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**DEBUGGING LUNG DISEASES: APPLYING  
MATHEMATICAL TECHNIQUES, INVOLVING MODELLING,  
DATA INTEGRATION AND MACHINE LEARNING FOR  
PRECISION MEDICINE**

**QUALIFYING EXAMINATION REPORT**

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MATRICULATION NUMBER : G1902804D**

# Contents

<b>1</b>	<b>Title1</b>	<b>3</b>
1.1	Introduction . . . . .	3
1.2	Methods . . . . .	4
1.2.1	Integrative-microbiomics, a webtool . . . . .	4
1.2.2	Longitudinal assessment of Exacerbation . . . . .	7
1.2.3	Antibiotic action simulation . . . . .	7
1.2.4	“Time to next exacerbation” prediction . . . . .	7
1.2.5	Validation of the interactome . . . . .	8
1.3	Results . . . . .	8
1.3.1	Math Cheat Sheet . . . . .	8
1.3.2	Table Cheat Sheet . . . . .	9
1.4	Discussion . . . . .	9
1.5	Future works . . . . .	10
<b>2</b>	<b>Title2</b>	<b>11</b>
2.1	Methods . . . . .	11
2.1.1	Study population . . . . .	11
2.1.2	Data-preprocessing . . . . .	12
2.1.3	Co-occurrence analysis . . . . .	12
2.1.4	. . . . .	12
2.2	Results . . . . .	12
2.2.1	Significant overlap of fungal communities of lung and gut contrary to bacteria . . . . .	12
2.3	Discussion . . . . .	14

2.4	Future works . . . . .	14
<b>3</b>	<b>Title3</b>	<b>16</b>
3.1	Introduction . . . . .	16
3.2	Methods . . . . .	17
3.3	Results . . . . .	19
3.3.1	Math Cheat Sheet . . . . .	19
3.3.2	Table Cheat Sheet . . . . .	20
3.4	Discussion . . . . .	20
3.5	Future works . . . . .	21
<b>4</b>	<b>Discussion</b>	<b>22</b>
<b>5</b>	<b>Future works</b>	<b>1</b>

# List of Figures

1.1	A figure illustrating the different sequencing approaches used to derive the human microbiome, consisting of interacting bacteria, fungi and viruses. Adapted from: [14] . . . . .	4
1.2	(a) A schematic representing, overview of analysis performed on the CAMEB cohort (n=217). Methodologies: Weighted SNF and Co-occurrence analysis were used for microbiome integration and intreactome construction. (b) A patient similarity matrix with each cell representing the integrated similarity between patients. Two clusters of low (black) and high (red) risk patients identified by wSNF are highlighted by boxes. Visualization of the interactome of low (c) and high (d) risk clusters. Interactions between microbes are classified as negative if the sign of the edge weights between them is negative (coloured red) with positive interactions indicated by green colouration. The strength of the interaction is indicated by the colour depth . . . . .	5
1.3	A figure describing the workflow of integrative microbiomics. The input microbiome datasets, are converted into patient/sample similarity networks based on the user-specified similarity measures: 1) Bray-Curtis, 2) Gower, 3) Canberra and 4) Jaccard; before merging them using the user-specified algorithm: 1) SNF, 2) wSNF. Further, the tool then implements a spectral clustering algorithm to allow cluster analysis on the merged dataset. . . . .	6
1.4	Plot of Exponential Function. . . . .	8
1.5	Plot of 3-D Function. . . . .	9
1.6	Two functions in one plot. . . . .	9
2.1	A histogram illustrating all available publications (including original articles and perspectives) matching the keyword “lung-gut axis” from 1900 to 2020 in the web of science database. . . .	12
2.2	A boxplot illustrating the difference in Shannon-diversity index of the Microbiome (Ochre) and Mycobioime (Blue) between the sputum (Lung) and stool (Gut) samples. Statistical significance of these differences calculated using ‘wilcoxon test’ are indicated above as p-values. . . .	13
3.1	A figure illustrating the different sequencing approaches used to derive the human microbiome, consisting of interacting bacteria, fungi and viruses. Adapted from: [14] . . . . .	17

3.2	(a) A schematic representing, overview of analysis performed on the CAMEB cohort (n=217). Methodologies: Weighted SNF and Co-occurrence analysis were used for microbiome integration and interactome construction. (b) A patient similarity matrix with each cell representing the integrated similarity between patients. Two clusters of low (black) and high (red) risk patients identified by wSNF are highlighted by boxes. Visualization of the interactome of low (c) and high (d) risk clusters. Interactions between microbes are classified as negative if the sign of the edge weights between them is negative (coloured red) with positive interactions indicated by green colouration. The strength of the interaction is indicated by the colour depth	18
3.3	Plot of Exponential Function. . . . .	19
3.4	Plot of 3-D Function. . . . .	19
3.5	Two functions in one plot. . . . .	20

# List of Tables

1.1	Caption . . . . .	10
3.1	Caption . . . . .	20

## Abstract

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# Introduction

Introduction of the thesis



# Chapter 1

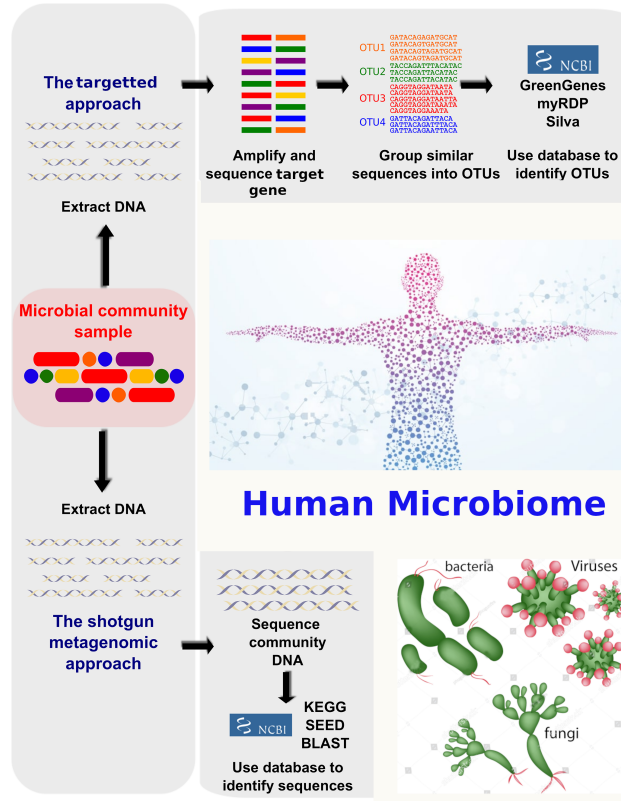
## Title1

### 1.1 Introduction

The term microbiome is used to refer to the collection of genes within a community of microbes (including bacteria, fungi, virus, protists and bacteriophages). In the last few years, microbiome research has helped us gained new insights into how microbes shape our human biology and have brought paradigm-shifting implications for translational research and clinical care. The human microbiota is crucial for our body to maintain its homeostasis. Disruption of this can lead to diseases such as obesity, inflammatory bowel disease, malnutrition, Parkinson's, Autism, Asthma, dental caries, bacterial vaginosis, and depression [10]. Currently, microbiome researchers use culture-independent techniques that involve DNA sequencing to derive the microbiome. Broadly, the community taxonomy/microbiome can be identified using two approaches (see Figure3.1) 1) Targeted and 2) Metagenomic. Targeted sequencing approach uses the PCR amplified, target gene markers (16S rRNA in case of bacteria or ITS in case of Fungi) derived from the samples to reference it against gene-marker databases (Silva, Green Genes, etc.). In contrast, the metagenomic sequencing approach directly sequence the whole community DNA and compares it to reference genomes [14].

Present microbiome studies focus on a single profile of the human microbiome in isolation, even though bacteria, fungi and viruses coexist and interact in the body as a community. Thus, it is essential to look at these biological components together in an integrated fashion to understand more holistically the true underlying in vivo state. However, one of the primary reasons for the lack of multi-biomic research is the lack of methods to merge microbiome datasets and integrative analysis. Consequently, I tried addressing some of these challenges in my master's thesis, using microbiome datasets derived from bronchiectasis patients as an example. Bronchiectasis, is a chronic inflammatory respiratory disease associated with progressive, irreversible dilatation of the airway. It is crucial to study bronchiectasis because in most cases it is known to be idiopathic(unknown cause) [3] and it is a significant contributor to lung diseases globally with a substantial four-fold higher predominance in Asian populations [16].

Previously in my master's thesis, I developed weighted similarity network fusion (wSNF) to allow weightage of input datasets during integration, otherwise unaccounted by conventional SNF [17]. Ensemble-based co-occurrence analysis strategy developed by Faust et al. [5] was extended to allow weightage of individual methods in the ensemble along with other modification to better infer microbial association networks. Microbiome and Mycobiome derived using targeted amplicon sequencing of the 16S and ITS regions from the sputum samples of the CAMEB cohort [12]; virome from qPCR on an extensive panel of 17 respiratory viruses, were used as the example dataset to integrate the microbiomes (Figure3.2a). Multi-biome (Microbiome, Mycobiome and Virome) integration by wSNF identifies a high-risk exacerbation cluster



**Figure 1.1:** A figure illustrating the different sequencing approaches used to derive the human microbiome, consisting of interacting bacteria, fungi and viruses. Adapted from: [14]

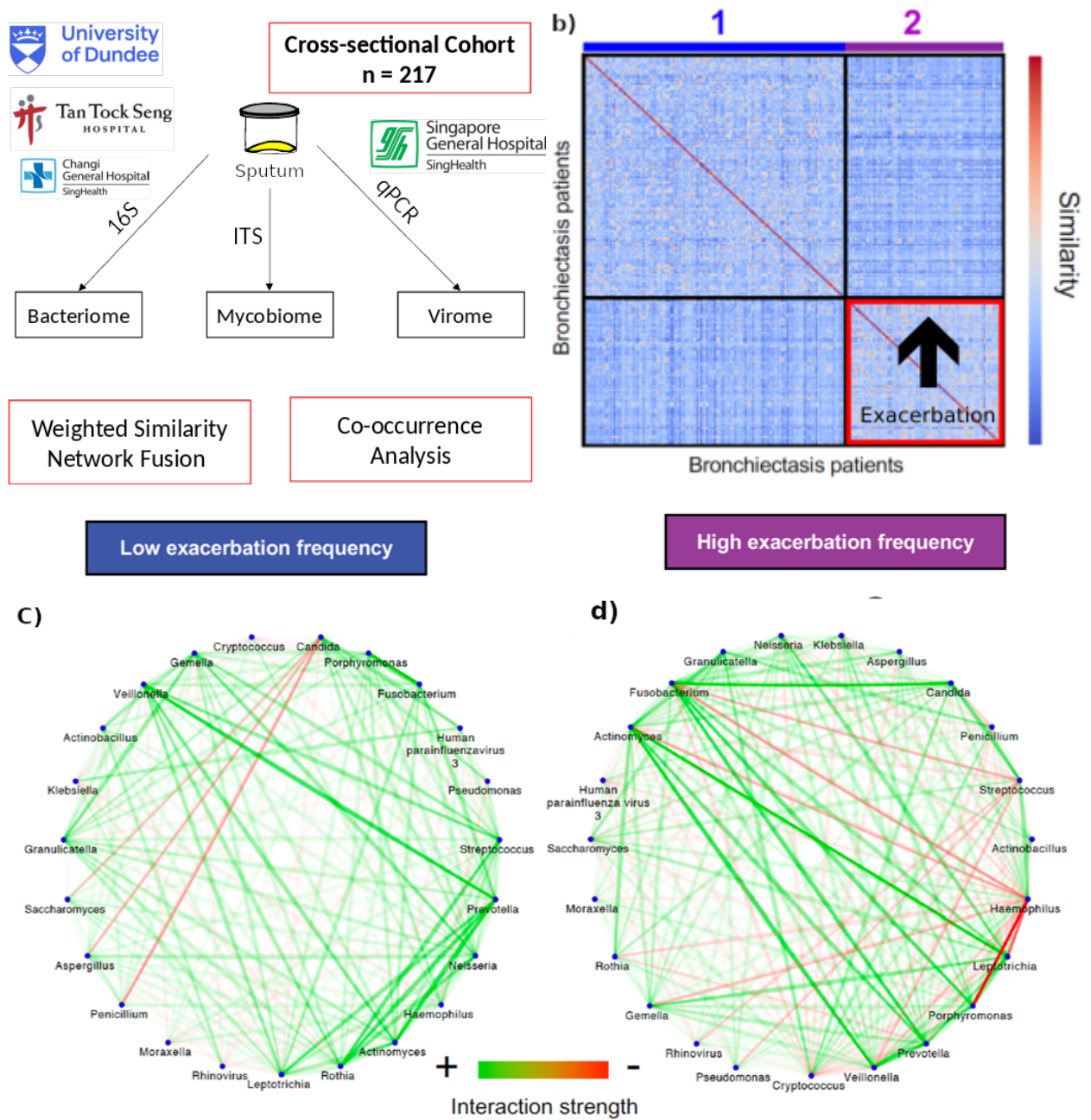
with increased precision (Figure3.2b). Co-occurrence network analysis of this high-risk cluster revealed an elevated antagonistic interactome with reduced alpha-diversity (Figure3.2c) [15].

Having developed the wSNF and shown its increased precision to identify exacerbators (clinical outcomes); here in this chapter of my PhD thesis, I attempt to extend my results further. I aim to develop a web tool to enable users to integrate their microbiome datasets and to illustrate its advantages using publicly available microbiome datasets. The tool would motivate clinicians and microbiome researchers to explore multi-biome strategies for their problem and aid them in integrating their datasets. Secondly, I aim to study exacerbation events, antimicrobial perturbations and “Time to next exacerbation” using the developed “Interactome” framework. Thirdly, I aim to validate the “high-risk” exacerbation cluster of Bronchiectasis patients and its “interactome” as derived in my previous work [15] using an alternate sequencing approach: metagenomics. Further, we also pick an interaction from the interactome of the high and low-risk clusters and validate it experimentally.

## 1.2 Methods

### 1.2.1 Integrative-microbiomics, a webtool

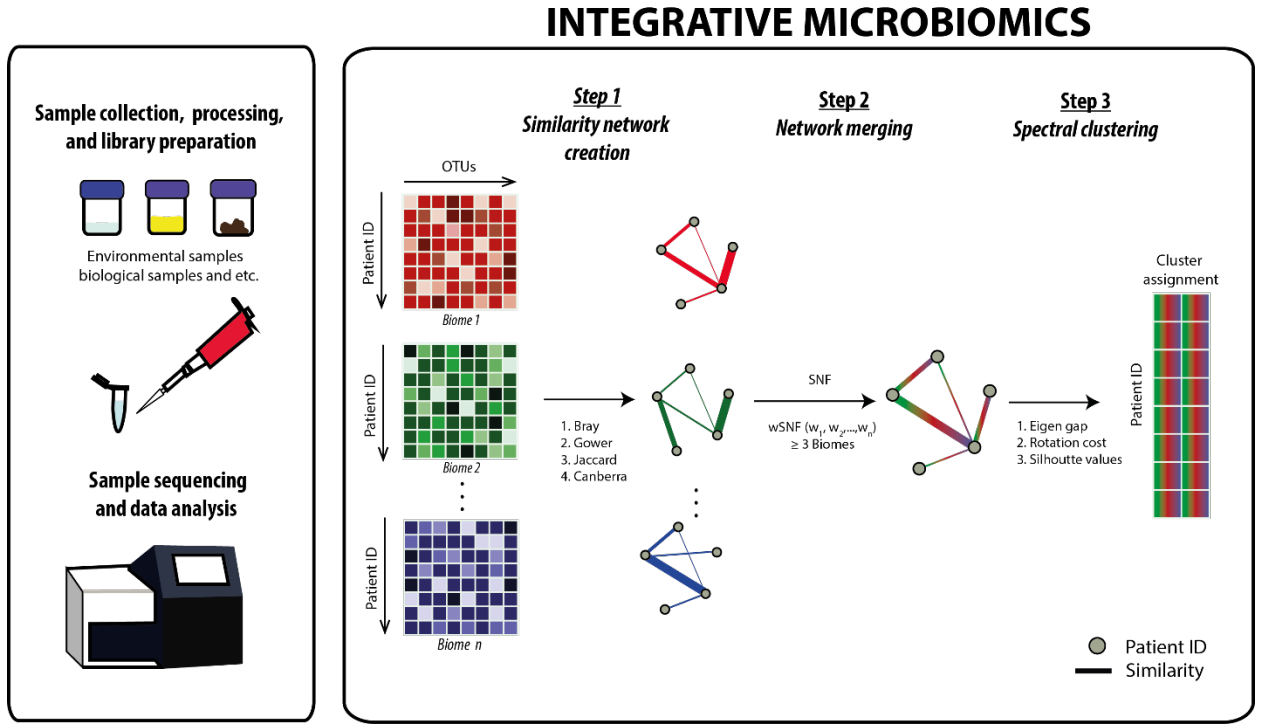
Given the input microbiome datasets, the tool converts them into patient/sample similarity networks for each view based on the user-specified similarity measure before merging them using the user-specified algorithm. Further, the tool then implements a spectral clustering algorithm to allow cluster analysis on the merged dataset outputting the cluster assignments for each sample/patient. The optimum default number of clusters is computed using ensemble-based voting of three differing methodologies: Best Eigen Gap, Rotation cost and average silhouette method (Figure1.3). For a given value of ‘k’ (the number of clusters), we calculate a



**Figure 1.2:** (a) A schematic representing, overview of analysis performed on the CAMEB cohort (n=217). Methodologies: Weighted SNF and Co-occurrence analysis were used for microbiome integration and interactome construction. (b) A patient similarity matrix with each cell representing the integrated similarity between patients. Two clusters of low (black) and high (red) risk patients identified by wSNF are highlighted by boxes. Visualization of the interactome of low (c) and high (d) risk clusters. Interactions between microbes are classified as negative if the sign of the edge weights between them is negative (coloured red) with positive interactions indicated by green colouration. The strength of the interaction is indicated by the colour depth

score/vote using the below rules

1. If the average silhouette score  $\geq 0.7 \rightarrow \text{Score} = \text{Score} + 3$
2. If  $0.5 \leq \text{average silhouette score} < 0.7 \rightarrow \text{Score} = \text{Score} + 2$
3. If  $0.3 \leq \text{average silhouette score} < 0.5 \rightarrow \text{Score} = \text{Score} + 1$
4. If k equals the first best value as derived from eigen gap method  $\rightarrow \text{Score} = \text{Score} + 3$
5. If k equals the second-best value as derived from eigen gap method  $\rightarrow \text{Score} = \text{Score} + 2$



**Figure 1.3:** A figure describing the workflow of integrative microbiomics. The input microbiome datasets, are converted into patient/sample similarity networks based on the user-specified similarity measures: 1) Bray-Curtis, 2) Gower, 3) Canberra and 4) Jaccard; before merging them using the user-specified algorithm: 1) SNF, 2) wSNF. Further, the tool then implements a spectral clustering algorithm to allow cluster analysis on the merged dataset.

6. If  $k$  equals the first best value as derived from rotation cost method  $\rightarrow \text{Score} = \text{Score} + 3$
7. If  $k$  equals the second-best value as derived from rotation cost method  $\rightarrow \text{Score} = \text{Score} + 2$

The value of  $k$  for which the Score is the highest is chosen as the default optimum number of clusters. In addition, the tool also outputs the integrated similarity matrix which can be used for downstream analysis such as for label propagation and survival analysis [17].

The tool presently provides four similarity measures 1) Bray-Curtis, 2) Gower, 3) Canberra and 4) Jaccard, appropriate for microbiome datasets which is used to construct patient/sample similarity network and two approaches 1) SNF, 2) wSNF to integrate these networks. For the implementation of wSNF the following formula in SNF

$$P^{(v)} = S^{(v)} \times \frac{\sum_{k=v} p^k}{(m-1)} \times (S^{(v)})^T, v = 1, 2, 3, \dots, m$$

was modified into

$$P^{(v)} = S^{(v)} \times \frac{\sum_{k=v} \omega_k \times p^{(k)}}{\sum_{k \neq v} \omega_k} \times (S^{(v)})$$

$v = 1, 2, 3, \dots, m$  where  $\omega_k$  is the weight of the  $k^{th}$  dataset,  $m$  the total number of views,  $P$  the status matrix and  $S$  the kernel matrix as defined by Wang et.al [17].

This webtool allows the users to integrate multiple microbiome datasets obtained from different sites in a patient/biological entity or from various methods (targeted sequencing, metagenomics and qPCR) from the same site. For example, the lung microbiome (bacteria) with the gut microbiome (bacteria) or the lung microbiome (bacteria) with lung mycobium. The tool assumes each input microbiome datasets represent a view of an underlying biological mechanism or a disease. Reliable estimation of each view is assumed when using SNF [9]. However, it may not be always practical to reliably estimate each view, although they

play an equal role in the underlying biological process. This is due to the limitations and differing rates of development, in the present technologies and reference databases. In such cases, a weighted SNF approach is preferred, which still assumes the input datasets share an underlying biological mechanism but accounts for inconsistency of the microbiome data based on the user specified weights. The default weights are assigned based on the taxonomical richness (i.e. the number of microbes present) of the datasets.

The interface of the webtool was developed using Rshiny and is available through Shiny Server (Open Source) in confluence with nginx-1.19.1. The tool is powered by custom scripts written in python2.7 and R; and containerized using Docker for ease of offline implementation. The developed webtool can be accessed at <https://integrative-microbiomics.ntu.edu.sg>.

### 1.2.2 Longitudinal assessment of Exacerbation

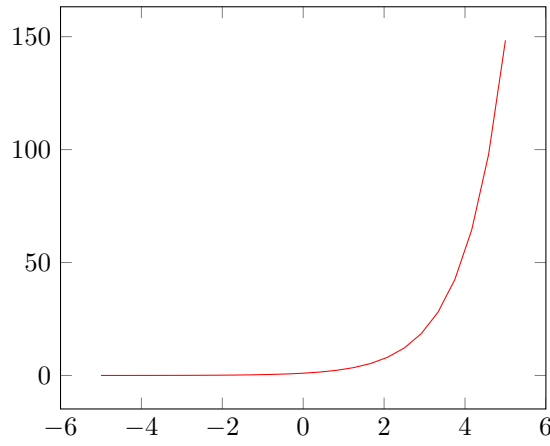
A longitudinal cohort of n=17 patients were recruited from two hospitals in the east of Scotland (2016-2017) to study changes in the microbiome during exacerbation and following antibiotic treatment. DNA and RNA extraction were performed on sputum samples obtained from each patient and on a blank sterile PBS (Phosphate buffer solution). The extracted DNA was subjected to targeted amplicon sequencing of the 16S rRNA and ITS2 regions of the genome to derive the Microbiome and Mycobiome, by mapping them to green genes and UNITE databases, respectively. Blank samples contained read counts many orders of magnitude lower than test samples and hence unlikely to have any influence on the observed microbiome. RT-qPCR (real time quantitative polymerase chain reaction) was performed on the cDNA derived from the extracted RNA to quantify the viral burden of the 17 viruses investigated in each patient.  $\alpha$  and  $\beta$  diversity of the multi-biome was calculated from the concatenated microbiome and the integrated patient similarity matrix using the vegan package in R.

### 1.2.3 Antibiotic action simulation

To predict the impact of antibiotics on the interactome,  $\beta$ -lactam antibiotic action was simulated by a 75% reduction in the relative abundance of the microbes targeted by this antibiotic in the baseline (pre-antibiotic) state including the following genera: *Streptococcus*, *Staphylococcus*, *Haemophilus*, *Moraxella*, *Actinomyces*, *Arachnia*, *Bacteroides*, *Bifidobacterium*, *Eubacterium*, *Fusobacterium*, *Lactobacillus*, *Leptotrichia*, *Peptococcus*, *Peptostreptococcus*, *Propionibacterium*, *Selenomonas*, *Treponema* and *Veillonella*. In order to remove interactions resulting from random noise at the expense of sensitivity to weak signals and to allow comparison between the derived interactomes, the following abundance and prevalence filters were applied followed by co-occurrence analysis; retention of microbes present at greater than 1% abundance in at least three subjects; in the pre OR post OR modelled antibiotic state.

### 1.2.4 “Time to next exacerbation” prediction

To predict Time to next exacerbation, Microbiome datasets were CLR (Centred log ratio) transformed before concatenation and microbes that are present in at least 4 patients at an abundance of 1% were considered for further analysis. To derive pairwise microbial interactions for each patient, LIONESS [11], a single patient network inference framework was implemented with General Boosted Linear model (GBLM) as the network inference algorithm. Correlation between the abundance of each microbes and interaction strength with time to next exacerbation was assessed using Spearmans rank correlation with statistical testing. Multivariate adaptive regression spline (MARS) [6], a non-linear regression model was implemented with microbes or



**Figure 1.4:** Plot of Exponential Function.

interaction strength as the predictor variable to predict time to next exacerbation groups; defined as (Time to exacerbation: <12 weeks and >12weeks). The goodness of the fit of the model was evaluated by computing the R-squared (RSq) and the Generalized R-squared metric (GRsq). A feature importance plot based on Generalized Cross validation score (gcv) was also computed on the feature selected (microbes) by the model. All the above analysis was implemented in R using the following packages 1)Hmisc 2) earth 3)vegan 4)compositions 5)lionessR.

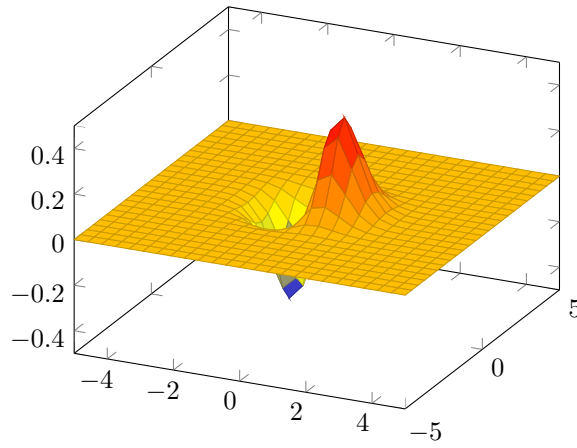
### 1.2.5 Validation of the interactome

Experimental microbiological validation of *Pseudomonas aeruginosa* and *Aspergillus fumigatus* interaction was performed using one strain *Aspergillus fumigatus* (Af293) and three strains of *Pseudomonas aeruginosa*: (1) lab strain (PAO1) as control and (2,3) two clinical isolates of *Pseudomonas aeruginosa* derived from low-risk and high-risk patient clusters. The interaction was investigated using the disk inhibition method as described by Homa et al. [8]. An independent cohort of 166 patients was recruited from 4 sites (3 in Singapore and 1 in Dundee, Scotland) to validate the high-risk cluster and its interactome. DNA extraction was performed on the collected sputum samples of each patient. A shotgun metagenomic sequencing was performed at the NTU core sequencing facility on these samples according to the methods described by Gusareva et al. [7]. Kaiju [13] with default parameters was implemented on the raw sequences after human read removal to estimate the taxonomic composition by referencing against NCBI BLAST nr+euk database. Estimation of the viruses that include prokaryotic phages and eukaryotic viruses was implemented using a custom pipeline that uses Demovir (<https://github.com/feargalr/Demovir>).

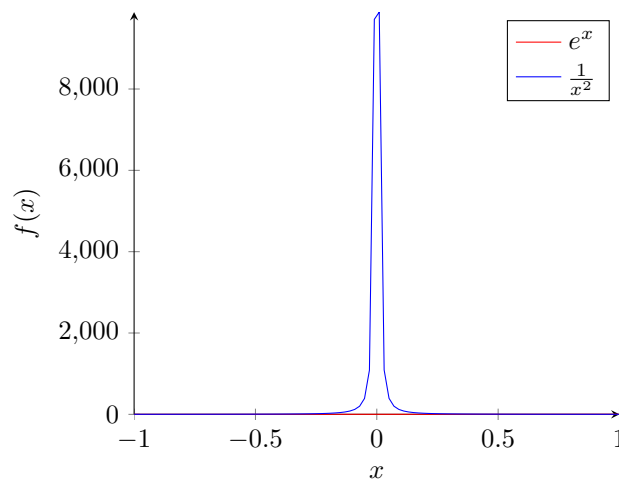
## 1.3 Results

### 1.3.1 Math Cheat Sheet

Figure 3.3, Figure 3.4, and Figure 3.5 are generated from function in L<sup>A</sup>T<sub>E</sub>X.



**Figure 1.5:** Plot of 3-D Function.



**Figure 1.6:** Two functions in one plot.

### 1.3.2 Table Cheat Sheet

## 1.4 Discussion

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	Apple	Oranges	Strawberries
A	1	2	3
B	1	2	3
C	1	2	3
D	1	2	3

**Table 1.1:** Caption

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## 1.5 Future works

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# Chapter 2

## Title2

### Introduction

The Gut-microbiome is by far the best and widely studied microbial ecosystem of the human anatomy, partly due to the rich microbial environment and partly due to the ease of sample collection (non-invasive) through faeces [2]. On the other hand, healthy lung was long considered to be sterile but with advent high-throughput sequencing techniques this has been proven otherwise [cite]. Extensive research on the gut-microbiota has shown that gut microbiota is capable of influencing other organs, such as the brain, liver or lungs [1]. This has led to the coining of terms such as the ‘gut-brain axis’ and the ‘lung-gut axis’.

The epithelial surfaces of the gut and lung are exposed to diverse microbes; ingested microorganisms can access both sites and the microbiota from the gut can enter the lungs through processes such as micro-aspiration [2]. Furthermore, the lung and gut can interact through the systemic cytokines released by host immune cells in response to microbes or microbes from one-site may secrete metabolites which are absorbed into the blood stream and thus regulate the organs [4]. A study used germ free mice, which lack an appropriately developed immune system and showed mucosal alterations, both of which is restored through colonization with gut microbiota. Thus, supplementing the concept of ‘lung-gut’ axis [2].

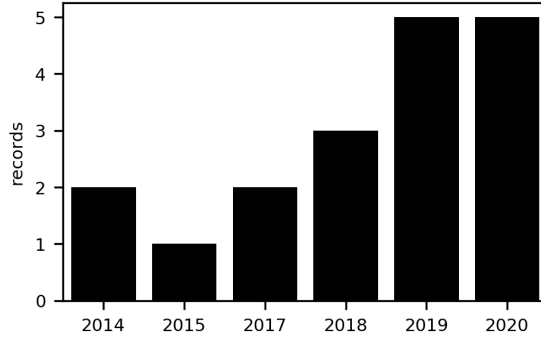
Literature survey using the keyword ‘lung-gut axis’ shows that this concept was first introduced in 2004 and increasing work is being done 2.1. This increasing evidence also suggests, a potential existence of lung-gut axis and its effectual role in lung diseases. Although the gutlung axis is only beginning to be understood, emerging evidence indicates that there is potential for manipulation of the gut microbiota in the treatment of lung diseases. Despite this, the influence of microbial gut health in Bronchiectasis lung is poorly studied. Hence, in the second chapter of my PhD thesis

Want to check if microbes interact

## 2.1 Methods

### 2.1.1 Study population

57 patients with stable bronchiectasis were recruited as a part of this study by our collaborators in Milan, Italy. Recruitment of patients was performed cross-sectionally as a part of the Bronchiectasis Program of



**Figure 2.1:** A histogram illustrating all available publications (including original articles and perspectives) matching the keyword “lung-gut axis” from 1900 to 2020 in the web of science database.

Fondazione IRCCS Ca’ Granda Ospedale Maggiore Policlinico, Milan, Italy. Patients were enrolled during their clinical stability (at least one month apart from the last exacerbation and antibiotic course) and underwent clinical, radiological and microbiological evaluation. Patients were asked to provide a sputum and stool sample with a maximum gap of 12hrs. between the sputum and stool sample. DNA was extracted by our lab members from the sputum and stool samples as described previously [12]. The extracted DNA was subjected to targeted amplicon sequencing of the 16S rRNA and ITS2 regions of the genome to derive the Microbiome and Mycobiome, by mapping them to green genes and UNITE databases, respectively.

### 2.1.2 Data-preprocessing

Read counts of Microbiome and Mycobiome datasets from the sputum and stool samples of the 57 samples were converted into relative abundances. Only microbes present  $\geq 1\%$  in at least 5 patients were considered for further analysis.

### 2.1.3 Co-occurrence analysis

### 2.1.4

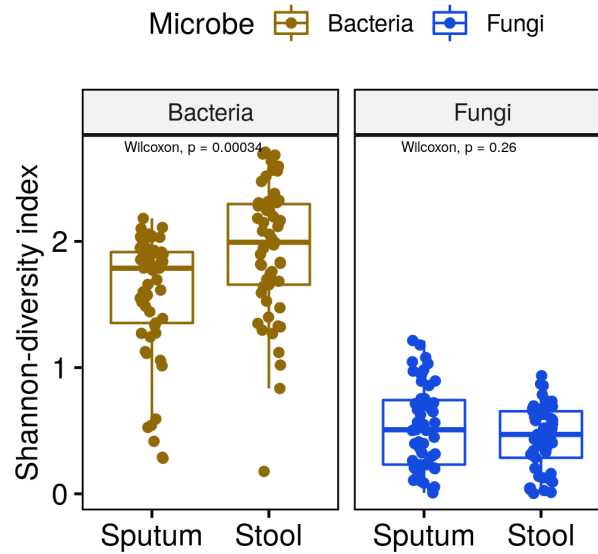
We report the first integration of lung-gut microbiome (bacteria and fungi) in bronchiectasis (n=57) performed using MOFA2 and a weighted similarity network fusion approach following spectral clustering. ALDEX2 was implemented to identify discriminant taxa. Co-occurrence analysis was employed using GBLM to derive microbial association networks.

## 2.2 Results

### 2.2.1 Significant overlap of fungal communities of lung and gut contrary to bacteria

Intersection analysis of bacterial and fungal communities between sputum and stool samples reveals increased overlap of fungal communities between the lung and gut, contrary to bacteria. Three bacterial genera including *Lactobacillus*, *Prevotella* and *Streptococcus* compared to six fungal genera including *Candida*, *Cryptococcus*, *Curvularia*, *Debaryomyces*, *Lodderomyces* and *Saccharomyces* were present in both sputum

and stool samples. Interestingly, upon assessment of diversity between the sputum and stool samples, a similar pattern is observed. Overall, mycobiome exhibits a decreased diversity compared to microbiome. Further, an increased diversity of bacteria is found in the gut compared to the lung whereas the fungal diversity doesn't change.



**Figure 2.2:** A boxplot illustrating the difference in Shannon-diversity index of the Microbiome (Ochre) and Mycobiome (Blue) between the sputum (Lung) and stool (Gut) samples. Statistical significance of these differences calculated using ‘wilcoxon test’ are indicated above as p-values.

Co-occurrence analysis reveals lung gut microbial (bacteria and fungi) interactions suggestive of a potential lung-gut axis.

MOFA2 analysis reveals factors, highly contributed by the Gut bacteria and associated with exacerbations.

Integrating microbiomes (bacteria and fungi) from lung and the gut, following clustering identifies patients with increased risk of exacerbation, Reiff score and FACED with no difference in lung function.

High-risk patients exhibit significantly increased *Candida* in Gut, *Fusobacterium* in Lung, increased lung-gut microbial interaction (35% $\downarrow$ 29%) and movement of *Streptococcus* between lung and gut, illustrating a dysregulated lung-gut axis.

## 2.3 Discussion

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## 2.4 Future works

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# Chapter 3

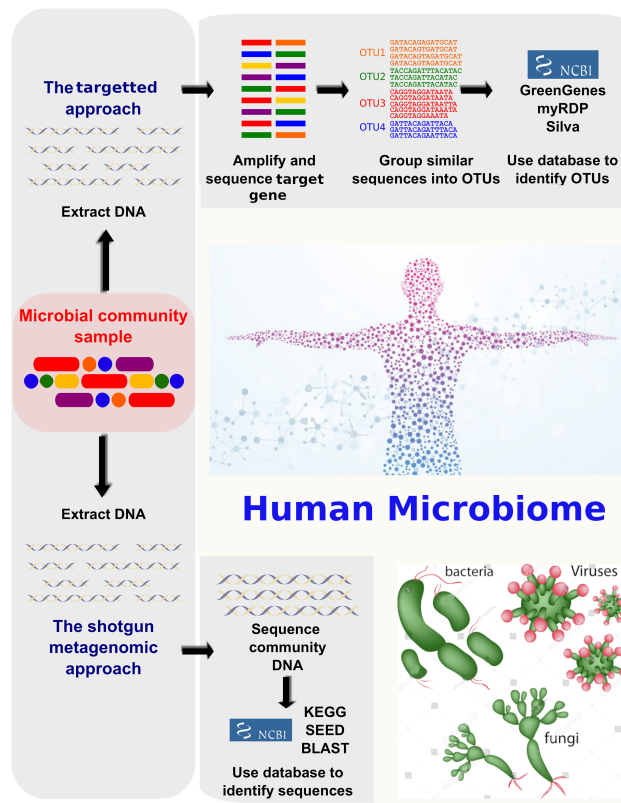
## Title3

### 3.1 Introduction

The term microbiome is used to refer to the collection of genes within a community of microbes (including bacteria, fungi, virus, protists and bacteriophages). In the last few years, microbiome research has helped us gained new insights into how microbes shape our human biology and have brought paradigm-shifting implications for translational research and clinical care. The human microbiota is crucial for our body to maintain its homeostasis. Disruption of this can lead to diseases such as obesity, inflammatory bowel disease, malnutrition, Parkinson's, Autism, Asthma, dental caries, bacterial vaginosis, and depression [10]. Currently, microbiome researchers use culture-independent techniques that involve DNA sequencing to derive the microbiome. Broadly, the community taxonomy/microbiome can be identified using two approaches (see Figure3.1) 1) Targeted and 2) Metagenomic. Targeted sequencing approach uses the PCR amplified, target gene markers (16S rRNA in case of bacteria or ITS in case of Fungi) derived from the samples to reference it against gene-marker databases (Silva, Green Genes, etc.). In contrast, the metagenomic sequencing approach directly sequence the whole community DNA and compares it to reference genomes [14].

Present microbiome studies focus on a single profile of the human microbiome in isolation, even though bacteria, fungi and viruses coexist and interact in the body as a community. Thus, it is essential to look at these biological components together in an integrated fashion to understand more holistically the true underlying in vivo state. However, one of the primary reasons for the lack of multi-biomic research is the lack of methods to merge microbiome datasets and integrative analysis. Consequently, I tried addressing some of these challenges in my master's thesis, using microbiome datasets derived from bronchiectasis patients as an example. Bronchiectasis, is a chronic inflammatory respiratory disease associated with progressive, irreversible dilatation of the airway. It is crucial to study bronchiectasis because in most cases it is known to be idiopathic(unknown cause) [3] and it is a significant contributor to lung diseases globally with a substantial four-fold higher predominance in Asian populations [16].

Previously in my master's thesis, I developed weighted similarity network fusion (wSNF) to allow weightage of input datasets during integration, otherwise unaccounted by conventional SNF [17]. Ensemble-based co-occurrence analysis strategy developed by Faust et al. [5] was extended to allow weightage of individual methods in the ensemble along with other modification to better infer microbial association networks. Microbiome and Mycobiome derived using targeted amplicon sequencing of the 16S and ITS regions from the sputum samples of the CAMEB cohort [12]; virome from qPCR on an extensive panel of 17 respiratory viruses, were used as the example dataset to integrate the microbiomes (Figure3.2a). Multi-biome (Microbiome, Mycobiome and Virome) integration by wSNF identifies a high-risk exacerbation cluster



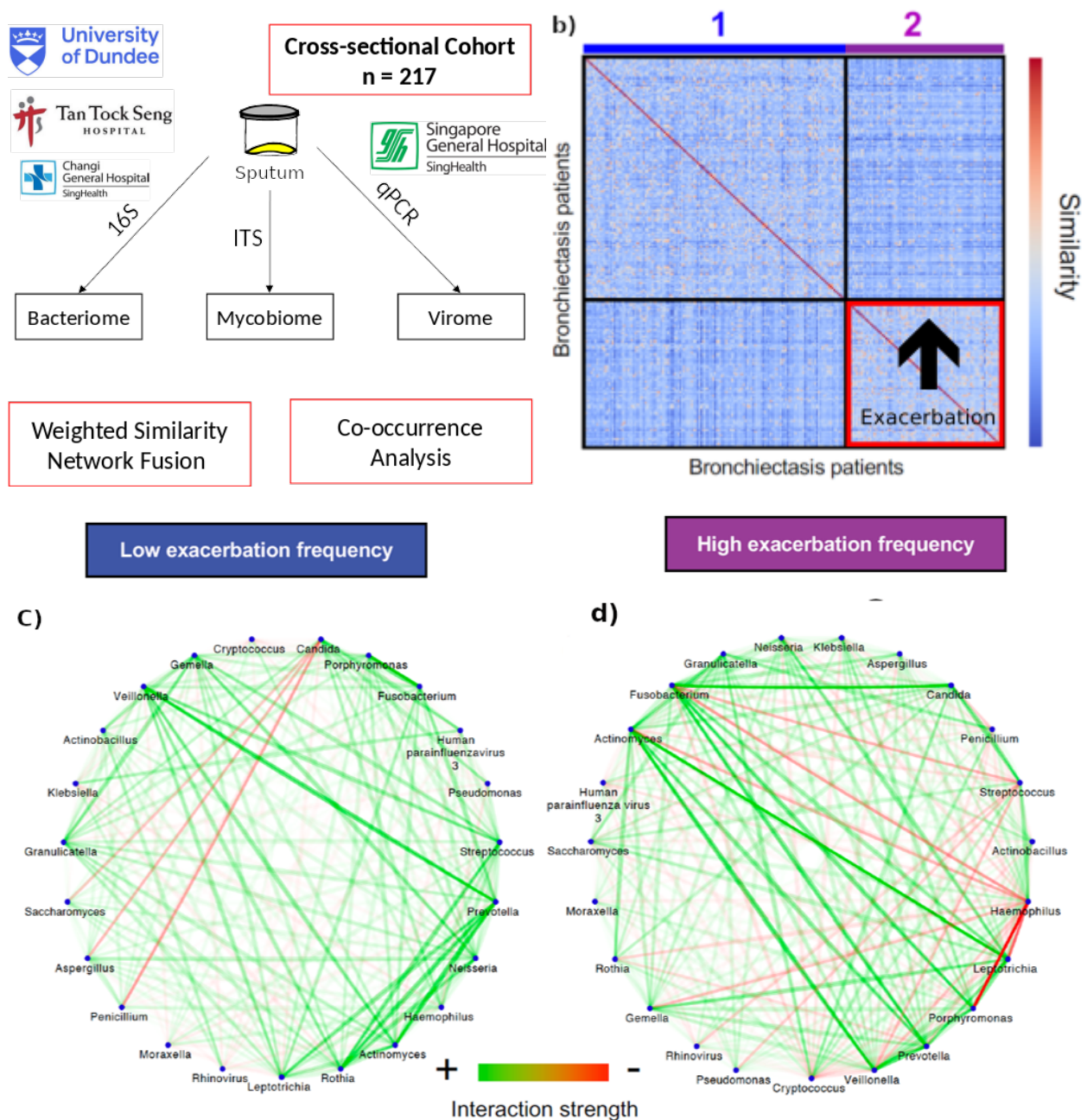
**Figure 3.1:** A figure illustrating the different sequencing approaches used to derive the human microbiome, consisting of interacting bacteria, fungi and viruses. Adapted from: [14]

with increased precision (Figure3.2b). Co-occurrence network analysis of this high-risk cluster revealed an elevated antagonistic interactome with reduced alpha-diversity (Figure3.2c) [15].

Having developed the wSNF and shown its increased precision to identify exacerbators (clinical outcomes); here in my PhD thesis, I attempt to extend my results further. I aim to develop a web tool to enable users to integrate their microbiome datasets and to illustrate its advantages using publicly available microbiome datasets. The tool would motivate clinicians and microbiome researchers to explore multi-biome strategies for their problem and aid them in integrating their datasets. Secondly, I aim to study exacerbation events, antimicrobial perturbations and “Time to next exacerbation” using the developed “Interactome” framework. Thirdly, I aim to validate the “high-risk” exacerbation cluster of Bronchiectasis patients and its “interactome” as derived in my previous work [15] using an alternate sequencing approach: metagenomics. Further, we also pick an interaction from the interactome of the high and low-risk clusters and validate it experimentally.

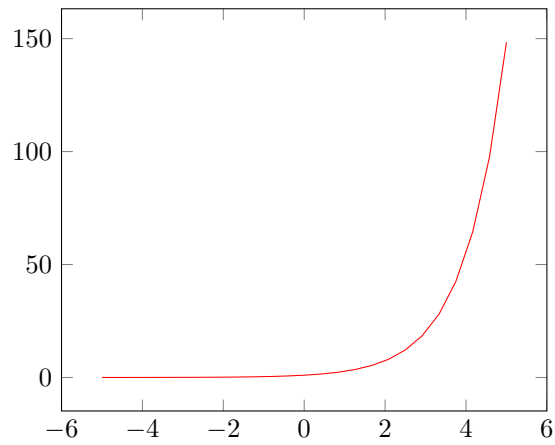
## 3.2 Methods

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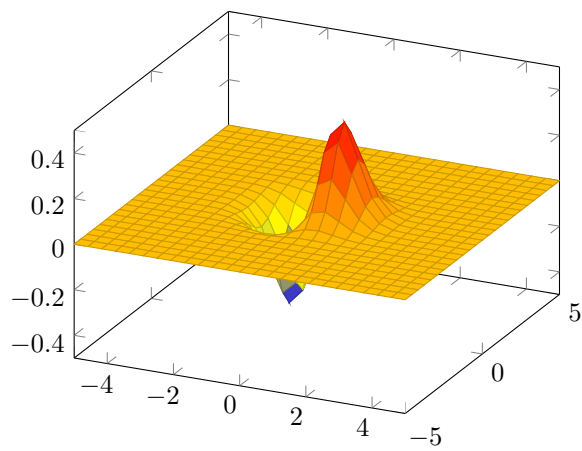


**Figure 3.2:** (a) A schematic representing, overview of analysis performed on the CAMEB cohort (n=217). Methodologies: Weighted SNF and Co-occurrence analysis were used for microbiome integration and interactome construction. (b) A patient similarity matrix with each cell representing the integrated similarity between patients. Two clusters of low (black) and high (red) risk patients identified by wSNF are highlighted by boxes. Visualization of the interactome of low (c) and high (d) risk clusters. Interactions between microbes are classified as negative if the sign of the edge weights between them is negative (coloured red) with positive interactions indicated by green colouration. The strength of the interaction is indicated by the colour depth

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**Figure 3.3:** Plot of Exponential Function.



**Figure 3.4:** Plot of 3-D Function.

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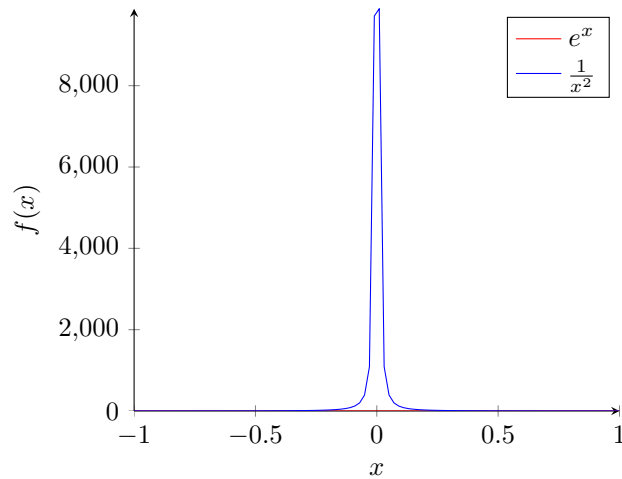
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## 3.3 Results

### 3.3.1 Math Cheat Sheet

Figure 3.3, Figure 3.4, and Figure 3.5 are generated from function in  $\text{\LaTeX}$ .





**Figure 3.5:** Two functions in one plot.

	Apple	Oranges	Strawberries
A	1	2	3
B	1	2	3
C	1	2	3
D	1	2	3

**Table 3.1:** Caption

### 3.3.2 Table Cheat Sheet

## 3.4 Discussion

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### 3.5 Future works

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## Chapter 4

# Discussion

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## Chapter 5

# Future works

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