

Thesis title

Subtitle of the thesis

Author Name



Thesis title

Subtitle of the thesis

Author Name

Bitte passen Sie den Lehrstuhlnamen in tumuser.sty an. Fakultät für Elektrotechnik und Informationstechnik Technische Universität München



Thesis title

Subtitle of the thesis

Author Name

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.

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

Abstract

The abstract of your thesis goes here.

Lorem ipsum dolor sit amet, consectetuer adipiscing elit. Ut purus elit, vestibulum ut, placerat ac, adipiscing vitae, felis. Curabitur dictum gravida mauris. Nam arcu libero, nonummy eget, consectetuer id, vulputate a, magna. Donec vehicula augue eu neque. Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas. Mauris ut leo. Cras viverra metus rhoncus sem. Nulla et lectus vestibulum urna fringilla ultrices. Phasellus eu tellus sit amet tortor gravida placerat. Integer sapien est, iaculis in, pretium quis, viverra ac, nunc. Praesent eget sem vel leo ultrices bibendum. Aenean faucibus. Morbi dolor nulla, malesuada eu, pulvinar at, mollis ac, nulla. Curabitur auctor semper nulla. Donec varius orci eget risus. Duis nibh mi, congue eu, accumsan eleifend, sagittis quis, diam. Duis eget orci sit amet orci dignissim rutrum.

Nam dui ligula, fringilla a, euismod sodales, sollicitudin vel, wisi. Morbi auctor lorem non justo. Nam lacus libero, pretium at, lobortis vitae, ultricies et, tellus. Donec aliquet, tortor sed accumsan bibendum, erat ligula aliquet magna, vitae ornare odio metus a mi. Morbi ac orci et nisl hendrerit mollis. Suspendisse ut massa. Cras nec ante. Pellentesque a nulla. Cum sociis natoque penatibus et magnis dis parturient montes, nascetur ridiculus mus. Aliquam tincidunt urna. Nulla ullamcorper vestibulum turpis. Pellentesque cursus luctus mauris.

Contents

Αb	stra	ct		ix									
1	Intro	oduction		1									
	1.1	1 Pathophysiology of chronical lung diseases											
			nopulmonary Dysplasia (BPD)										
			a										
			c Obstructive Pulmonary Disease (COPD)	1									
			hic Pulmonary Fibrosis (IPF)										
	1.2		I biology and chronic lung diseases	1									
			mics data integration	1									
			I prediction	1									
			ns biology	1									
		,	cell transcriptomics										
	1.3	_											
		7		•									
2	Met	hodology		3									
	2.1		g	4									
			。 ata	4									
			n data	4									
			data	4									
	2.2			4									
			, lization	4									
			nputation	4									
			effect detection	4									
	2.3		pression analysis	4									
				4									
			12	4									
	2.4	-	nalysis	4									
			ist functional enrichment analysis	4									
	2.5		ctor analysis (MOFA)	4									
	2.6		orrelation	5									
			regression	5									
			ial regression	5									
			I regression	5									
			omial logistic regression	5									
			et regression	5									
	2.7		g of Lasso models dealing with missing values	5									
	,	_	edge guided multi-level network inference	5									
			eps based models	5									
			e covariance based methods	5									
	2.8		relation	5									
	0		m forest	5									
			manova, log-reg										

3		eroxia-induced cell cycle arrest drives long-term impairment of lung development and
	3.1	repair in neonates
	_	Summary
	3.2	Transcriptional characterization of <i>in vitro</i> and <i>in vivo</i> mice under hyperoxia and mechanical
		ventilation
		3.2.1 <i>in vitro</i> samples
	0.0	3.2.2 <i>In vivo</i> samples
	3.3	Transcriptional commonalities between <i>in vitro</i> samples
		3.3.1 Transcriptional commonalities between AT1/2, EC and MFB
	0.4	3.3.2 Transcriptional commonalities between AT1/2 and MFB
	3.4	Transcriptional singularities between <i>in vitro</i> samples
		3.4.1 Alveolar type 1/2 (AT1/2)
		3.4.2 Myofibroblast (MFB)
	3.5	Deep transcriptional characterization of cell-cycle arrest under hyperoxia
		3.5.1 Pre-replication complex hypothesis
		3.5.2 Experimental validation
	3.6	Transcriptional comparison between in vitro and in vivo samples
		3.6.1 Multi-systemic development arrest hypothesis
	3.7	Discussion
		3.7.1 Limitations
		3.7.2 Outlooks
4		-omic integration characterizes major endotypes of bronchopulmonary dysplasia linke
		ult chronic lung disease
	4.1	Summary
	4.2	Feature selection based on differential abundance analysis
		4.2.1 Proteomics
		4.2.2 Metabolomics
	4.3	Enrichment analysis of differentially abundant proteins between BPD and no-BPD samples
	4.4	Latent factor identification as potential BPD endotypes
		4.4.1 Factor 1:
		4.4.2 Factor 2:
		4.4.3 Factor 3:
		4.4.4 Factor 4:
		4.4.5 Factor 5:
	4.5	Summary of BPD endotypes
		4.5.1 Acute BPD signature
		4.5.2 Late/chronic BPD sugnature
	4.6	Correlation between BPD endotypes and chronical adult lung diseases
		4.6.1 Use of imbalanced random forest to separate between COPD and IPF patients using
		BPD latent factor loadings
		4.6.2 Characterization of most explanatory features per significant BPD endotype regard-
		ing COPD and IPF
	4.7	Discussion
	,	4.7.1 Limitations
		4.7.2 Outlooks
5	Mul	-Omics Regulatory Network Inference in the Presence of Missing Data
	5.1	Summary
	•	Experimental set-up
	-	5.2.1 Data preprocessing
		5.2.2 Parameter selection

Α	App	endix		21
8	Disc	cussion	1	19
7	7.1	A sect	Derived from Nasal Epithelial Lining Fluid in Patients with Asthma ion	17 17 17
6	6.1	A sect	Graphical Interface for Single-Cell Transcriptomics Workflow Development ion	15 15 15
		5.5.1 5.5.2	Limitations	13 13
	5.5	5.4.2	Performance evaluation over down-sampling	13 13 13
	5.4	5.3.2 5.3.3 Gener	Single-omics random missingness	13 13 13
	5.3		Missingness simulated scenarios	

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 Cumputational biology and chronic lung diseases

- 1.2.1 Multi-omics data integration
- 1.2.2 Clinical prediction
- 1.2.3 Systems biology
- 1.2.4 Single-cell transcriptomics
- **1.3 Aims**

2 Methodology

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)

Lorem ipsum dolor sit amet, consectetuer adipiscing elit. Ut purus elit, vestibulum ut, placerat ac, adipiscing vitae, felis. Curabitur dictum gravida mauris. Nam arcu libero, nonummy eget, consectetuer id, vulputate a, magna. Donec vehicula augue eu neque. Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas. Mauris ut leo. Cras viverra metus rhoncus sem. Nulla et lectus vestibulum urna fringilla ultrices. Phasellus eu tellus sit amet tortor gravida placerat. Integer sapien

est, iaculis in, pretium quis, viverra ac, nunc. Praesent eget sem vel leo ultrices bibendum. Aenean faucibus. Morbi dolor nulla, malesuada eu, pulvinar at, mollis ac, nulla. Curabitur auctor semper nulla. Donec varius orci eget risus. Duis nibh mi, congue eu, accumsan eleifend, sagittis quis, diam. Duis eget orci sit amet orci dignissim rutrum.

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 Hyperoxia-induced cell cycle arrest drives long-term impairment of lung development and DNA repair in neonates

3.1 Summary

3.2 Transcriptional characterization of *in vitro* and *in vivo* mice under hyperoxia and mechanical ventilation

3.2.1 in vitro samples

Alveolar type 1/2 (AT1/2)

Endothelial cells (EC)

Myofibroblast (MFB)

3.2.2 In vivo samples

3.3 Transcriptional commonalities between *in vitro* samples

- 3.3.1 Transcriptional commonalities between AT1/2, EC and MFB
- 3.3.2 Transcriptional commonalities between AT1/2 and MFB
- 3.4 Transcriptional singularities between in vitro samples
- 3.4.1 Alveolar type 1/2 (AT1/2)
- 3.4.2 Myofibroblast (MFB)
- 3.5 Deep transcriptional characterization of cell-cycle arrest under hyperoxia
- 3.5.1 Pre-replication complex hypothesis
- 3.5.2 Experimental validation
- 3.6 Transcriptional comparison between in vitro and in vivo samples
- 3.6.1 Multi-systemic development arrest hypothesis
- 3.7 Discussion
- 3.7.1 Limitations
- 3.7.2 Outlooks

4 Multi-omic integration characterizes major endotypes of bronchopulmonary dysplasia linked to adult chronic lung disease

4.1 Summary

4.2 Feature selection based on differential abundance analysis

- 4.2.1 Proteomics
- 4.2.2 Metabolomics

4.3 Enrichment analysis of differentially abundant proteins between BPD and no-BPD samples

4.4 Latent factor identification as potential BPD endotypes

4.4.1 Factor 1:

Clinical variable correlation

Systems biology of Factor 1

4.4.2 Factor 2:

Clinical variable correlation

Systems biology of Factor 2

4.4.3 Factor 3:

Clinical variable correlation

Systems biology of Factor 3

4.4.4 Factor 4:

Clinical variable correlation

Systems biology of Factor 4

4.4.5 Factor 5:

Clinical variable correlation

Systems biology of Factor 5

Lorem ipsum dolor sit amet, consectetuer adipiscing elit. Ut purus elit, vestibulum ut, placerat ac, adipiscing vitae, felis. Curabitur dictum gravida mauris. Nam arcu libero, nonummy eget, consectetuer id, vulputate a, magna. Donec vehicula augue eu neque. Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas. Mauris ut leo. Cras viverra metus rhoncus sem. Nulla et lectus vestibulum urna fringilla ultrices. Phasellus eu tellus sit amet tortor gravida placerat. Integer sapien est, iaculis in, pretium quis, viverra ac, nunc. Praesent eget sem vel leo ultrices bibendum. Aenean faucibus. Morbi dolor nulla, malesuada eu, pulvinar at, mollis ac, nulla. Curabitur auctor semper nulla. Donec varius orci eget risus. Duis nibh mi, congue eu, accumsan eleifend, sagittis quis, diam. Duis eget orci sit amet orci dignissim rutrum.

4.5 Summary of BPD endotypes

- 4.5.1 Acute BPD signature
- 4.5.2 Late/chronic BPD sugnature
- 4.6 Correlation between BPD endotypes and chronical adult lung diseases
- 4.6.1 Use of imbalanced random forest to separate between COPD and IPF patients using BPD latent factor loadings
- 4.6.2 Characterization of most explanatory features per significant BPD endotype regarding COPD and IPF

Factor 1

Factor 4

Factor 5

- 4.7 Discussion
- 4.7.1 Limitations
- 4.7.2 Outlooks

5 Multi-Omics Regulatory Network Inference in the Presence of Missing Data

This is the third project of the thesis.

5.1 Summary

5.2 Experimental set-up

- 5.2.1 Data preprocessing
- 5.2.2 Parameter selection
- 5.2.3 Missingness simulated scenarios
- 5.2.4 Performance evaluation criteria

5.3 Performance evaluation over different missingness scenarios

- 5.3.1 Single-omics random missingness
- 5.3.2 Multi-omics random missingness
- 5.3.3 Block-wise random missingness

5.4 General method performance evaluation

- 5.4.1 Performance evaluation over down-sampling
- 5.4.2 Computational runtime evaluation
- 5.5 Discussion
- 5.5.1 Limitations
- 5.5.2 Outlooks

6 scNodes: Graphical Interface for Single-Cell Transcriptomics Workflow Development

This is the forth project of the thesis.

Lorem ipsum dolor sit amet, consectetuer adipiscing elit. Ut purus elit, vestibulum ut, placerat ac, adipiscing vitae, felis. Curabitur dictum gravida mauris. Nam arcu libero, nonummy eget, consectetuer id, vulputate a, magna. Donec vehicula augue eu neque. Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas. Mauris ut leo. Cras viverra metus rhoncus sem. Nulla et lectus vestibulum urna fringilla ultrices. Phasellus eu tellus sit amet tortor gravida placerat. Integer sapien est, iaculis in, pretium quis, viverra ac, nunc. Praesent eget sem vel leo ultrices bibendum. Aenean faucibus. Morbi dolor nulla, malesuada eu, pulvinar at, mollis ac, nulla. Curabitur auctor semper nulla. Donec varius orci eget risus. Duis nibh mi, congue eu, accumsan eleifend, sagittis quis, diam. Duis eget orci sit amet orci dignissim rutrum.

6.1 A section

Nam dui ligula, fringilla a, euismod sodales, sollicitudin vel, wisi. Morbi auctor lorem non justo. Nam lacus libero, pretium at, lobortis vitae, ultricies et, tellus. Donec aliquet, tortor sed accumsan bibendum, erat ligula aliquet magna, vitae ornare odio metus a mi. Morbi ac orci et nisl hendrerit mollis. Suspendisse ut massa. Cras nec ante. Pellentesque a nulla. Cum sociis natoque penatibus et magnis dis parturient montes, nascetur ridiculus mus. Aliquam tincidunt urna. Nulla ullamcorper vestibulum turpis. Pellentesque cursus luctus mauris.

6.2 Another section

Nulla malesuada porttitor diam. Donec felis erat, congue non, volutpat at, tincidunt tristique, libero. Vivamus viverra fermentum felis. Donec nonummy pellentesque ante. Phasellus adipiscing semper elit. Proin fermentum massa ac quam. Sed diam turpis, molestie vitae, placerat a, molestie nec, leo. Maecenas lacinia. Nam ipsum ligula, eleifend at, accumsan nec, suscipit a, ipsum. Morbi blandit ligula feugiat magna. Nunc eleifend consequat lorem. Sed lacinia nulla vitae enim. Pellentesque tincidunt purus vel magna. Integer non enim. Praesent euismod nunc eu purus. Donec bibendum quam in tellus. Nullam cursus pulvinar lectus. Donec et mi. Nam vulputate metus eu enim. Vestibulum pellentesque felis eu massa.

7 Cytokines Derived from Nasal Epithelial Lining Fluid in Patients with Asthma

The fifth project.

Lorem ipsum dolor sit amet, consectetuer adipiscing elit. Ut purus elit, vestibulum ut, placerat ac, adipiscing vitae, felis. Curabitur dictum gravida mauris. Nam arcu libero, nonummy eget, consectetuer id, vulputate a, magna. Donec vehicula augue eu neque. Pellentesque habitant morbi tristique senectus et netus et malesuada fames ac turpis egestas. Mauris ut leo. Cras viverra metus rhoncus sem. Nulla et lectus vestibulum urna fringilla ultrices. Phasellus eu tellus sit amet tortor gravida placerat. Integer sapien est, iaculis in, pretium quis, viverra ac, nunc. Praesent eget sem vel leo ultrices bibendum. Aenean faucibus. Morbi dolor nulla, malesuada eu, pulvinar at, mollis ac, nulla. Curabitur auctor semper nulla. Donec varius orci eget risus. Duis nibh mi, congue eu, accumsan eleifend, sagittis quis, diam. Duis eget orci sit amet orci dignissim rutrum.

7.1 A section

Nam dui ligula, fringilla a, euismod sodales, sollicitudin vel, wisi. Morbi auctor lorem non justo. Nam lacus libero, pretium at, lobortis vitae, ultricies et, tellus. Donec aliquet, tortor sed accumsan bibendum, erat ligula aliquet magna, vitae ornare odio metus a mi. Morbi ac orci et nisl hendrerit mollis. Suspendisse ut massa. Cras nec ante. Pellentesque a nulla. Cum sociis natoque penatibus et magnis dis parturient montes, nascetur ridiculus mus. Aliquam tincidunt urna. Nulla ullamcorper vestibulum turpis. Pellentesque cursus luctus mauris.

7.2 Another section

Nulla malesuada porttitor diam. Donec felis erat, congue non, volutpat at, tincidunt tristique, libero. Vivamus viverra fermentum felis. Donec nonummy pellentesque ante. Phasellus adipiscing semper elit. Proin fermentum massa ac quam. Sed diam turpis, molestie vitae, placerat a, molestie nec, leo. Maecenas lacinia. Nam ipsum ligula, eleifend at, accumsan nec, suscipit a, ipsum. Morbi blandit ligula feugiat magna. Nunc eleifend consequat lorem. Sed lacinia nulla vitae enim. Pellentesque tincidunt purus vel magna. Integer non enim. Praesent euismod nunc eu purus. Donec bibendum quam in tellus. Nullam cursus pulvinar lectus. Donec et mi. Nam vulputate metus eu enim. Vestibulum pellentesque felis eu massa.

8 Discussion

This is the discussion of the thesis.

A Appendix

Quisque ullamcorper placerat ipsum. Cras nibh. Morbi vel justo vitae lacus tincidunt ultrices. Lorem ipsum dolor sit amet, consectetuer adipiscing elit. In hac habitasse platea dictumst. Integer tempus convallis augue. Etiam facilisis. Nunc elementum fermentum wisi. Aenean placerat. Ut imperdiet, enim sed gravida sollicitudin, felis odio placerat quam, ac pulvinar elit purus eget enim. Nunc vitae tortor. Proin tempus nibh sit amet nisl. Vivamus quis tortor vitae risus porta vehicula.