Dissertation zur Erlangung des Doktorgrades eingereicht am Fachbereich Mathematik und Informatik der Freien Universität Berlin

The COMMON DENOMINATOR PROCEDURE

A Novel Approach to Gene Expression Data Mining for Identification of Phenotype-Specific Genes

René Korn

2006

Betreuer:

PD Dr. Steffen Schulze-Kremer

Dr. Sascha Röhrig Dr. Ulrich Brinkmann

Gutachter:

PD Dr. Steffen Schulze-Kremer

Prof. Dr. Peter Buckel

Tag der Disputation:

28. April 2006

Dedicated to my beloved father Klaus Korn, who had to suffer from cancer for too many years.

Abstract

This thesis addresses the gap between the amount of on-hand expression data and the availability of information related to the function of those genes. To this end, a data mining procedure for the identification of genes that are associated with pre-defined phenotypes and/or molecular pathways was established. Based on the observation that pathway/phenotype associated genes are frequently expressed in same or nearby places and at identical or similar time points, an approach termed COMMON DENOMINATOR PROCEDURE (CDP) was devised. One unique feature of this novel approach is that the specificity and probability to identify desired phenotype/pathway-associated factors increases the more diverse the input data are. Three different approaches are discussed and compared: (i) a BASIC CDP, (ii) a GENETIC ALGORITHM BASED CDP and (iii) an INDICATOR GENES BASED CDP. To show the feasibility of these approaches, the CGAP Expression Data combined with a defined set of angiogenic factors was used to identify additional and novel angiogenesis-associated genes. A multitude of these additional genes were known to be associated with angiogenesis according to published data, verifying our approach. Application of a high throughput functional genomics platform (XantoScreen[™]) provided further experimental evidence for association of candidate genes with angiogenesis.

Acknowledgement

First of all, I would like to thank PD Dr. Steffen Schulze-Kremer for being my supervisor and for supporting this work with his beneficial ideas and constructive criticism. I would also like to kindly thank Prof. Dr. Peter Buckel for taking over the part of the second referee. I would like to thank Dr. Ulrich Brinkmann for the original impulse to this work and his commitment.

I also appreciate all my friends and colleagues from Xantos, for their helpful feedback and their friendship. I want to thank Dr. Irene Boche, Stefan Hess, Piia Lämmlein, Dr. Dieter Link, Dr. Stephan Reschauer and Dr. Jürgen Zitzler for their friendship, a nice time and exciting badminton matches. Special thanks go to Dr. Sascha Röhrig, my patient superior, mentor and friend, as well as my closest colleagues from the Bioinformatics and IT department, Dr. Bettina Ehring, Dr. Beate Gawin, Fabian Weiß, Alexander Felber, Dr. Björn Kesper, Dr. Reinhold Köckerbauer and Dr. Alexander Spychaj. I am particularly grateful for the support from the high throughput screening team, Johannes Görl, Dr. Kerstin König-Hoffmann, Dr. Rolf Schäfer and Michael Kazinski.

I want to demonstrate my deepest respect to Xantos Biomedicine AG, especially to Stephan Wehselau and again to Prof. Dr. Peter Buckel, for there investment in my future and their commitment during exciting, interesting and turbulent times.

I am also thankful for the possibility to submit my work to the Department of Mathematics and Computer Science at the Free University of Berlin.

Last but not least I want to thank my family, especially my partner in life Janine Christ, my mother Brigitte Korn, my sister Carolin Korn and my godfather Rainer Spitzenpfeil as well as all my friends, especially Roman Egle and Daniel Godau, for encouragement, for proofreading, for putting up with me all the time, and for just being there.

Contents

	Abs	tract	j
	Ack	nowledgement	i
	Con	itents	iii
	List	of Figures	V
	List	of Tables	vi
	Abb	previations	/ i i
1	Tntr	roduction	1
1	1.1	Knowledge Discovery in Databases	1
	1.2	Biological Background	4
		1.2.1 Central Dogma of Molecular Biology	4
		1.2.2 Gene Expression	7
	1.3	Biological Challenge	7
		1.3.1 Common Denominator Concept	8
		1.3.2 Phenotype Angiogenesis	9
	1.4	Outline	10
2	Sys	tem and Methods	2
	2.1	Infrastructure	12
	2.2		13
		2.2.1 Adaptation to CGAP Expression Data	13
		· · · · · · · · · · · · · · · · · · ·	14
			14
	2.3		15
		· /	17
			20
			22
			23
			23
	2.4		- 25
			27

3	Res	ults	29				
	3.1	Basic CDP	30				
		3.1.1 Definition of Input Data	30				
		3.1.2 Determination of the LIBRARYPROFILE	32				
		3.1.3 Determination of the GENESCORE	32				
		3.1.4 Selection of Candidate Genes	33				
		3.1.5 Procedure Control and Validation	33				
	3.2	GENETIC ALGORITHM BASED CDP	37				
		3.2.1 Definition of Input Data	37				
		3.2.2 Determination of the LIBRARYPROFILE	39				
		3.2.3 Determination of the GENESCORE	39				
		3.2.4 Selection of Candidate Genes	39				
		3.2.5 Procedure Control and Validation	40				
	3.3	INDICATOR GENES BASED CDP	43				
		3.3.1 Definition of Input Data	43				
		3.3.2 Determination of the LIBRARYPROFILE	45				
		3.3.3 Determination of the GENESCORE	45				
		3.3.4 Selection of AngioProfiles	46				
		3.3.5 Selection of Candidate Genes	46				
		3.3.6 Procedure Control and Validation	48				
	3.4	Summary	53				
		3.4.1 Internal Procedure Control	54				
		3.4.2 Procedure Validation - Experimental	55				
		3.4.3 Procedure Validation - Literature	56				
4	ъ.		- -				
4			57				
	4.1	Comparison of the Procedures	58				
	4.2	Comparison to Established Procedures	60				
	4.3	Extensibility	61				
	4.4	Future Perspective	63				
\mathbf{R}	e fere :	nces	66				
\mathbf{A}	Dat	a Sources	75				
В	Imp	lementation	7 8				
\mathbf{C}	C Anhang gemäß Promotionsordnung						
_		Erklärung	80 80				
		Lebenslauf	81				
	\circ . \circ	Zusammenfassung	82				

List of Figures

1.1	Different Steps of Knowledge Discovery in Databases	2
1.2	Central Dogma of Molecular Biology	5
1.3	Different Steps of Protein Synthesis	6
2.1	Key Steps of the IGCDP	16
2.2	Example of a Genetic Algorithm	19
2.3	Schematic Candidate Gene Selection	26
3.1	Flowchart of the BASIC CDP	31
3.2	Flowchart of the GENETIC ALGORITHM BASED CDP	38
3.3	Flowchart of the Indicator Genes Based CDP	44
3.4	Validation of the Indicator Genes Based CDP	51
4.1	Distribution of UniGene Clusters within CGAP Expression Data	62
В.1	Entity Relationship Diagram	78
B.2	UML Class Diagram	79

List of Tables

2.1	Number of AngioTestGroup Genes in the Selected CGAP Libraries	18
3.1	Top Candidate Genes of the BASIC CDP	34
3.2	Expectation of AngioTestGroup Genes and Screen Hits	35
3.3	Number of Candidate Genes of the BASIC CDP	36
3.4	Top Candidate Genes of the GENETIC ALGORITHM BASED CDP	41
3.5	Number of Candidate Genes of the Genetic Algorithm Based CDP $$	42
3.6	Detailed Information for the Selected AngioProfiles	47
3.7	Top Candidate Genes of the Indicator Genes Based CDP	49
3.8	Number of Candidate Genes of the Indicator Genes Based CDP	50
3.9	Known Modulators of Angiogenesis for the Indicator Genes Based CDP	53
4.1	Comparison of the COMMON DENOMINATOR PROCEDURES	59
A.1	CGAP Libraries Selected as Data Source	76
A.2	Tissue Distribution of the Selected CGAP Libraries	77
A.3	Protocol Distribution of the Selected CGAP Libraries	77
A.4	Histology Distribution of the Selected CGAP Libraries	77

Abbreviations

NIH

NHGRI

PDGF

вCDP BASIC COMMON DENOMINATOR PROCEDURE cDNAComplementary DNA CDP COMMON DENOMINATOR PROCEDURE **CGAP** NCI's Cancer Genome Anatomy Project CPU Central Processing Unit DDIT4 HIF-1 Responsive RTP801 DMEM Dulbecco's Modified Eagle Medium DNA Deoxyribonucleic Acid **ECBM** Endothelial Cell Basal Medium, Promocell® **ECGF** Endothelial Cell Growth Factor 1 **ECGM** Endothelial Cell Growth Medium, Promocell® Endothelial PAS Domain Protein 1 EPAS1 ERD Entity Relationship Diagram EST Expressed Sequence Tag FDA U.S. Food and Drug Administration FCS Foetal Calf Serum, Invitrogen® GA Genetic Algorithm GB Gigabyte GHz **Gigahertz** GENETIC ALGORITHM BASED COMMON DENOMINATOR PROCEDURE GACDP GO Gene Ontology **GRIF** Gene References Into Function **HEK293** Human Embryonal Kidney Cells Hypoxia-inducible Factor 1, Alpha Subunit HIF1A Human Umbilical Cord Vein Endothelial Cells HUVEC **IGCDP** INDICATOR GENES BASED COMMON DENOMINATOR PROCEDURE IGFR1 Insulin-like Growth Factor 1 Receptor **JGAP** Java Genetics Algorithms Package MB Megabyte mRNA Messenger RNA **NCBI** U.S. National Center for Biotechnology Information NCI U.S. National Cancer Institute

U.S. National Human Genome Research Institute

U.S. National Health Institute

Platelet-derived Growth Factor

RAM Random Access Memory

RNA Ribonucleic Acid

SAGE Serial Analysis of Gene Expression VEGF Vascular Endothelial Growth Factor

UniProt Universal Protein Resource

RefSeq Protein Sequence Databases (Reference Sequence)

GenBank Nucleotide Sequence Database

EMBL European Molecular Biology Laboratory

UML Unified Modeling Language