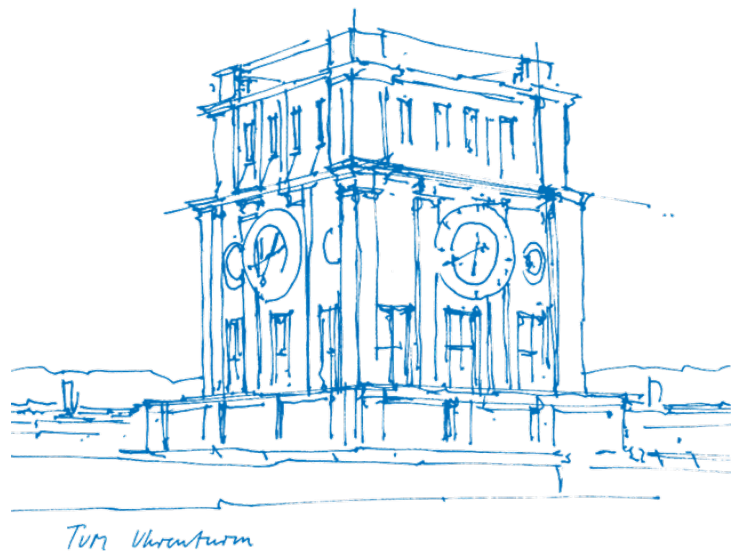


# Thesis title

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Author Name





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Vollständiger Abdruck der von der Fakultät für Elektrotechnik und Informationstechnik der Technischen Universität München zur Erlangung des akademischen Grades eines

**Doktor-Ingenieurs (Dr.-Ing.)**

genehmigten Dissertation.

**Vorsitzende(r):**

Prof. Franz X. Gabelsberger

**Prüfer der Dissertation:**

1. Prof. Dr. Georg Simon Ohm
2. Prof. James Clerk Maxwell

Die Dissertation wurde am 29.04.2016 bei der Technischen Universität München eingereicht und durch die Fakultät für Elektrotechnik und Informationstechnik am 11.07.2016 angenommen.



*To Franz X. Gabelsberger, inventor of the street named after him.*





# Abstract

The abstract of your thesis goes here.

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# **1 Introduction**

This is the introduction of the thesis.

## **1.1 Pathophysiology of chronical lung diseases**

### **1.1.1 Bronchopulmonary Dysplasia (BPD)**

### **1.1.2 Asthma**

### **1.1.3 Chronic Obstructive Pulmonary Disease (COPD)**

### **1.1.4 Idiopathic Pulmonary Fibrosis (IPF)**

## **1.2 Computational biology and chronic lung diseases**

### **1.2.1 Multi-omics data integration**

### **1.2.2 Clinical prediction**

### **1.2.3 Systems biology**

## **1.3 Aims**



## **2 Methodology**

This is the methodology of the thesis.

## **2.1 Data gathering**

### **2.1.1 Mice data**

Transcriptomics

### **2.1.2 Human data**

Transcriptomics

Metabolomics

### **2.1.3 Public data**

Multi-omics bulk data

Neonatal single-cell transcriptomics

## **2.2 Preprocessing**

### **2.2.1 Normalization**

DESeq2

Pareto scaling

Size-effect

### **2.2.2 Data imputation**

Random-forest

knn-Imputation

### **2.2.3 Batch-effect detection**

Principal component analysis (PCA)

Hierarchical clustering

K-BET

## **2.3 Differential expression analysis**

### **2.3.1 Limma**

### **2.3.2 DESeq2**

## **2.4 Enrichment analysis**

### **2.4.1 Gene list functional enrichment analysis**

## **2.5 Multi-omics factor analysis (MOFA)**

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## **2.6 Clinical data correlation**

### **2.6.1 Linear regression**

### **2.6.2 Binomial regression**

### **2.6.3 Ordinal regression**

### **2.6.4 Multinomial logistic regression**

### **2.6.5 Dirichlet regression**

## **2.7 Benchmarking of Lasso models dealing with missing values**

### **2.7.1 Knowledge guided multi-level network inference**

### **2.7.2 Two-steps based models**

Grouped adaptive Lasso (GALasso)

Stacked adaptive Lasso (SALasso)

### **2.7.3 Inverse covariance based methods**

Convexed conditioned Lasso (CoCoLasso)

Lasso with high missing rate (HMLasso)

## **2.8 Adult data correlation**

### **2.8.1 Random forest**

Imbalanced random forest

Nested cross-validation in random forest

### **2.8.2 t-test, manova, log-reg**



### 3 Summary of publications

1. Juan Henao, Alida Kindt, Tanja Seegmüller, Kai Foerster, Andreas Flemmer<sup>3</sup>, Juergen Behr<sup>4</sup>, Nikolaus Kneidinger, Marion Frankenberger, Fabian Theis, Benjamin Schubert, Markus List, Anne Hilgendorff. Multi-omic signatures relate to the severity of pulmonary outcome in neonates traced into adult disease.

**Summary:** kfkfkfkfk

2. Erika Gonzalez Rodriguez<sup>1</sup>, Juan Henao<sup>2</sup>, Motaharehsadat Heydarian<sup>1</sup>, Tina Pritzke<sup>1</sup>, Alida Kindt<sup>3</sup>, Anna M. Dmitrieva<sup>1</sup>, Heiko Adler<sup>4, 5</sup>, Melanie Markmann<sup>6</sup>, Valeria Viteri-Alvarez<sup>1</sup>, Prajakta Oak<sup>1</sup>, Markus Koschlig<sup>1</sup>, Xin Zhang<sup>1</sup>, Kai M. Foerster<sup>7</sup>, Andreas Flemmer<sup>7</sup>, Hamid Hossain<sup>6,8</sup>, Xavier Pastor<sup>2</sup>, Holger Kirsten<sup>9</sup>, Peter Ahnert<sup>9</sup>, Juergen Behr<sup>10</sup>, Tushar J. Desai<sup>11</sup>, Benjamin Schubert<sup>2</sup>, Anne Hilgendorff<sup>1,12</sup>. Hyperoxia-induced cell cycle arrest drives long-term impairment of lung development and DNA repair in neonates.
3. Juan David Henao Sanchez<sup>3,14</sup>, Mustafa Abdo<sup>1,2</sup>, MD, MSc, Benjamin Schubert<sup>3,14</sup>, PhD, Markus List<sup>4</sup>, PhD, Henrik Watz<sup>2,14</sup>, MD, Frauke Pedersen<sup>1,2,14</sup>, PhD, Alina Bauer<sup>3,15</sup>, MSc, Dominik Thiele<sup>5,14</sup>, MSc, Adam M. Chaker<sup>6,7</sup>, MD, Constanze A. Jakwerth<sup>7,15</sup>, PhD, Benjamin Waschki<sup>1,8,14</sup>, MD, Anne Kirsten<sup>2,14</sup>, MD, Markus Weckmann<sup>9,14</sup>, PhD, Oliver Fuchs<sup>9,10,14</sup>, MD, PhD, Gesine Hansen<sup>11,16</sup>, MD, Matthias V. Kopp<sup>9,14</sup>, MD, Erika v. Mutius<sup>12,13,15</sup>, MD, MSc, Inke R. König<sup>4,14</sup>, PhD, Klaus F. Rabe<sup>1,14</sup>, MD, PhD, Thomas Bahmer<sup>1,14</sup>, MD, Carsten B. Schmidt-Weber<sup>7,15</sup>, PhD, Ulrich M. Zissler<sup>7,15</sup>, PhD, and the ALLIANCE Study Group\*. Cytokines Derived from Nasal Epithelial Lining Fluid in Patients with Asthma.
4. Henao, J. D., Lauber, M., Azevedo, M., Grekova, A., Theis, F., List, M., ... & Schubert, B. (2023). Multi-omics regulatory network inference in the presence of missing data. *Briefings in Bioinformatics*, 24(5), bbad309.



## 4 Discussion

This is the discussion of the thesis.



# A Appendix

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