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## Unique aspects of microbiome analysis

#### • Expression Analysis

- Unit of analysis: Transcript (an isoform of mRNA produced from a gene)
- Measurement: Quantitative
- Variant Analysis
  - Unit of analysis: Variant (a version of a genomic segment)
  - Measurement: number of copies, usually 0, 1, or 2; or 0 vs 1+
- Microbiome Analysis
  - Unit of analysis: Abundance of variants of a 16S rRNA gene amplicon region
  - Measurement: Count of observed sequence variants in the specimen
  - Analogy: variant analysis in an omniploid organism

#### Additional caveats

- Sequencing errors
  - A big problem when you need to get 100x coverage of a gene in a diploid organism;
  - A huge problem, when the coverage is 10,000x in an omniploid microbiome.
- Functional multiplicity
  - Many microbes fill the same role
- Compositional effects
  - Inference about absolute quantity of microbes is hard with amplicon data
- Causal considerations

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# What is the role of microbiome in human health?

#### We are more microbes than we are humans?

- Human shelter 10 trillion microbes (10<sup>13</sup>) in their gut alone, (we are made of 10 trillion cells).
- Only 1 in 10 cells in your body carries 'your' DNA. Recent evidence suggests as many bacterial cells as human.
- It is estimated that there are 1000 species of bacteria living in the human gut.
- Compare also the number of human genes (~25,000) to the number of genes and variants that bacterial communities may carry (~4,000,000, see e.g. doi:10.1038/ncomms3151).







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# A conceptual role of the microbiome in human disease, an infectious disease approach

#### • Robert Koch's (1843 - 1910) postulates:

- 1. The microorganism must be found in abundance in all organisms suffering from the disease, but should not be found in healthy organisms.
- 2. The microorganism must be isolated from a diseased organism and grown in pure culture.
- 3. The cultured microorganism should cause disease when introduced into a healthy organism.
- 4. The microorganism must be reisolated from the inoculated, diseased experimental host and identified as being identical to the original specific causative agent.
- Do these apply to specific microbiota?











## 'New' ways to 'look' at microbiomes

