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**FACULTY OF ENGINEERING &
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INTRODUCTION

- The term **metagenomics** first used by **Jo Handelsman, Jon Clardy, Robert M. Goodman** and first appeared in publication in **1998**.
- Metagenomics defined as “**the genomics analysis of microorganism by direct extraction and cloning DNA from an assemblage of microorganism.**”
- In Greek, **meta** means “**transcendent**” (combination of separate analysis) **Genomics** refers to the study of the **genome**



Jo Handelsman



Introduction

- Metagenomics is the study of metagenome, genetics material, recovered directly from environmental sample such as soil, water or faeces.
- Metagenomics is based on the genomics analysis of microbial DNA directly from the communities present in samples
- Metagenomics technology – genomics on a large scale will probably lead to great advances in medicine, agriculture, energy production and bioremediation.
- Metagenomics can unlock the massive uncultured microbial diversity present in the environment for new molecule for therapeutic and biotechnological application.
- Metagenomic studies have identified many novel microbial genes coding for metabolic pathways such as energy acquisition, carbon and nitrogen metabolism in natural environments that were previously considered to lack such metabolism

Cont...

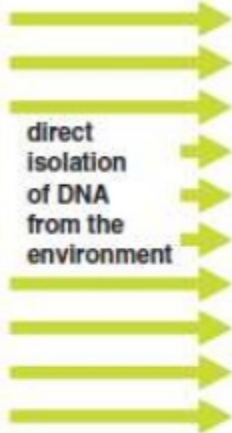
- The science of metagenomics, only a few years old, will make it possible to investigate microbes in their natural environments, the complex communities in which they normally live.
- It will bring about a transformation in biology, medicine, ecology, and biotechnology that may be as profound as that initiated by the invention of the microscope.
- All plants and animals have closely associated microbial communities that make necessary nutrients(carbon, nitrogen, oxygen, and sulfur) metals, and vitamins available to their hosts.
- We depend on microbes to remediate toxins in the environment—both the ones that are produced naturally and the ones that are the byproducts of human activities, such as oil and chemical spills.



WHY METAGENOMICS?

- Science of metagenomics make it possible to investigate resource for the development of novel genes, enzymes and chemical compounds for use in biotechnology.
- Microbes, as communities, are key players in maintaining environmental stability.
- Investigate microbes in their natural environment, the complex communities in which they normally live in.
- High-throughput gene-level studies of communities.





direct
isolation
of DNA
from the
environment

metagenomics



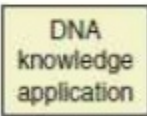
DNA
knowledge
application



Metagenomics can in principle
access 100% of the genetic
resources of an environment.



cultivation



DNA
knowledge
application

isolation
of DNA



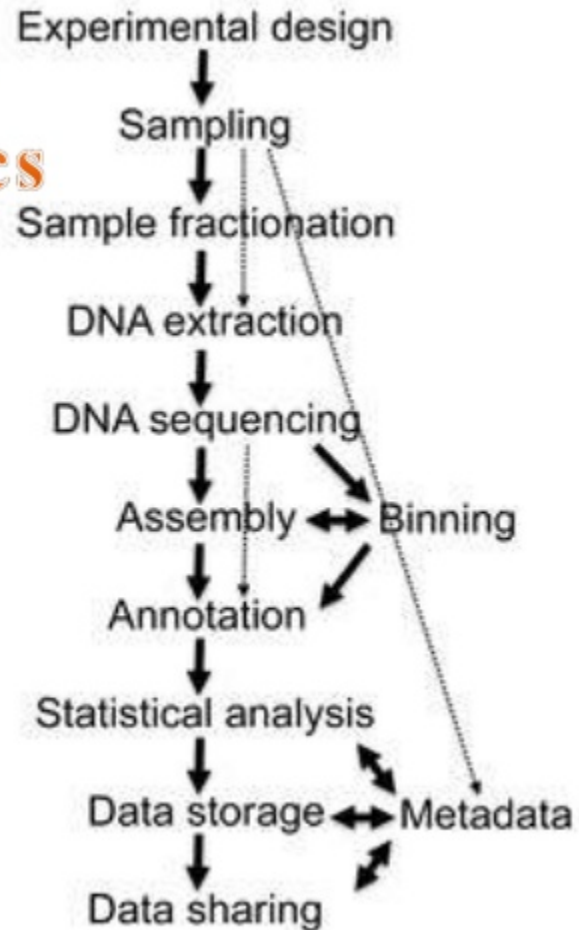
cultivable
species

genomics



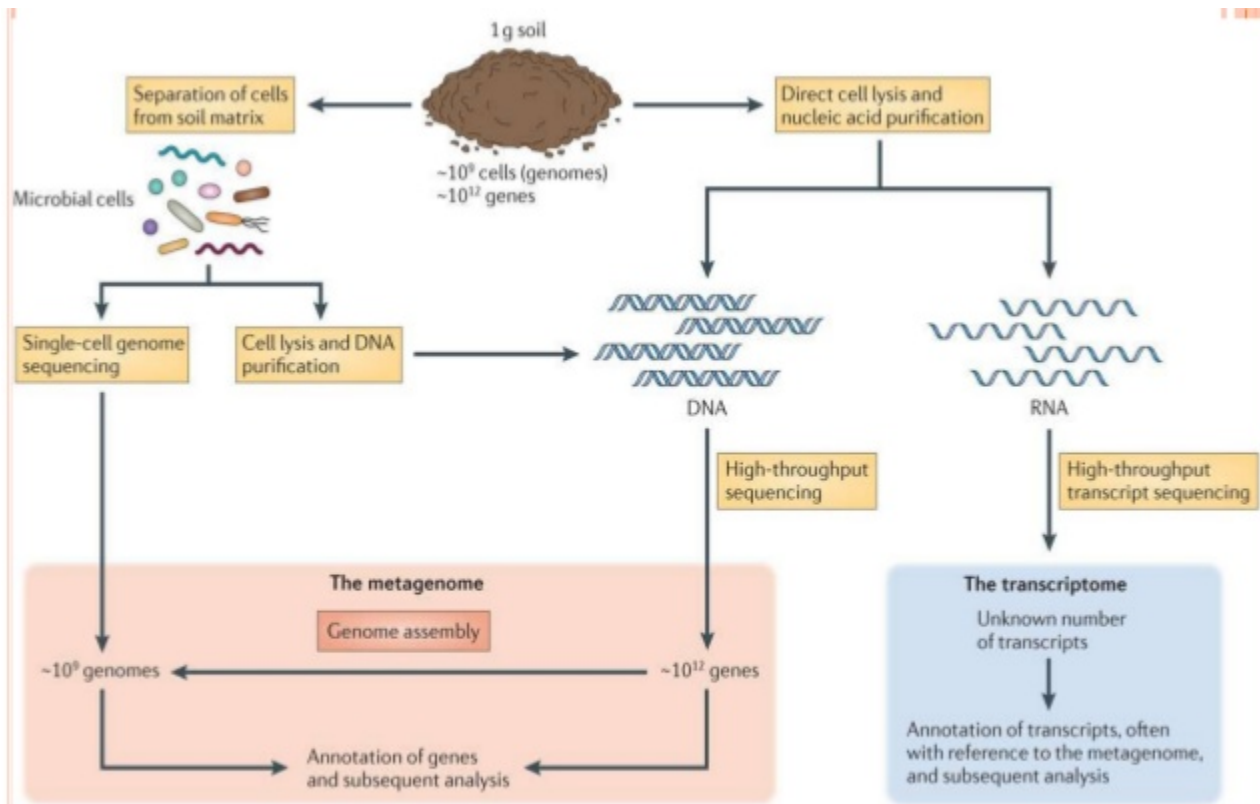
Traditional cultivation methods
and traditional genomics can at
best access 1%.

Overview of metagenomics



Sampling and processing

- Sample processing is the first and most crucial step in metagenomics.
- DNA extracted should be representative of all cells present in the sample and sufficient amounts of high quality nucleic acids must be obtained for subsequent library production and sequencing.
- Sample fractionation steps should be checked to ensure that sufficient enrichment of the target is achieved and that minimal contamination of non-target material occurs.
- Physical separation and isolation of cells from the samples might also be important to maximize DNA yield or avoid co-extraction of enzymatic inhibitors that might interfere with subsequent processing.
- Direct lysis of cells versus indirect lysis has a quantifiable bias in terms of microbial diversity, DNA yield, and resulting sequence fragment length.
- Some type of sample such as biopsies or ground water often yield very small amounts of DNA but in library production for most sequencing technologies require high amounts of DNA (ng or μg), and hence **amplification** of starting material might be required.
- Multiple displacement amplification (MDA) using **random hexamers** and **phage phi29 polymerase** is one option employed to increase DNA yields, this method has been widely used in single-cell genomics and to a certain extent in metagenomics.



Type of metagenomics

- There are two basic types of Metagenomics studies
 - I. **Sequence-based Metagenomics**- involves sequencing and analysis of DNA from environmental samples
 - II. **Function-based Metagenomics** involves screening for a particular function or activity

