

Group meeting

Parties present:

Claire
Howard
Soroush
Alex
Ryan
Avril

Minutes taken by:

Alex

Agenda:

- Finalize data set we will use for final project
- Decide on a research question

Howard khchen1219@gmail.com:

Question 1: Does age affect differences in gut microbiota composition among COVID-19 patients during the acute and recovery phases?

Data: PRJNA769052

- Research gap:
 - Age-specific differences in gut microbiota composition are only seen in hamster models, with age-related dysfunctions, though not yet explored in humans -> Brito Rodrigues P, de Rezende Rodovalho V, Sencio V, et al. Integrative metagenomics and metabolomics reveal age-associated gut microbiota and metabolite alterations in a hamster model of COVID-19. *Gut Microbes*. 2025;17(1):2486511. doi:10.1080/19490976.2025.2486511

Question 2: Age-specific differences in nasopharyngeal microbiota across various groups of COVID-19 patients (asymptomatic, mild, and severe infections)

Data: PRJNA1176675

Soroush (storfehn@student.ubc.ca):

Question 1: did the combination of antivirals and antibiotic drugs have an effect on the individuals response to inf

Paper Title: Meta-analysis of 16S rRNA microbial data identified alterations of the gut microbiota in COVID-19 patients during the acute and recovery phases

DOI: <https://doi.org/10.1186/s12866-022-02686-9>

PRJNA684070

Alex (aaelbaz@student.ubc.ca):

Data: PRJNA358103 (IAV infected Mallard ducks)

Potential Questions:

1. Are there differences in microbiome composition during infection with different IAV subtypes? ← This was briefly mentioned in the study, so may have to be more specific.
2. Sex differences in microbiome changes during IAV infection? By subtype?
 - a. Examining by sex & subtype is more likely to be truly novel; not sure how valuable of a project that is though.
3. Can influenza infection and subtype be predicted by microbiome composition in ducks?
 - a. Likely fairly novel, but not sure how valuable of a project it is.
 - b. <https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2022.979320/full> - kind of looks at something similar?

Data:

- RSV: PRJNA579491 (gut), PRJEB20811 (nasopharynx)
- COVID: PRJNA1176675 (nasopharynx), PRJNA769052 (gut?), PRJNA787810 (gut?), etc.

Potential Questions:

1. Are there differences in the shifts of the respiratory (e.g., lung/nose/throat) microbiomes and gut microbiomes during COVID and/or RSV infection?
 - a. Based on a quick search, this seems fairly novel. The challenge here would be combining datasets, but if it is doable, that might work to our advantage in having a more powerful study.

Data:

- COVID: PRJNA747262, PRJNA684070, PRJNA758913

Potential Questions:

1. Are there differences in gut and/or respiratory microbiome shifts during COVID, Influenza, and/or RSV infection based on antibiotic/antiviral treatments/history?
 - b. Seems fairly novel and might be pretty insightful in terms of a question to answer (especially in the case of RSV where a lot of concern surrounds infants and young children, in which concerns also exist about antibiotic usage).
 - c. <https://pmc.ncbi.nlm.nih.gov/articles/PMC5056860/> ← only paper I could find vaguely in the realm of this question after a brief search.

Ryan (ryanjchen5@gmail.com):

Question 1: Do sex-specific (or age) differences in the gut microbiome composition exist among RSV patients, and how are these differences associated with disease severity?

Data:

DOI: <https://doi.org/10.1186/s12866-020-01816-5>

Sequencing Data (Accession): PRJNA579491.

Dataset Links:

Paper Title: Altered gut microbiota in infants is associated with respiratory syncytial virus disease severity

DOI: <https://doi.org/10.1186/s12866-020-01816-5>

Sequencing Data (Accession): PRJNA579491.

Number of Runs: 95.

Metadata Location: Within sequencing data.

Metadata Contents: Age, sex.

Paper Title: Community-Level Differences in the Microbiome of Healthy Wild Mallards and Those Infected by Influenza A Viruses

DOI: <https://doi.org/10.1128/msystems.00188-16>

Sequencing Data (Accession): PRJNA358103.

Number of Runs: 115.

Metadata Location: Within sequencing data + seemingly more in an Excel file linked in the paper.

Metadata Contents: Geographic location, Influenza A subtype, Influenza A status (+/-), sex.

Paper Title: Haemophilus is overrepresented in the nasopharynx of infants hospitalized with RSV infection and associated with increased viral load and enhanced mucosal CXCL8 responses

DOI: <https://doi.org/10.1186/s40168-017-0395-y>

Sequencing Data (Accession): PRJEB20811.

Number of Runs: 100.

Metadata Location: Within sequencing data.

Metadata Contents: Age, condition (healthy/RSV), gender (encoded - need to figure out what 0/1 corresponds to), RSV severity.

Special Notes: Original dataset was presented under ENA as opposed to NCBI SRA, but the study accession seemed to retrieve the same data within NCBI SRA.

Paper Title: Identification of nasopharyngeal microbial dysbiosis in COVID-19 patients by 16S rRNA gene sequencing

DOI: <https://doi.org/10.3389/fmicb.2025.1631198>

Sequencing Data (Accession): PRJNA1176675.

Number of Runs: 81.

Metadata Location: Within sequencing data + more in Excel files linked in the paper (supplementary materials).

Metadata Contents: COVID status (+/-), disease phase, group (severity), age, sex, sampling facility.

Special Notes: Seems to have quite a bit of missing data.

Paper Title: Meta-analysis of 16S rRNA microbial data identified alterations of the gut microbiota in COVID-19 patients during the acute and recovery phases

DOI: <https://doi.org/10.1186/s12866-022-02686-9>

Sequencing Data (Accession): PRJNA769052.

Number of Runs: 128.

Metadata Location: Within sequencing data.

Metadata Contents: Age, BMI, gender, group, source.

Sequencing Data (Accession): PRJNA787810.

Number of Runs: 131.

Metadata Location: Within sequencing data.

Metadata Contents: Location, group, sex, birth year.

Sequencing Data (Accession): PRJNA747262.

Number of Runs: 212.

Metadata Location: Within sequencing data.

Metadata Contents: Age (categories), antibiotics y/n, heart disease y/n, dialysis y/n, ethnicity, fever y/n, hospitalization y/n, etc. (a LOT of features).

Sequencing Data (Accession): PRJNA684070.

Number of Runs: 297.

Metadata Location: Within sequencing data.

Metadata Contents: Age, antibiotics y/n, antivirals y/n, diseased y/n, disease severity, group, isolation source, sample type, sex.

Special Notes: This paper did not have original data itself but provided the accessions for several papers whose data this paper used (supplementary material; Table S8). The data presented for this entry are of those linked papers (which would be researched further and cited properly should the data end up being used).

Paper Title: Microbiome disturbance and resilience dynamics of the upper respiratory tract during influenza A virus infection

DOI: <https://doi.org/10.1038/s41467-020-16429-9>

Sequencing Data (Accession) - Infected: PRJNA240559.

Number of Runs: 146.

Metadata Location: Within sequencing data.

Metadata Contents: Location, age, sex, isolation source, influenza strain.

Sequencing Data (Accession) - Uninfected: PRJNA240562.

Number of Runs: 127.

Metadata Location: Within sequencing data.

Metadata Contents: Age, sex.

Paper Title: Robust cross-cohort gut microbiome associations with COVID-19 severity

DOI: <https://doi.org/10.1080/19490976.2023.2242615>

Sequencing Data (Accession): PRJNA758913.

Number of Runs: 219.

Metadata Location: Within sequencing data.

Metadata Contents: Age, disease severity, disease status, sex at birth, sex, BMI, antibiotic use.

Special Notes: This paper did not have original data itself but provided the accessions for several papers whose data this paper used (supplementary Excel file). The data presented for this entry is of one of those linked papers (which would be researched further and cited properly should the data end up being used).

Meeting minutes

Deciding on a research question & dataset:

- **Does age affect differences in gut microbiota composition among COVID-19 patients during the acute & recovery phases?**
 - Reasonable data, groups might get small when stratified by age.
- **Does antibiotic/antiviral treatment impact the microbiome composition of individuals in response to influenza infection in an age dependent fashion?**
 - Need to determine meaning of antibiotics y/n in the context of the data - i.e., is it antibiotics during infection, before infection, after infection, etc.
 - Has a lot of available data.
 - Novelty? Seems as though it is; research about antibiotics & COVID exists, but not a lot with respect to the microbiome.
- **Are there differences in microbiome composition during infection with different influenza A subtypes? Can subtype (or susceptibility) be predicted by the microbiome composition?**
 - Novelty? Yes - original paper did not thoroughly examine subtype differences.
 - Group sizes might be quite small depending on how samples are split.
 - Need to consider how to split samples into meaningful groups; might end up filtering out samples where group size is too small.
 - Worth looking into if there is research that relates specific influenza subtype infections with specific microbiome effects/changes.
 - Is there a certain H/N influenza subtype that shifts the microbiome more than others?
 - May be able to use the data to determine susceptibility of organisms (i.e., ducks) to strains of influenza based on microbiome composition.
 - May provide proof of concept for determining susceptibility of influenza carrier organisms (e.g., avian species) to specific influenza strains/subtypes of concern.
 - Can try for a predictive model, but group sizes may be too small to produce an effective/accurate model.
- **Are there differences in the shifts of the respiratory and gut microbiomes during COVID/RSV infection?**
 - Might have issues with combining datasets given that each dataset only looks at a single body site for their cohort.
 - Given that we don't have any data where individuals have both respiratory and gut microbiomes measured, wouldn't be able to easily determine relative patterns of microbiome shift.
 - Any patterns we might observe over the data could be a result of differences between the studied cohorts.

- Would have to be functional analysis over taxonomic analysis
 - Again, difficult to parse between noise & actual expressional differences (partly given the vast differences between the two microbiomes; aerobic vs. anaerobic, etc.)
- Would be a good graduate project probably...
- Do sex- or age-specific differences in the gut microbiome composition exist among RSV patients and how are these differences associated with disease severity?
 - Group imbalances in the relevant data may be problematic.

Meeting Summary:

- Top choice: Mallard ducks influenza subtype infection microbiome differences.
- Backup: Age dependent antibiotic treatment impacts on microbiomes of individuals infected with COVID-19.
 - Could examine cohort effects across the multiple datasets, analyze antivirals, make a predictive model, etc.

Action Items:

- Determine how to split the samples into groups in the mallard ducks dataset.
 - Split by H & N subtypes, just H, etc.
 - Look at the literature to determine what would be appropriate.
- Determine if sample size for each group is large enough to work with in the mallard ducks dataset.
 - Let Claire/Avril know as soon as we determine this to evaluate whether we will continue with this project or pivot to the backup.
- Start the literature review section of the first group assignment.
- Run the dataset through the QIIME2 pipeline once uploaded to the server.
 - Make sure to do so in the shared high performance container
 - CHECK IF SOMEONE ELSE HAS ALREADY DONE IT BEFORE RUNNING.