

Introduction to the ‘-omics’

Elliott J. Price

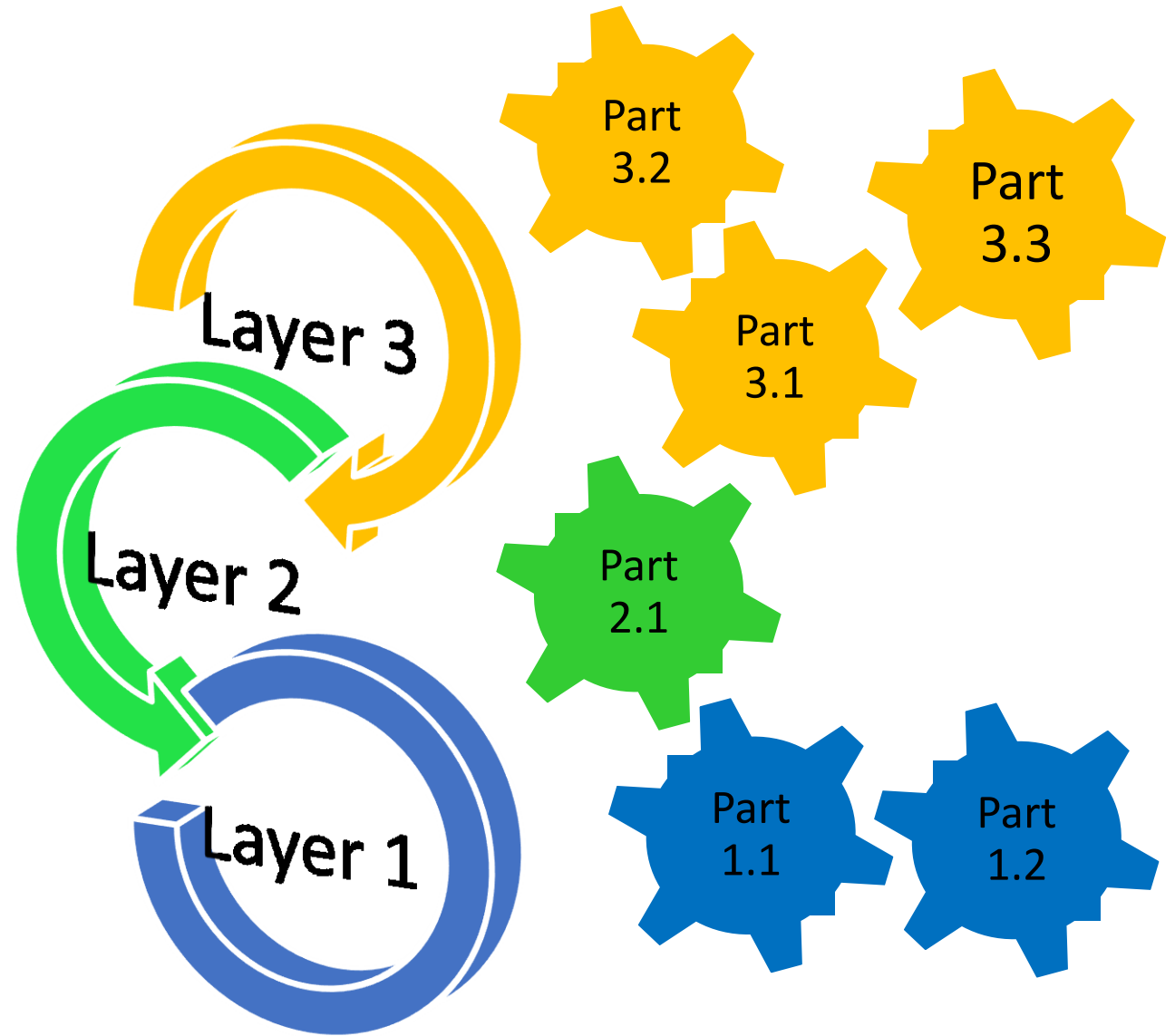
Outline

- What are the 'omics'?
- Common '-omics' technologies
- Multi-omics in environmental chemistry

What is “-omics”?

Systematic and comprehensive analysis
[of a cellular/ molecular layer]

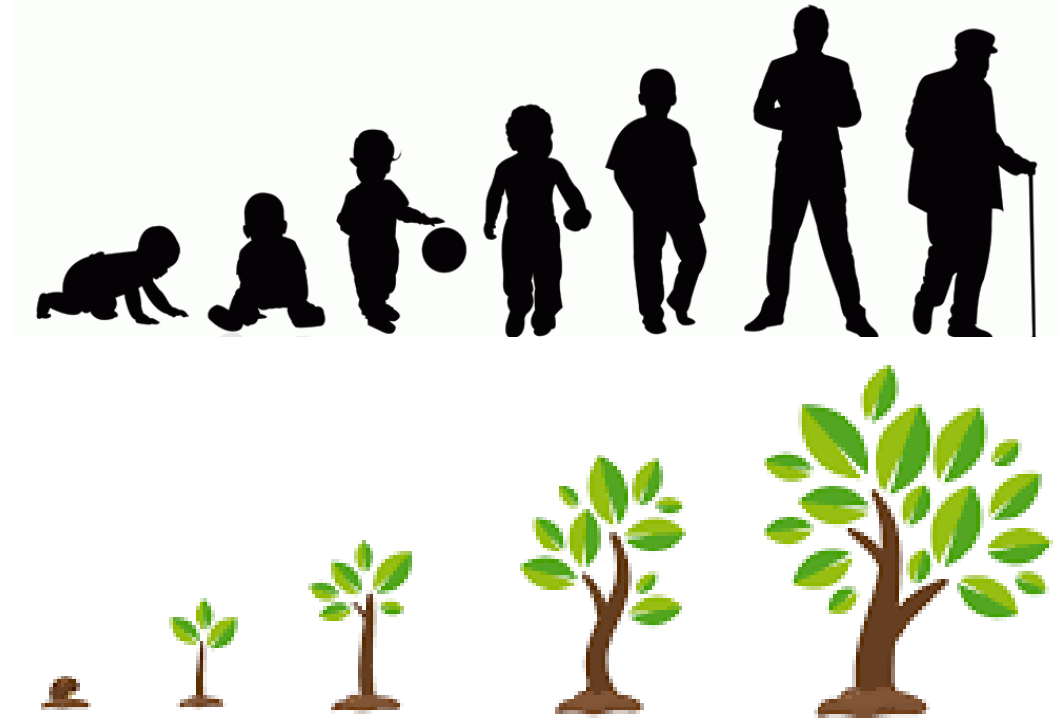
i.e. a subset of
[molecular] phenotyping



Phenotype

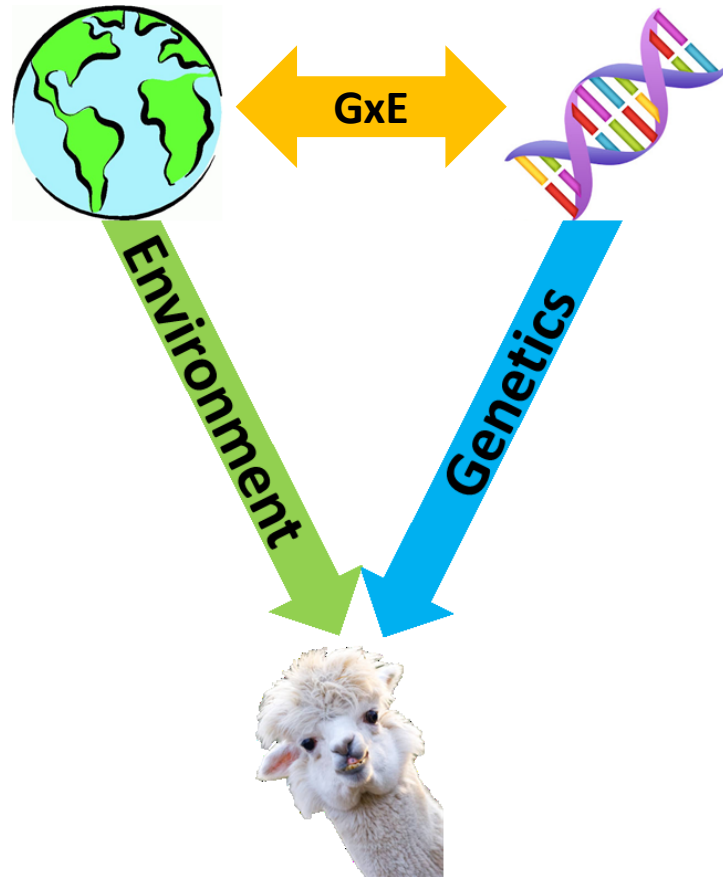
Phenotype =
characteristics [traits]
displayed by an entity
[organism]

Phenotype is dynamic
i.e. changes over time
[development]



Further material: [10.1006/jtbi.1996.0335](https://doi.org/10.1006/jtbi.1996.0335)

Nature and nurture



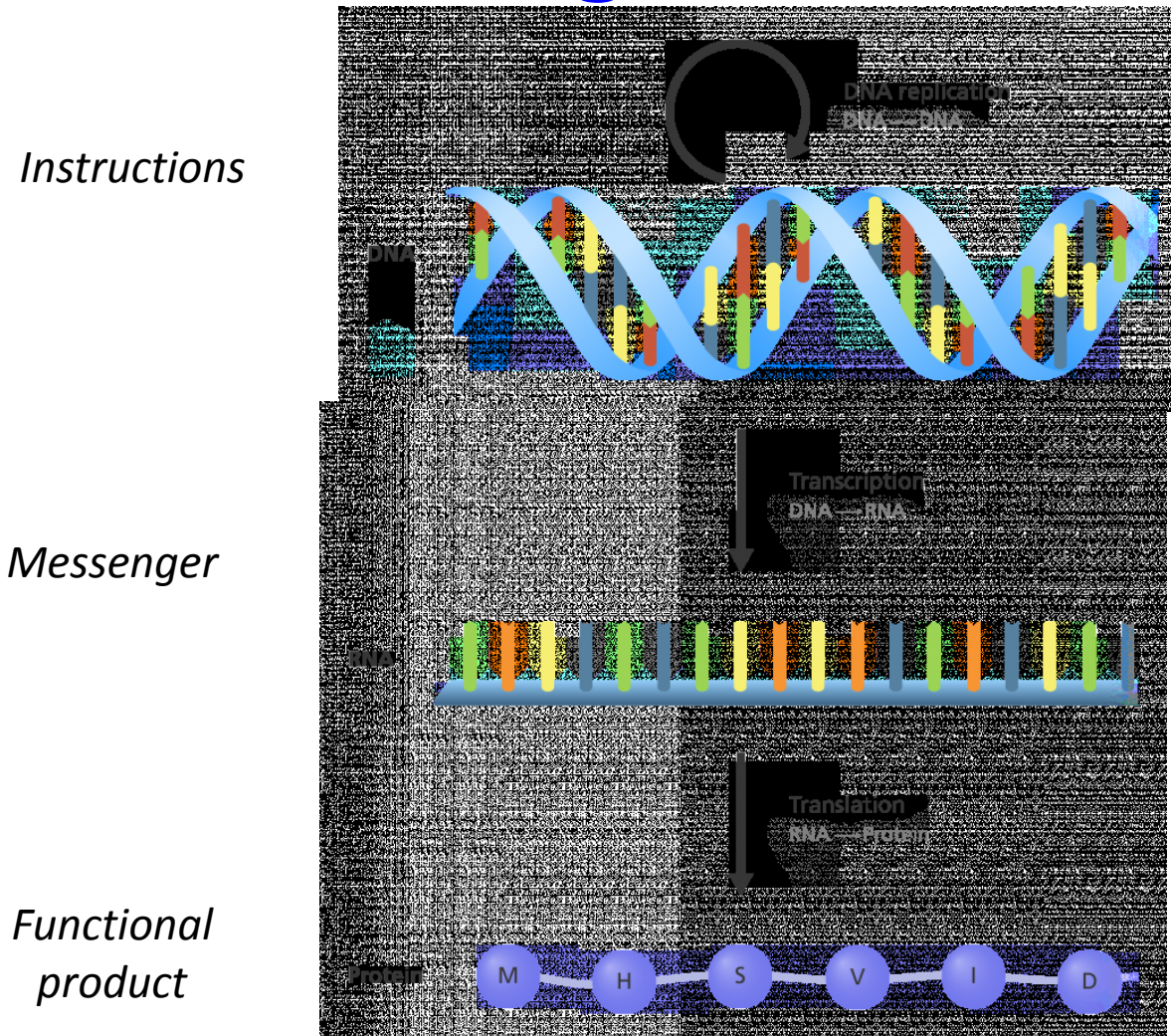
Phenotype is the results of genetics & environment

i.e. need to understand:

- Genotype
- Environment
- Genotype x Environment interaction (**GxE**)

Further material: [Nature via nurture](#)

Central dogma of molecular biology



Genome = all **inherited** genetic material [DNA] of an organism

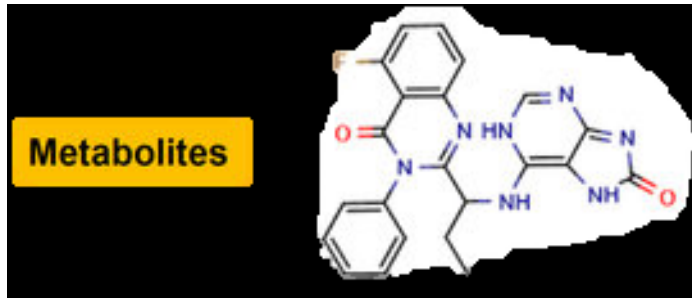
Transcriptome = all the transcribed genetic material [RNA] of an organism i.e. all expressed genes

Proteome = all the **proteins/peptides** of an organism i.e. all translated genetic material

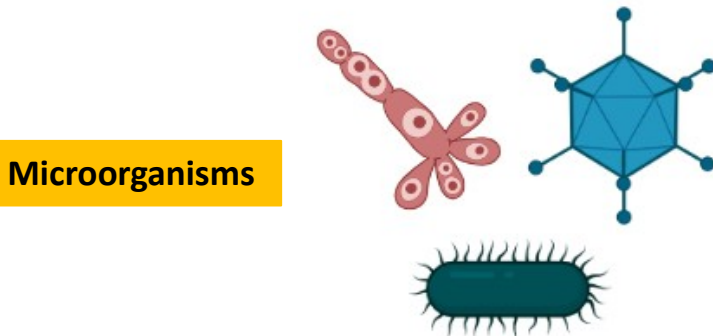
Image: Genome Research Limited



Additional layers of molecular biology



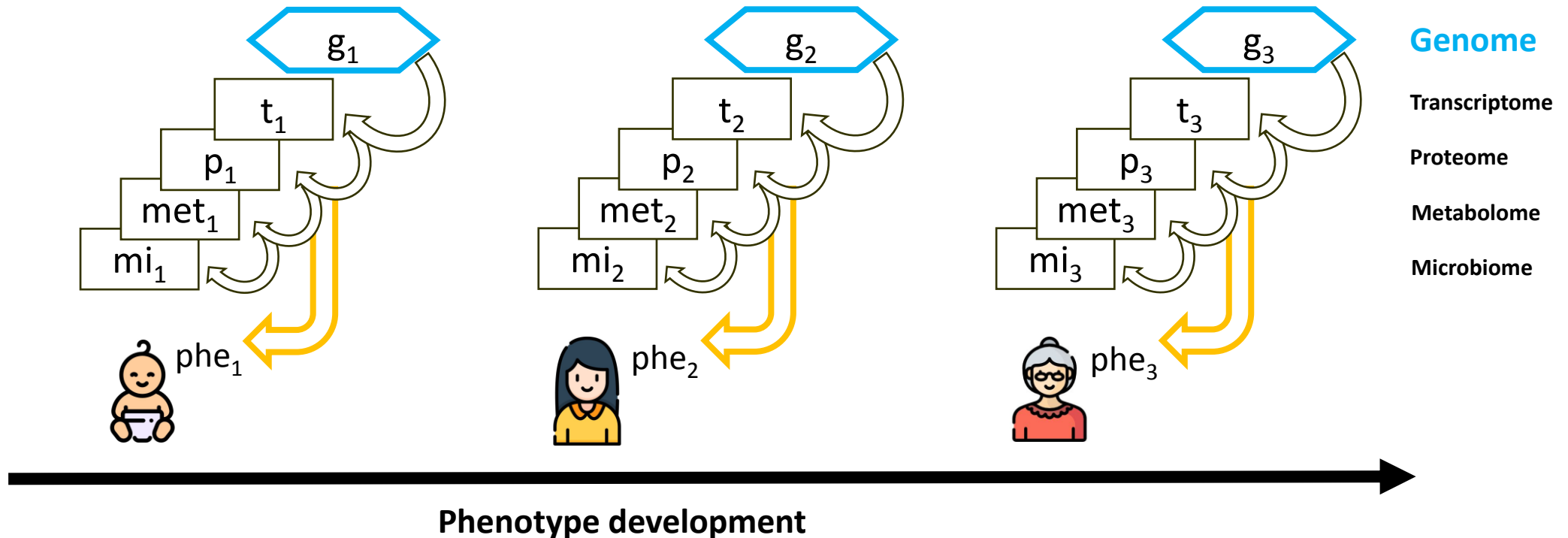
Metabolome = all the **metabolites (small molecules)** of an organism i.e. all small substances active in cellular processes



Microbiome = all the **microorganisms** [in direct contact with an organism]
each with their own genes-to-functions

Image: Biorender

Functional genomics - driven analysis



Further material: <https://youtu.be/D-Ljd5Uex0s>
Online course: [10.6019/TOL.FunGenI-c.2016.00001.1](https://www.fun-genl.com/courses/10.6019/TOL.FunGenI-c.2016.00001.1)

What is the environment?



Image: iStock by Getty images

Environmental exposure and the exposome

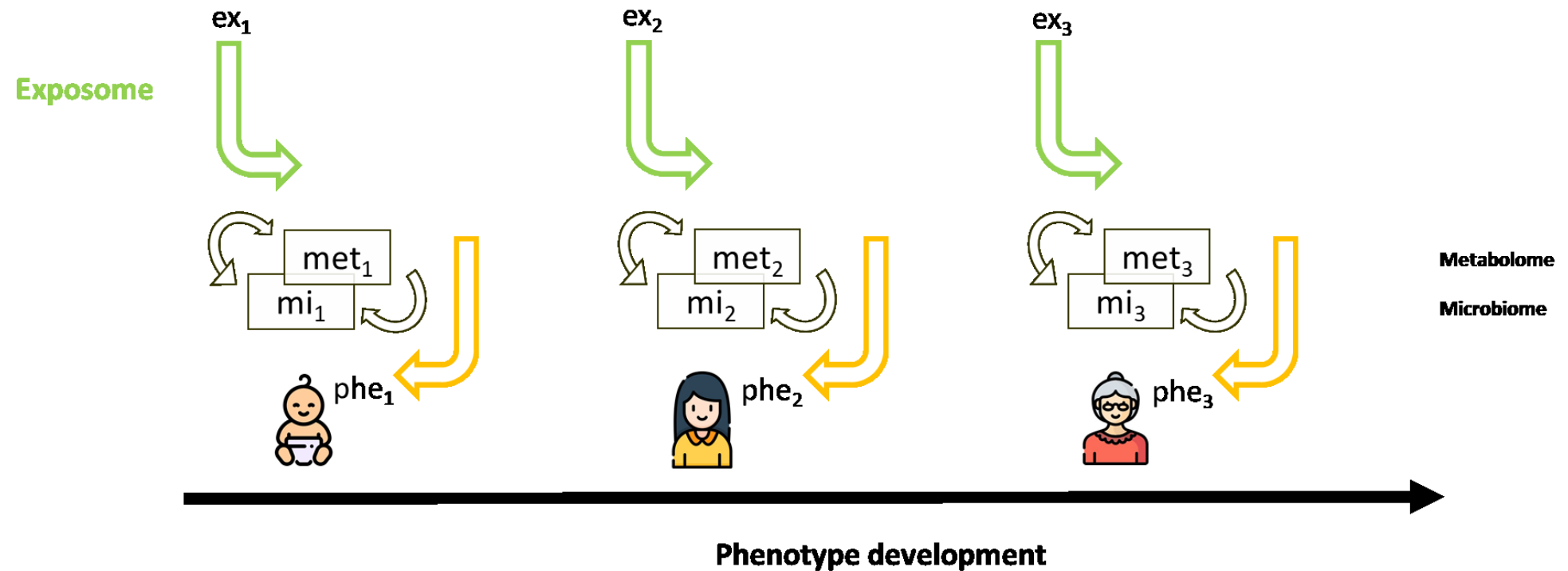
Environmental exposure: contact between an external factor (agent) and an entity.

Contact occurs at an [exposure] interface. Agent includes [external] psychosocial factors. The entity is any subject experiencing contact. A single exposure event is a continuous contact (exposure period).

Exposome: the totality of environmental exposures

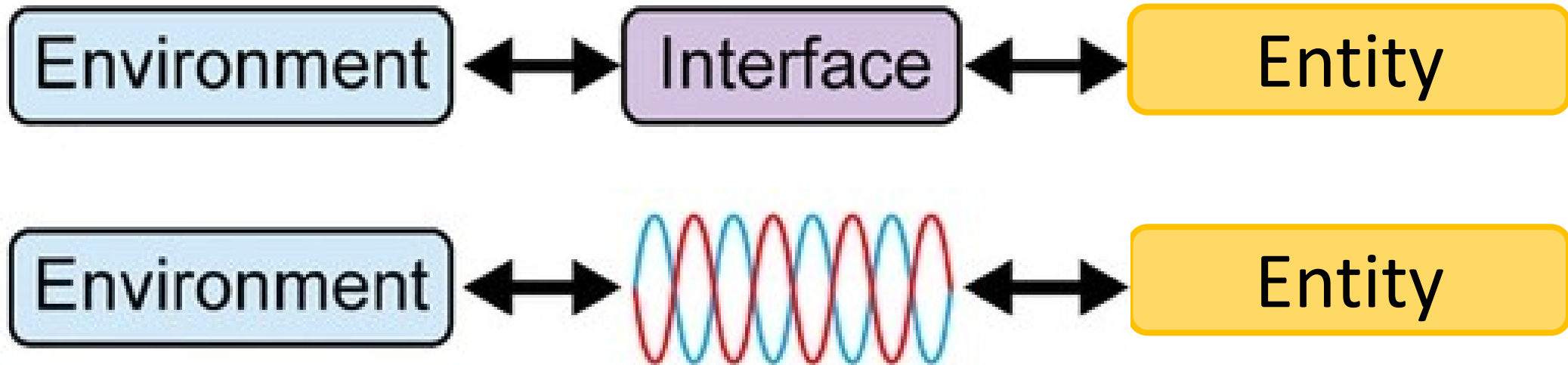
Functional exposomics

Environment-to-phenotype mapping?



Further material: [10.1073/pnas.1903232116](https://doi.org/10.1073/pnas.1903232116)

Biodynamic interfaces & GxE measurement

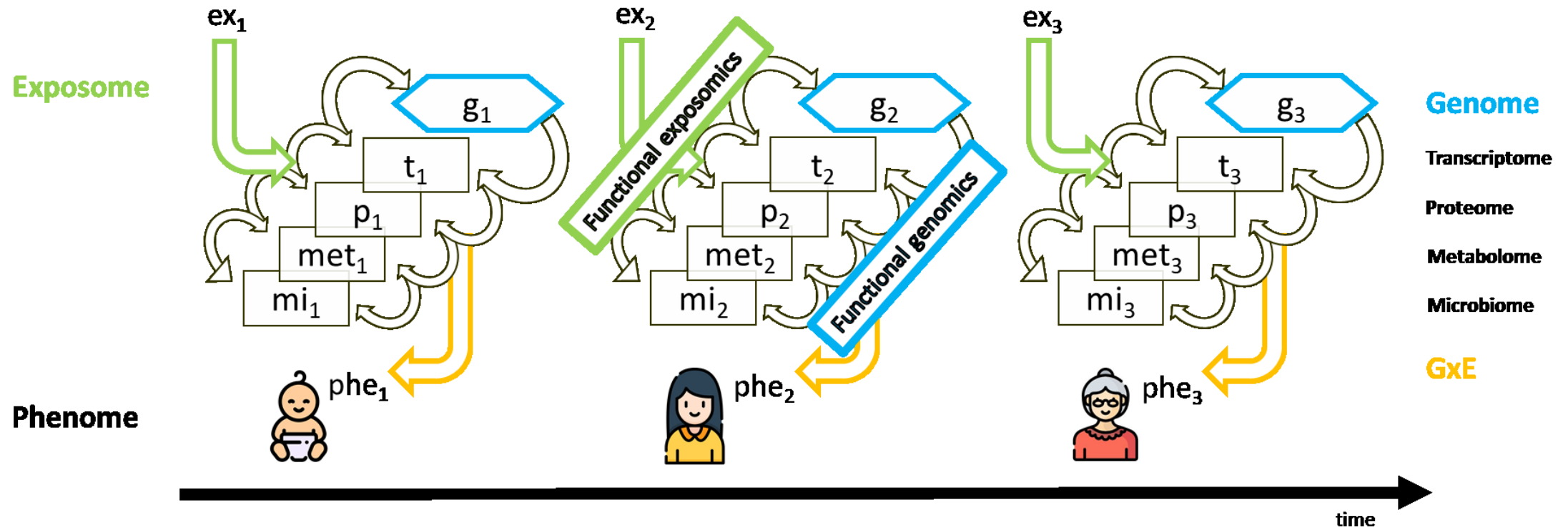


Modified from: [10.1002/bies.202000017](https://doi.org/10.1002/bies.202000017)

GxE interaction – need to understand both sides equally

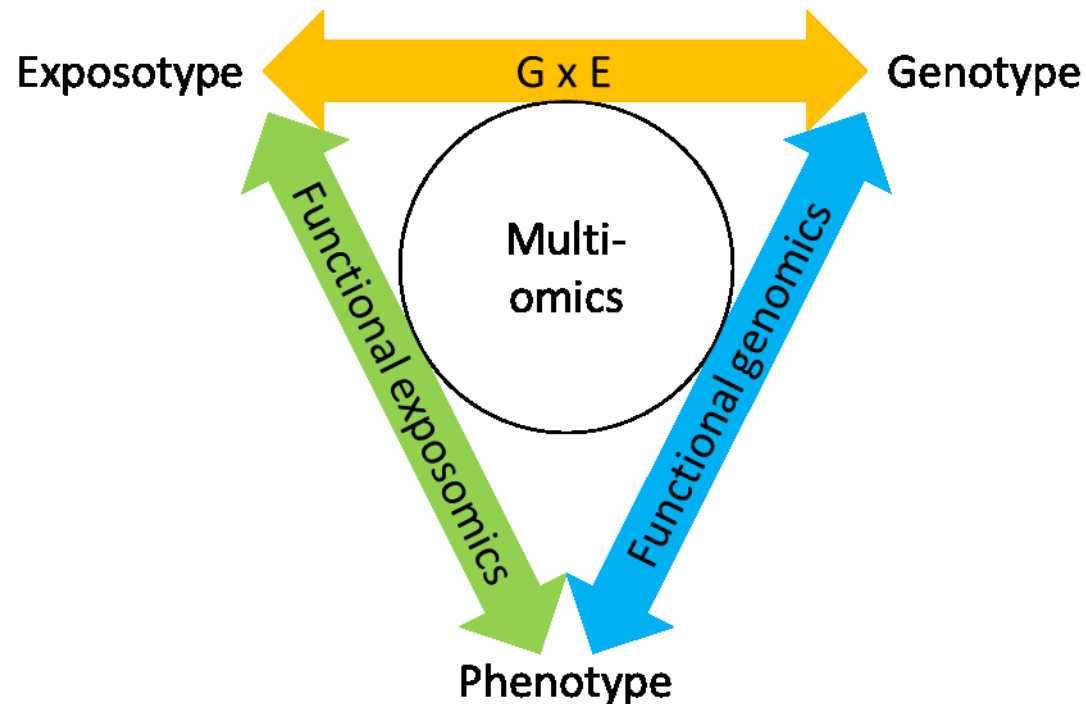
Further material: <https://youtu.be/XeyjeZeyo4o>

Multi-omics analysis



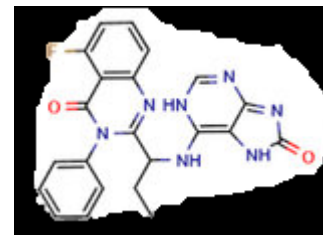
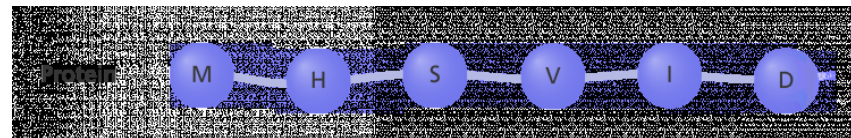
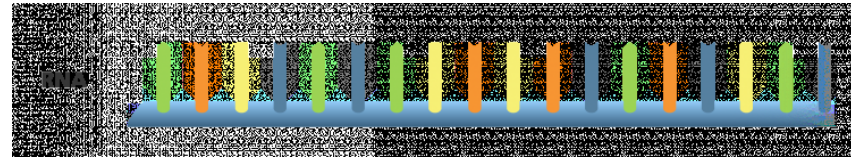
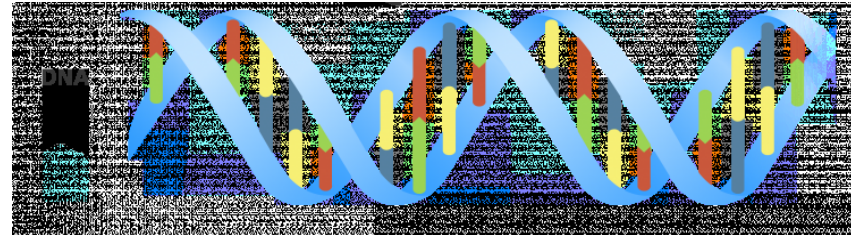
Further material: <https://doi.org/10.5281/zenodo.5579746>

Multi-omics integrated framework

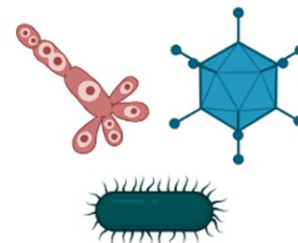


“More extensive characterization of the **exposome** and integration with molecular **multi-omics profiling** is set to advance the factoring of phenotypic variance into genetic and environmental components. Studying their interplay places **genotype-environment interaction** at the center of integrative biology towards deepening our understanding of **phenotype development** and **adaptation** to further **personal, population and ecosystem health.**”

Consideration for 'omics' analysis



Metabolites



Microorganisms

- Hypothesis or observation?
- Which layer(s)?

High-throughput technologies - NGS

- ❑ Next-generation sequencing (NGS)
- ❑ Measure genetic material (i.e. DNA, RNA, [microbiome])
- ❑ Measured via physical properties (e.g. optical fluorescence / electro-conductivity)

Online course: [10.6019/TOL.FunGenII-c.2016.00001.1](https://www.tol.fun-gen.org/courses/10.6019/TOL.FunGenII-c.2016.00001.1)

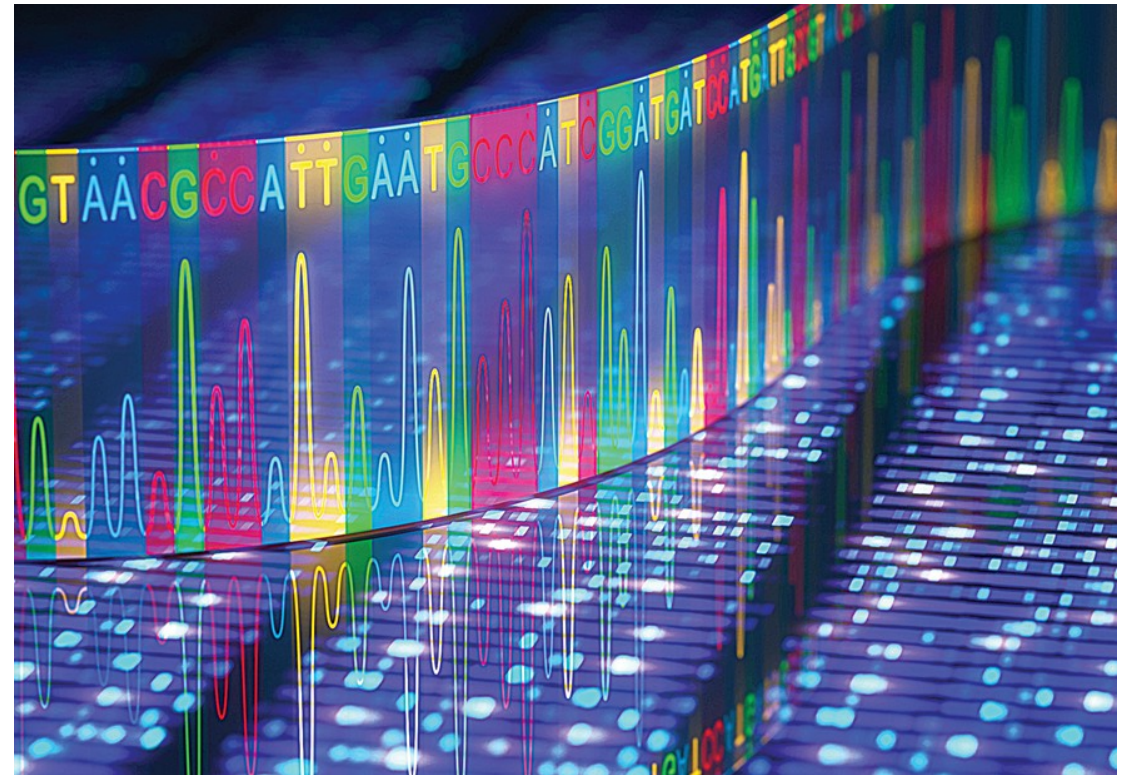


Image: LabManager

High-throughput technologies - NGS

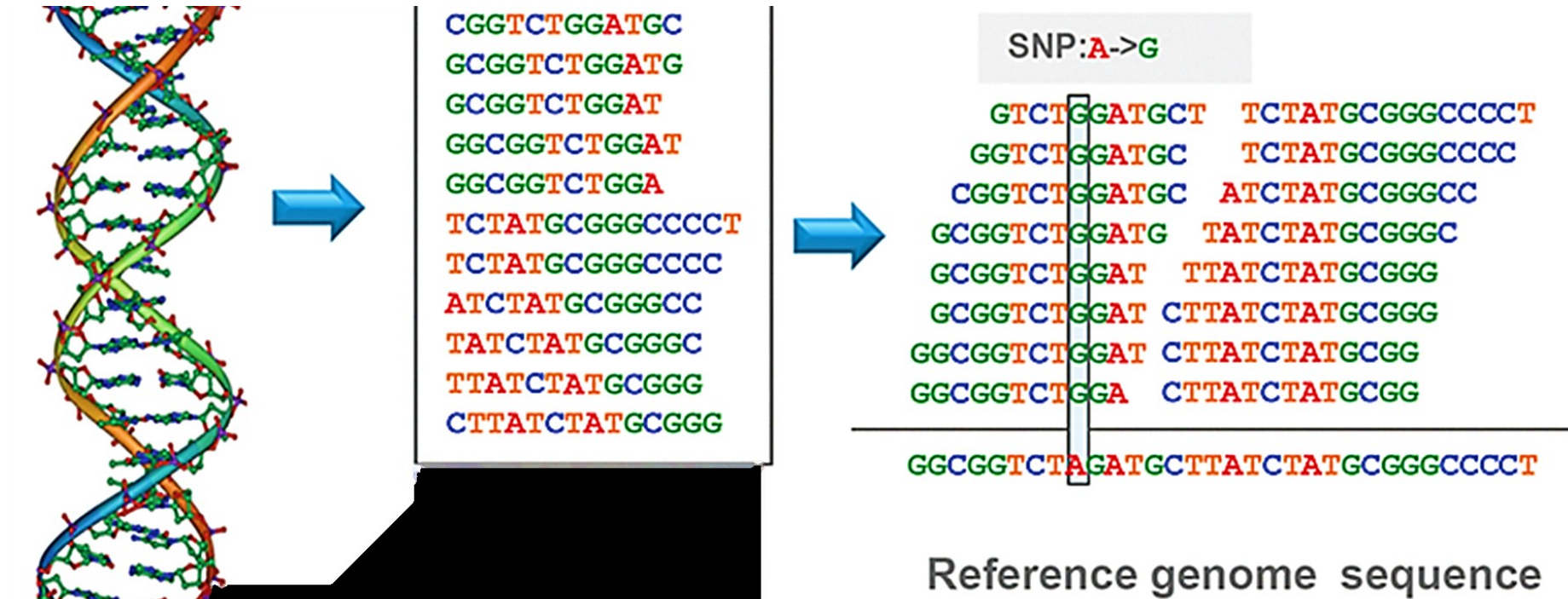


Image from DOI: [10.5772/66732](https://doi.org/10.5772/66732)

□ What genetic material are present?

High-throughput technologies - NGS

Short reads

- Relatively affordable
- Accurate base-pair identifications
- Difficult to assemble / map to scaffold

Long reads

Further material:

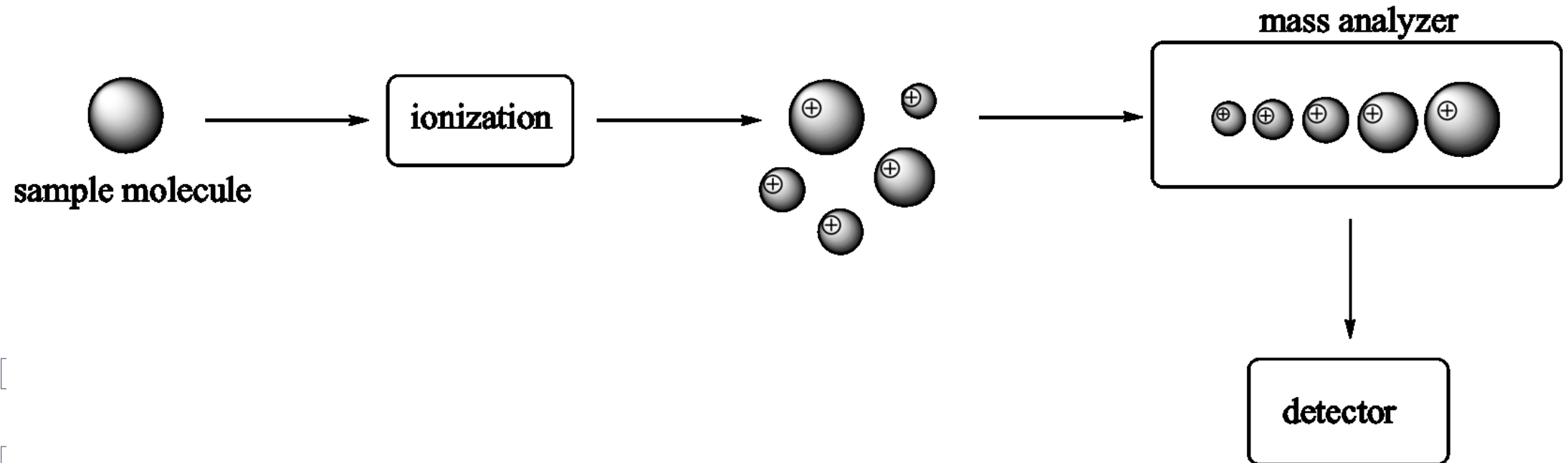
[10.1038/s41576-021-00367-3](https://doi.org/10.1038/s41576-021-00367-3)

- Relatively expensive (~5 times more)
- Less accurate base-pair identification
- Easy to assemble / map to scaffold

How much genetic material is active (expressed)?

- Typically achieve **relative amounts**
- Absolute quantification is possible, otherwise use [RT]-qPCR

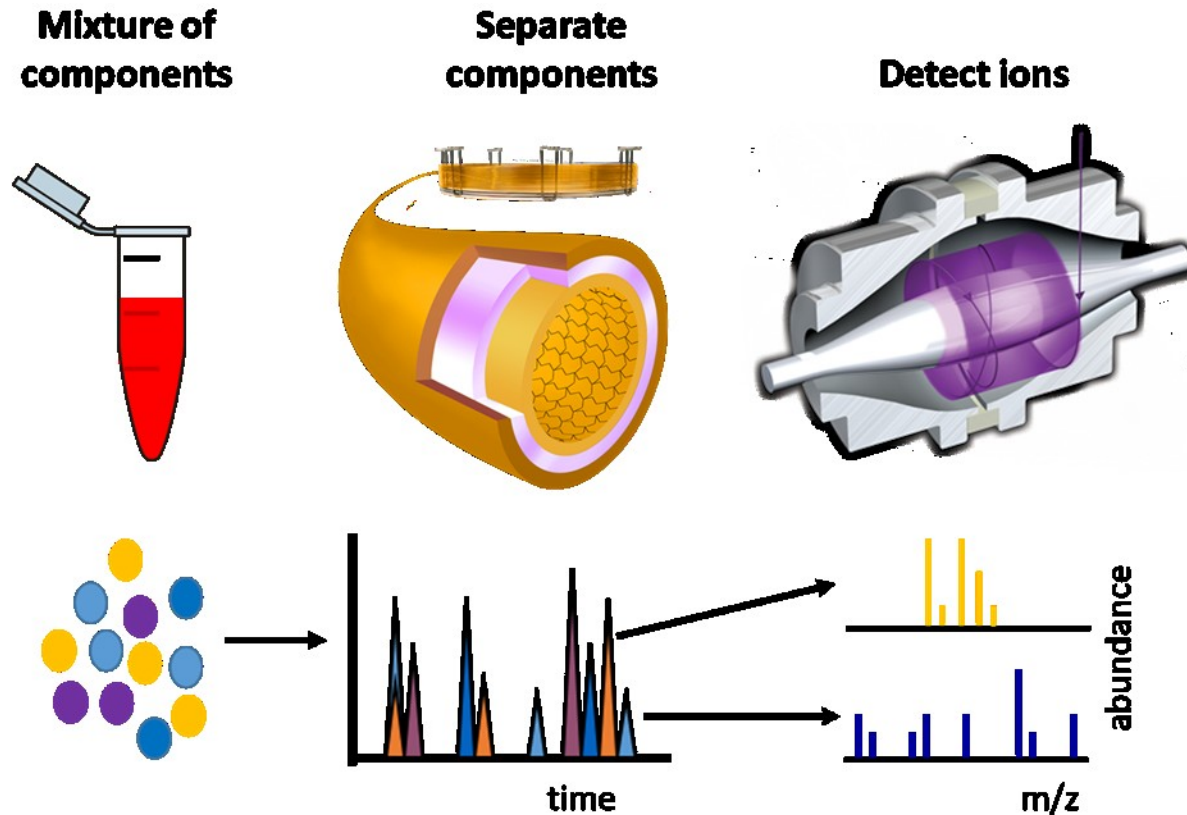
High-throughput technologies - MS



[m/z]) of ions to calculate **mass** & elucidate structure

- Widely applied for peptide/proteins & small molecules

High-throughput technologies – MS coupling

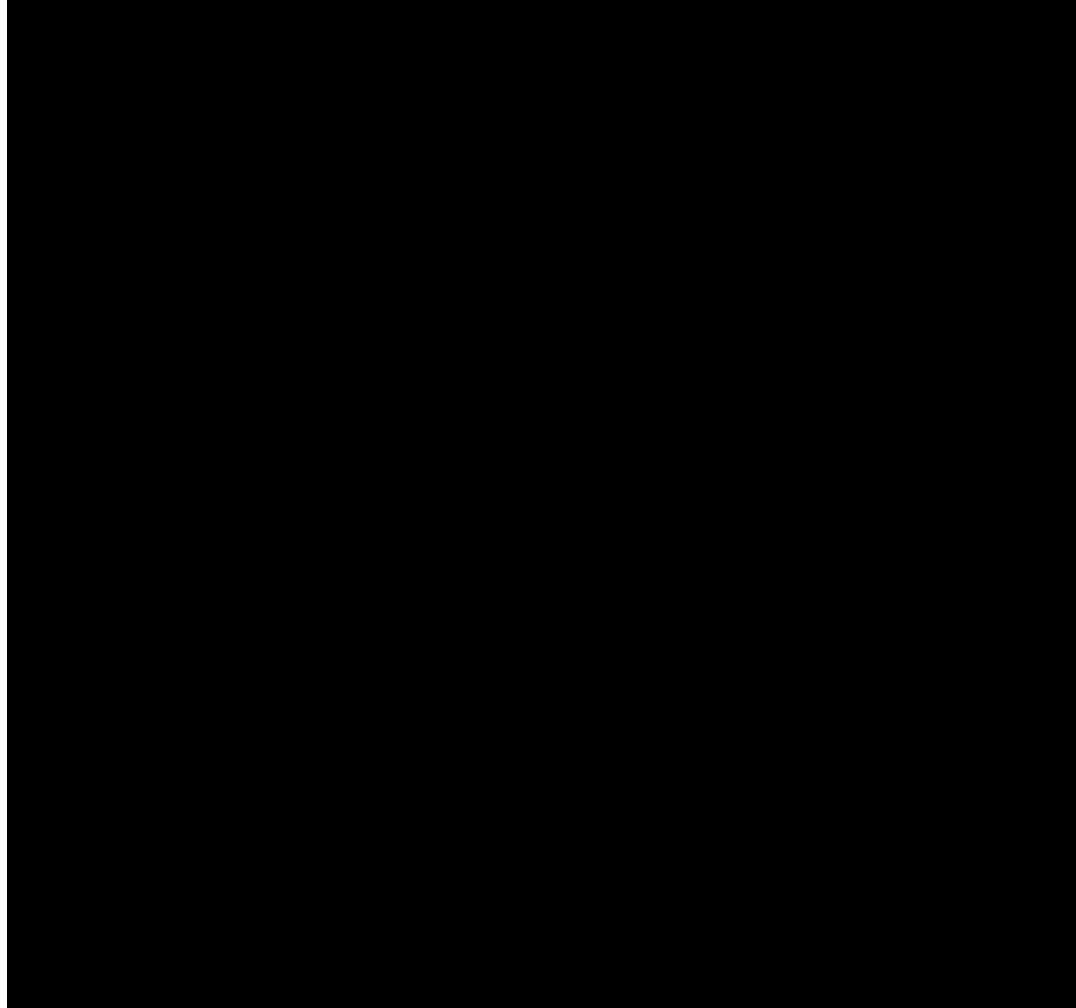


MS is often preceded by chromatography

Major approaches are:

- Full-scan (non-target)
- Selective (target)

High-throughput technologies - MS



Increasing
detection
sensitivity



Increasing
quantitative
accuracy



Decreasing
compound
coverage



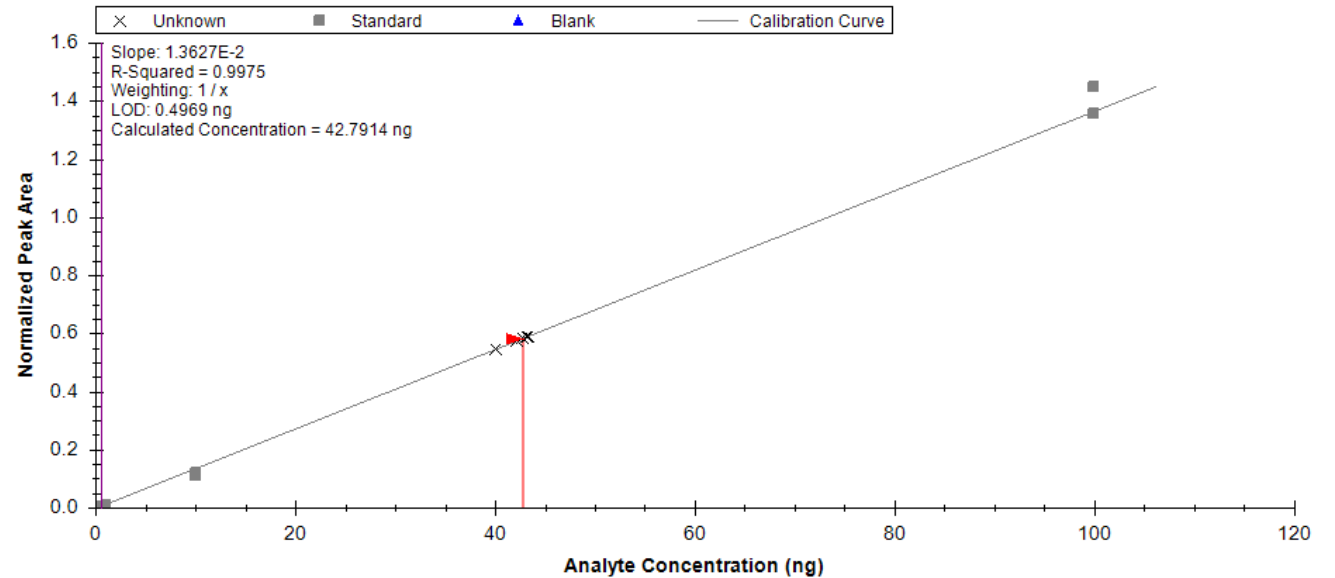
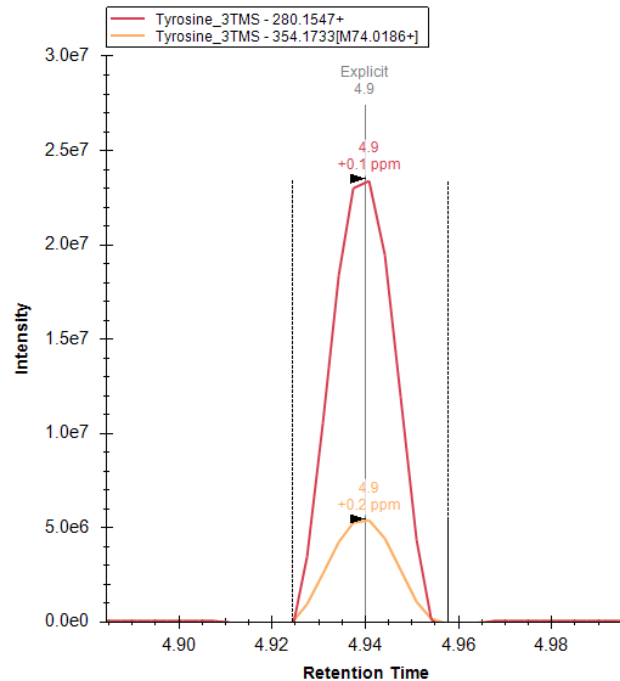
Decreasing
compound
coverage

Further material: <https://nontargetedanalysis.org/>

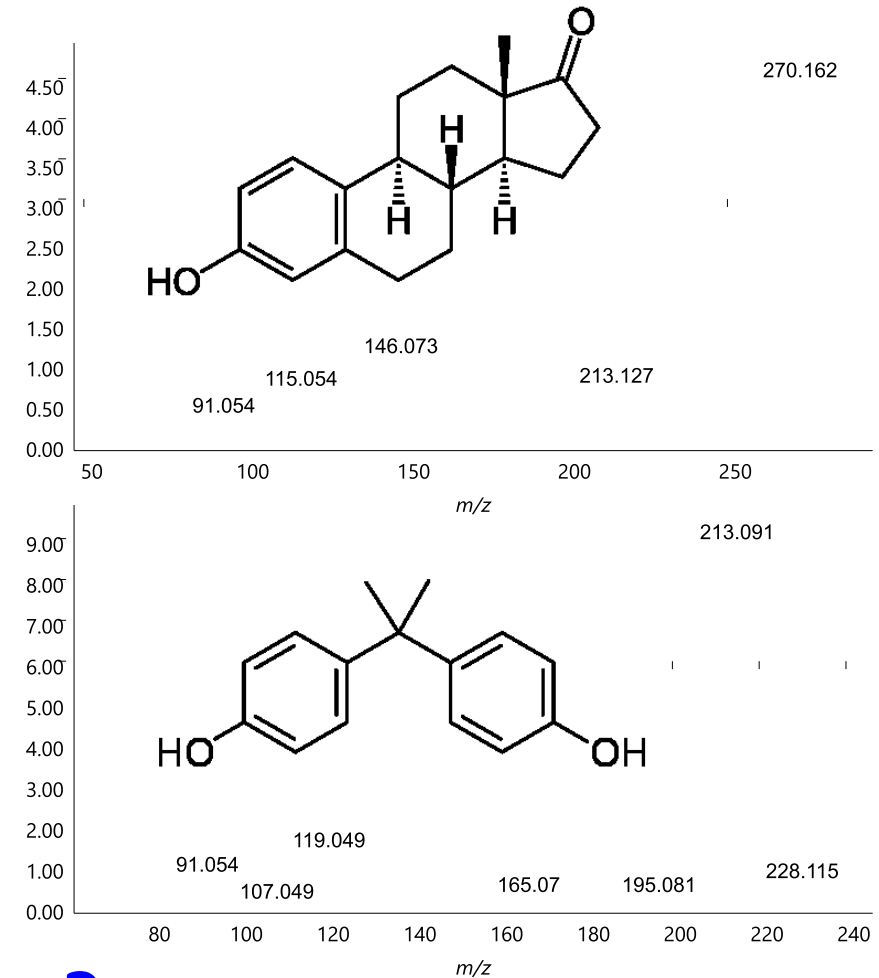
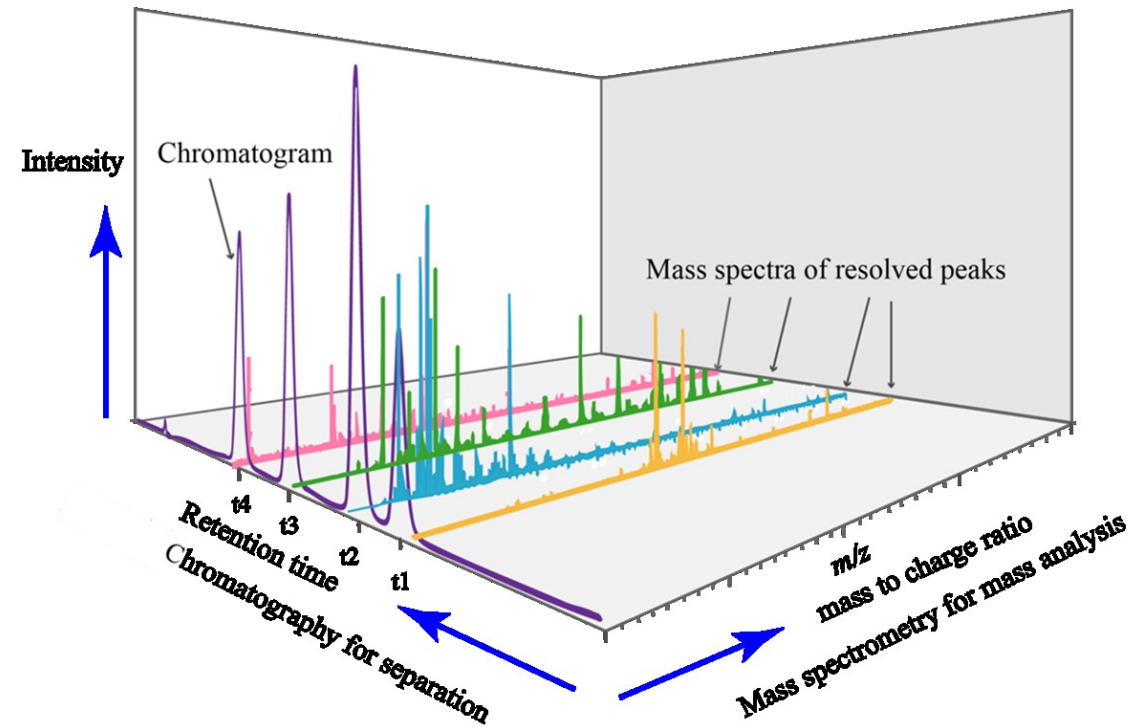
MUNI | RECETOX

Selective acquisition

- Scan selected ions (m/z) specific to molecules of interest
- **How much of molecule is present?**

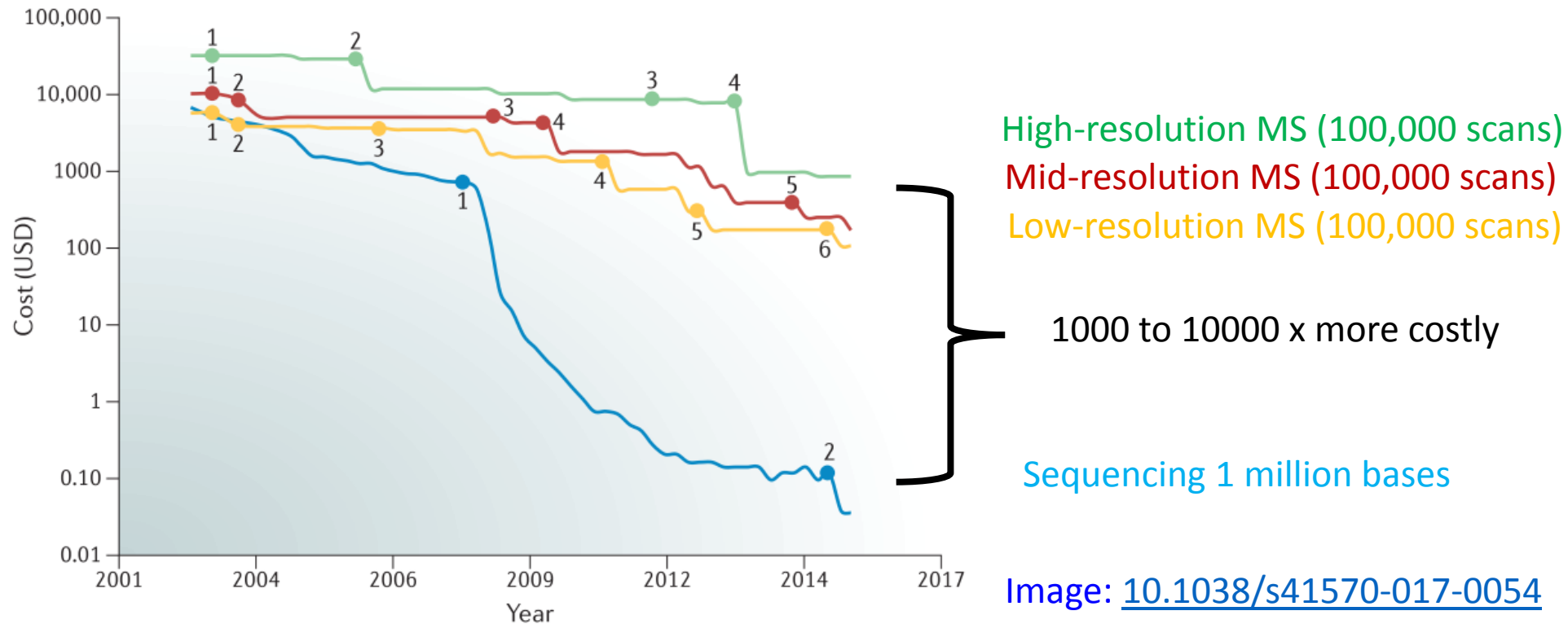


Full-scan analysis



- Identify what chemicals are present?
- Quantification (even relative) is difficult

Sequencing & mass spectrometry



Large-scale sequencing remains cheaper & easier than large-scale MS

Sequencing & mass spectrometry

- **Sequencing is more robust** than MS
- **MS** methods provide **finer details about phenotype** due to **greater inclusion of external factors**
- **Sequencing** shows **all potential biological reactions** that can occur
- **MS** shows **biological and non-biological reactions** that **occur**

Further material: [10.1038/s41437-019-0209-z](https://doi.org/10.1038/s41437-019-0209-z) & [10.1038/s41570-017-0054](https://doi.org/10.1038/s41570-017-0054)

Network biology

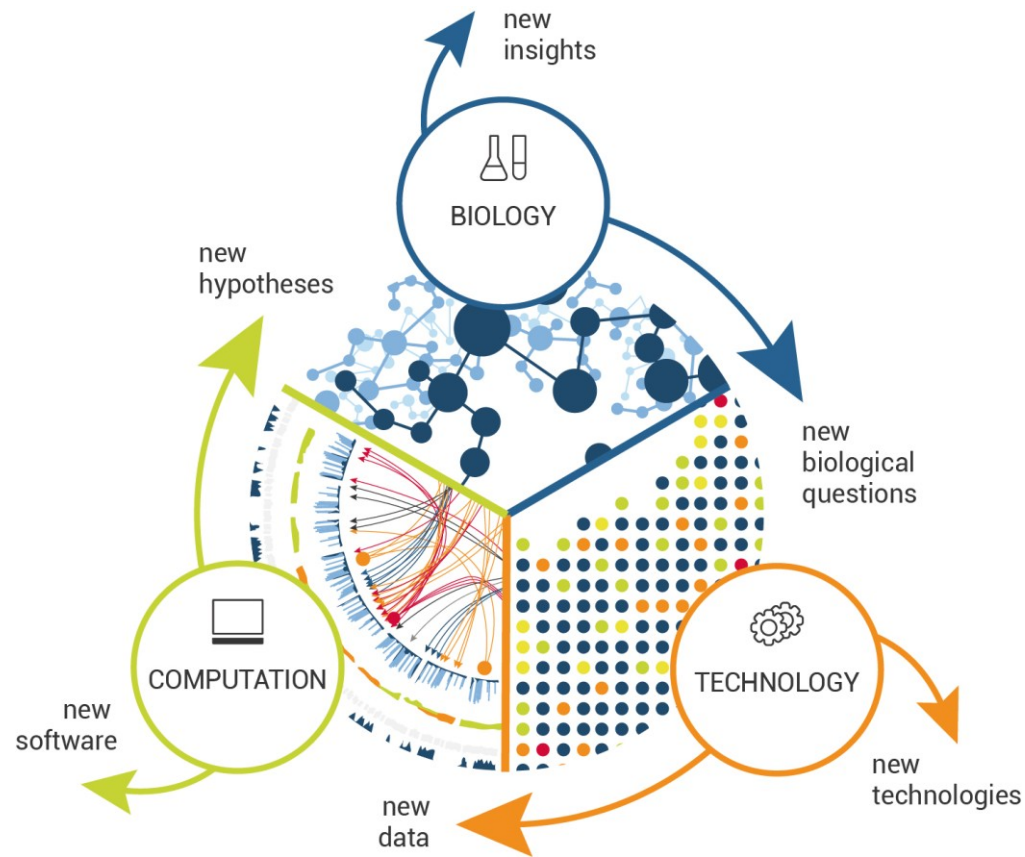


Image: [10.1016/B978-0-12-813762-8.00002-5](https://doi.org/10.1016/B978-0-12-813762-8.00002-5)



Informatics to integrate and understand big data is the major advance of 'omics' technologies

Systems biology

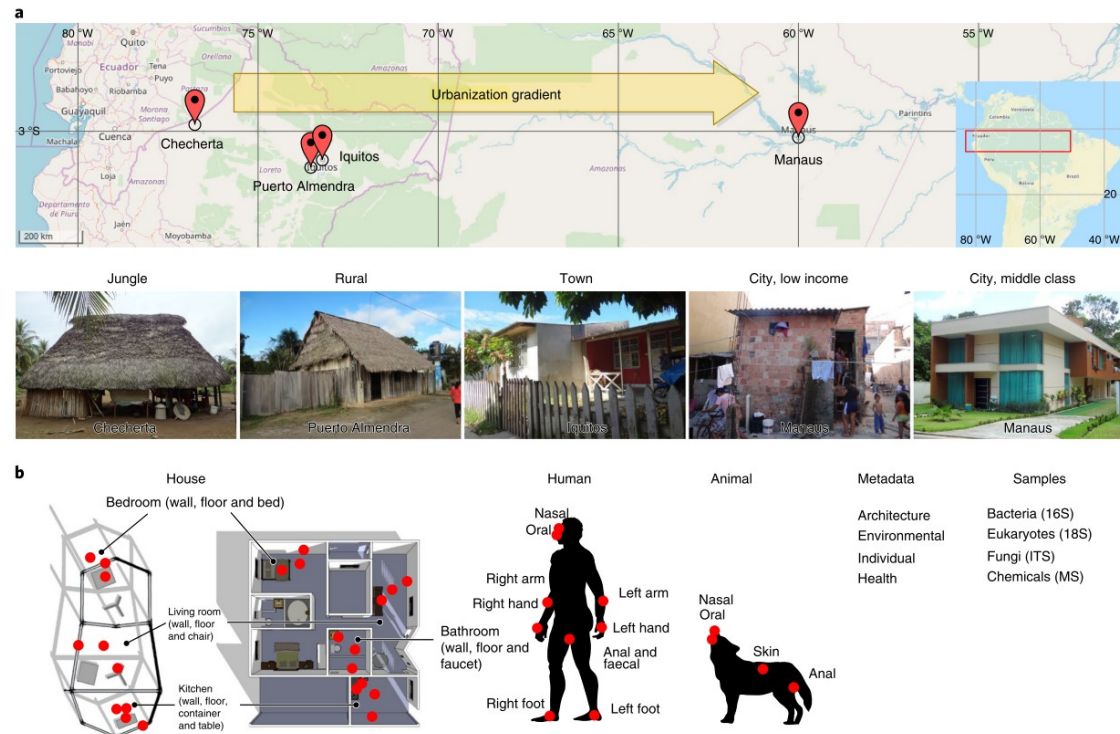
'Omics' technologies enable more observations but more observations does not equal more understanding

Benefit of the '-omics' all depends on **study design** being correct for the hypothesis you want to test / question you wish to explore



Multi-omics in environmental chemistry

McCall *et al.* Home chemical and microbial transitions across urbanization. *Nat Microbiol* **5**, 108–115 (2020). <https://doi.org/10.1038/s41564-019-0593-4>



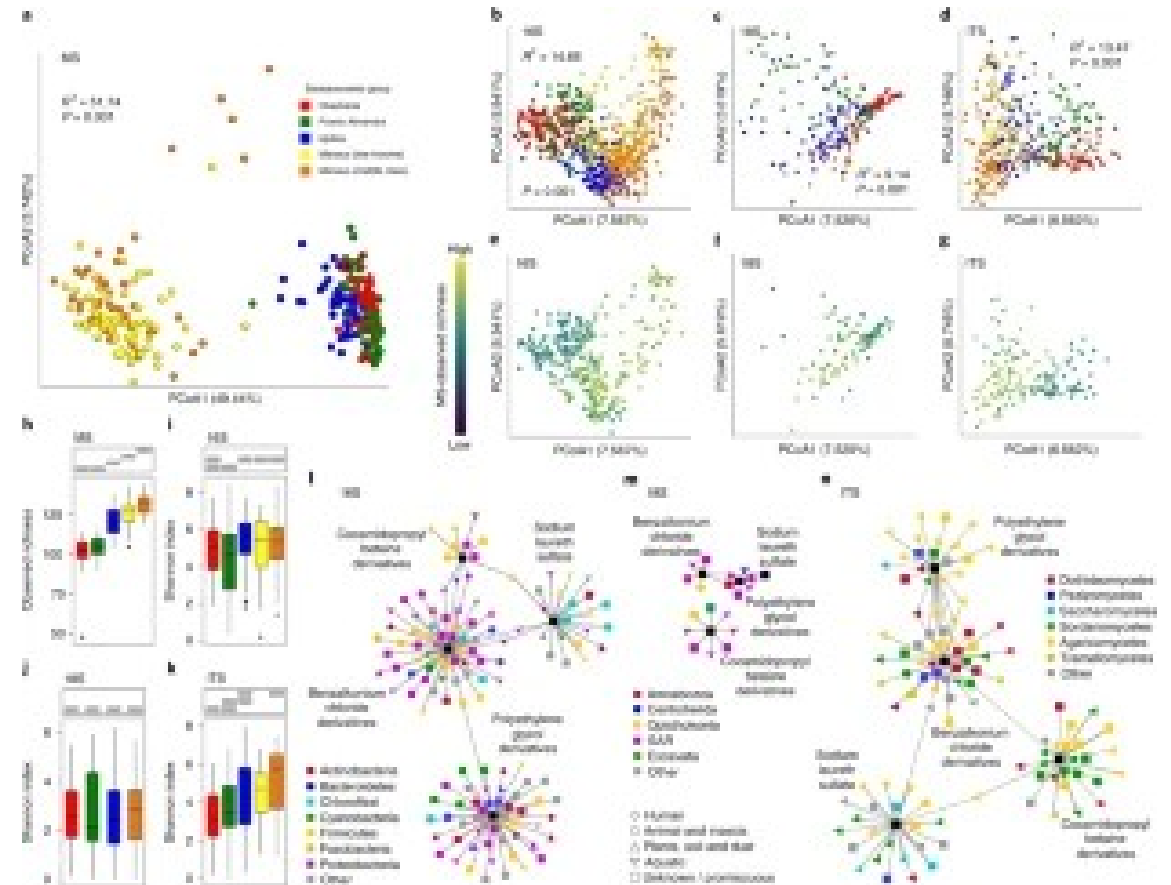
□ Took swab samples from inside homes and from their inhabitants across gradient of rainforest – city in Brazil

□ **NGS (microbiome) & MS (chemicals)**

Multi-omics in environmental chemistry

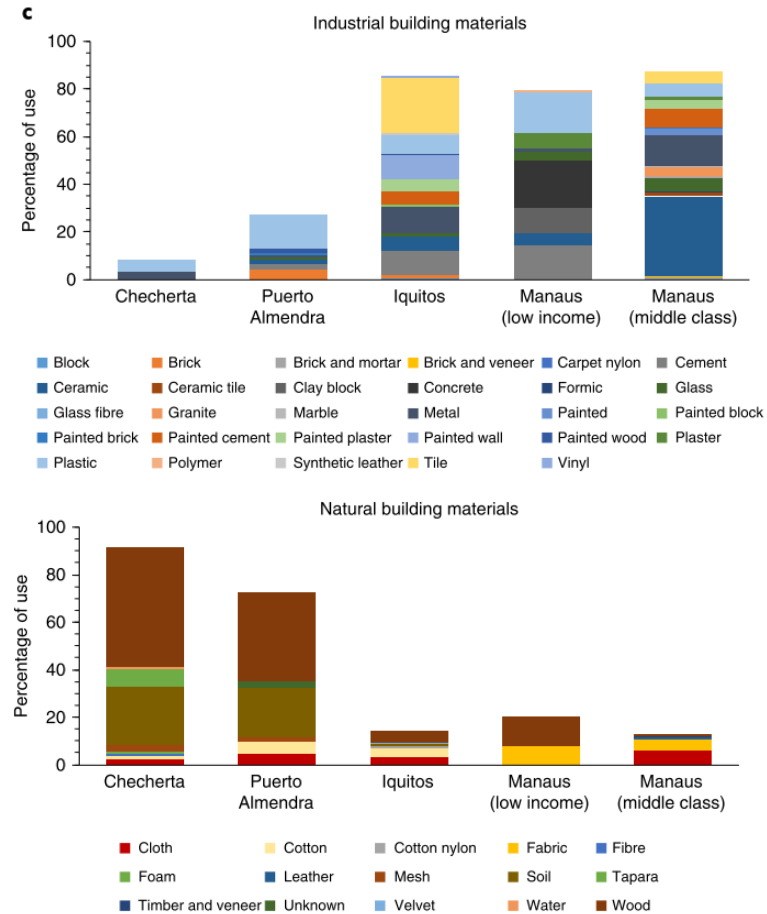
<https://doi.org/10.1038/s41564-019-0593-4>

- Urban homes showed higher levels of irritant cleaning products / detergents
- Urban homes had much greater fungal diversity & biomass



Multi-omics in environmental chemistry

<https://doi.org/10.1038/s41564-019-0593-4>

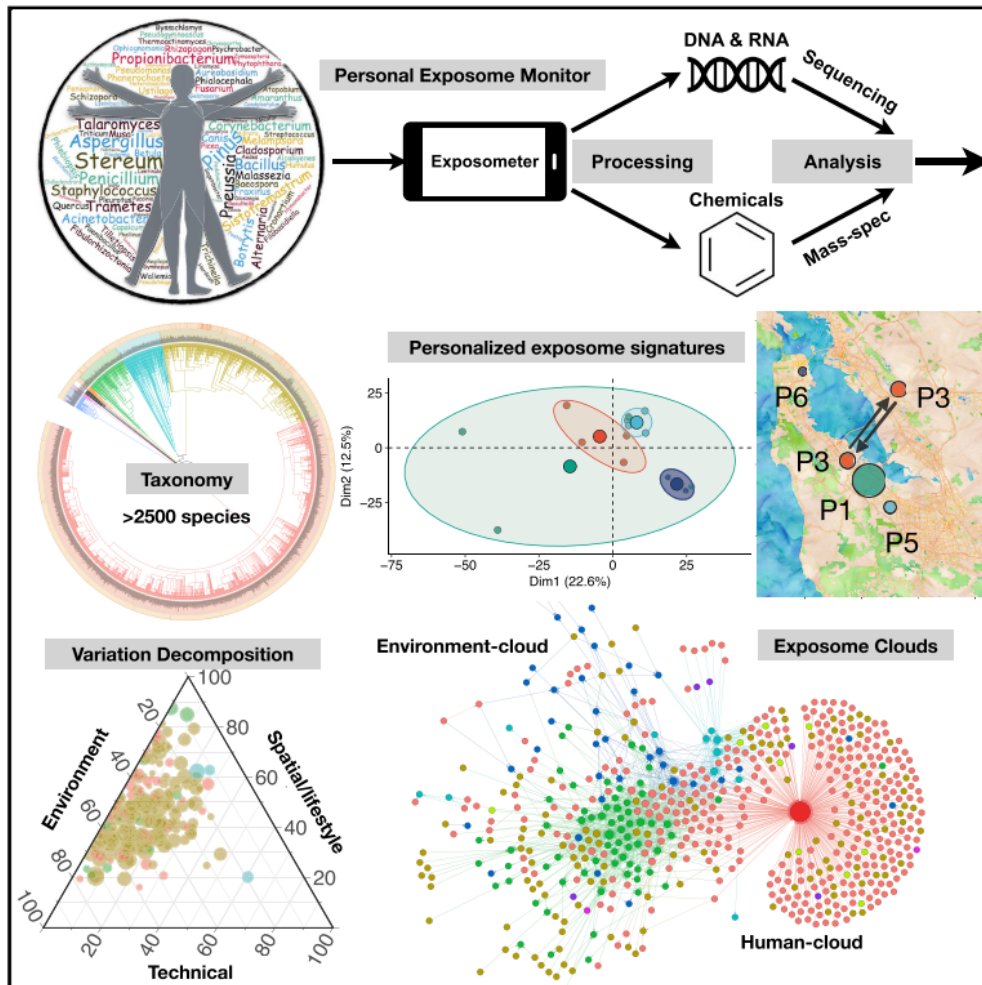


Industrial materials cover more surfaces in urban homes & were cleaned with antimicrobials more frequently

Fungus inside urban homes speculated to have developed resistance

Allergenic load higher in urban homes

Multi-omics in environmental chemistry



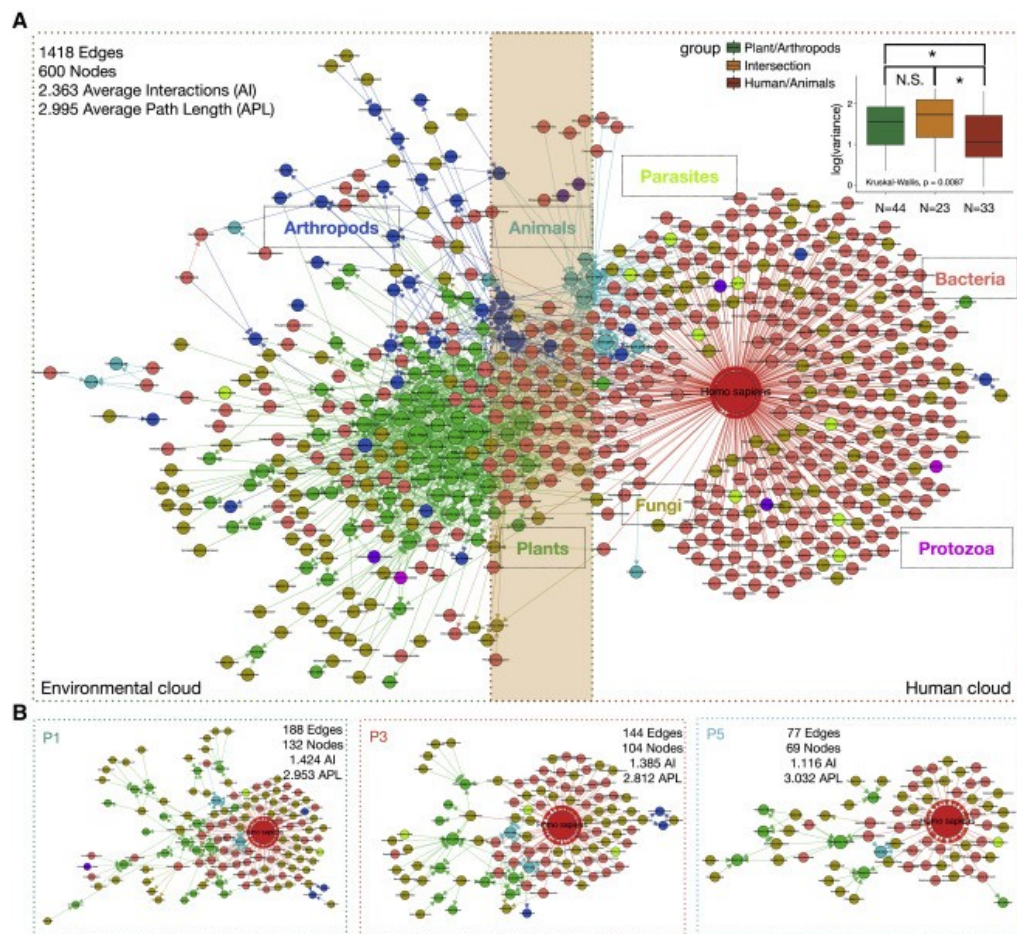
Jiang *et al.* Dynamic Human Environmental Exposome Revealed by Longitudinal Personal Monitoring. *Cell* **175**, 277–291 (2018).

<https://doi.org/10.1016/j.cell.2018.08.060>

- 15 people monitored for 800 days'
- Tracked location & air monitoring
- **Analysed airborne microbes (NGS) and chemicals (MS)**

Multi-omics in environmental chemistry

<https://doi.org/10.1016/j.cell.2018.08.060>



– Identified plant centric & human centric ‘exposure clouds’ with constant interaction mediated by bacteria & fungi

– Identified many location/lifestyle specific airborne pathogens & harmful toxins

'omics' takeaway messages

- 'omics' focus on **systems/network** study
- 'omics' techniques can easily collect **lots of data**
- **Theory and research questions are crucial for understanding**
- **Need to study the genetic – environment interface in order to understand phenotype development, adaptation, evolution etc.**
i.e. to fully investigate why anything is what it is