalogue established by metagenomic sequencing”. Nature,(464):59-65.

Demo case 2



Screen the microbe related with Type 2 Diabetes

Junjie Qin, et al. **unpublished.**

What do you think?



**How to make full use of our
Metagenomics tool?**



Welcome to participate

The First International EMP (Earth Microbiome Project) Conference



June 13th-15th 2011, in Shenzhen, China

<http://emp.genomics.org.cn>

A high-altitude mountain climbing scene. A line of climbers is ascending a steep, icy slope. The lead climber is wearing a red helmet and dark gear. The background shows rugged, snow-covered mountain peaks under a blue sky with some clouds.

BGI:

**YOUR PREMIER SCIENTIFIC
PARTNER**

Thanks!

tech@genomics.cn

Shenzhen, China