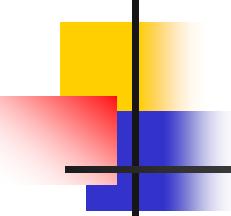




The urinary protein biomarker database

中国医学科学院基础医学研究所

邵晨

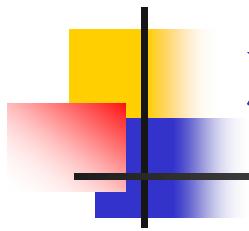


尿蛋白作为疾病标志物来源

- 可无创、大量地获得
- 可直接反映肾脏、膀胱等泌尿系统的变化
- 复杂度相对较低，更容易观察其中的低丰度蛋白的变化
- 能够在一定程度上反映血液的变化，因此也可以用来研究全身系统性的疾病

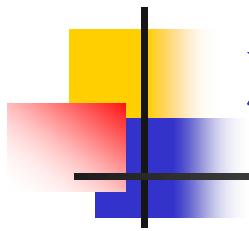
尿液的产生





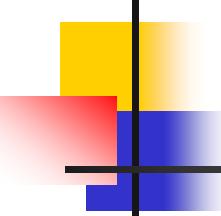
标志物的疾病特异性问题

- 仅比较疾病和正常样品，不能说明找到的标志物是否是这个疾病特有的。
- 没有实验室为了找到特异标志物可以全面地把所有相关的疾病都包含在研究中。



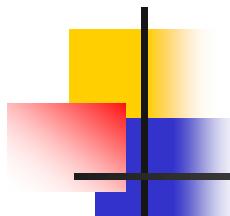
标志物的可信度问题

- 尿蛋白质组较大的动态变化范围和个体差异的存在、以及当前仪器水平的限制，对同一疾病，不同的实验室的得到的标志物差异很大



我们的工作

- 建立一个数据库，收录了目前文献报道的所有尿液中疾病标志物的研究成果（不限于蛋白质组研究）
- 内容包括：尿液中鉴定到的所有疾病的候选标志物（人和动物模型）；不包括：CE-MS, SELDI-MS等未鉴定蛋白序列的研究
- 通过数据分析，回答一些生物学问题



文献检索和数据收集

- 2005年以后综述引用的文献
- 直接Pubmed检索文献
- 采用人工阅读文献的方法收集biomarker的信息，以确保其准确性

根据疾病分类显示

Home Protein Browse Biomarker Search

Show: 10 entries Search:

HID	Disease	Protein Name	Protein ID	detection methods	Pubmed ID
h117	bladder cancer	gamma-synuclein (SNCG)	O76070	western blotting	15596044
h118	bladder cancer	catechol-o-methyltransferase (COMT)	P21964	western blotting	15596044
h119	bladder carcinoma	UBC (urinary cytokeratin 8 and 18 fragments)	no match	UBC Rapid and UBC ELISA	15596183
h131	bladder cancer	matrix metalloproteinase-2 (MMP-2)	P08253	gelatin-beads, 2D PAGE and MALDI-TOF MS	15964125
h132	bladder cancer	fibronectin	P02751	gelatin-beads, 2D PAGE and MALDI-TOF MS	15964125
h142	bladder cancer	zinc-alpha-glycoprotein	P25311	2DE,MALDI-TOF-MS(Axima CFR MALDI-TOF spectrometer)	16196100
h143	bladder cancer	BLCA-4	no match	sandwich immunoassay	16360453
h15	bladder cancer	Keratin, type I cytoskeletal 19	P08727	electrochemiluminescent immunoassay	10569545
h16	bladder cancer	urinary bladder cancer antigen	no match	ELISA	10569545
h17	bladder cancer	tissue polypeptide antigen	no match	immunoradiometric assay	10569545

Showing 1 to 10 of 57 entries

A set of small navigation icons typically found in web applications, including arrows for page navigation and other symbols.

标志物的具体信息

Home Protein Browse Biomarker Search

[return](#)

DATABASE ID: H117

DISEASE INFORMATION

Disease	bladder cancer
Sample details	Voided urine samples were obtained from 112 patients with bladder cancer and 230 control patients, including benign or malignant conditions (124 with benign prostatic hyperplasia, 7 with urinary tract infections (UTI), 6 with urinary stones, 6 with microscopic hematuria without known pathology, 58 with prostate cancer, 3 with renal cell carcinoma, 10 with breast cancer, and 16 with no definitive disorders).
Tissue	urine
Pubmed ID	15596044
Year	2004

BIOMARKER INFORMATION

Protein name	gamma-synuclein (SNCG)
Uniprot ID	O76070
IPI ID	IPI00297714
Fragment or variants	
Abundance change	upregulation
Molecular weight(experimental)	15kDa
pI(experimental)	4.8
PTM	
Detection methods and instruments	western blotting
Validation on distinct	

检索功能

Home Protein Browse Biomarker Search

IPI Search

Experiment
All

IPI

submit

Peptide Sequence Search

Sequence

submit

biomarker Search

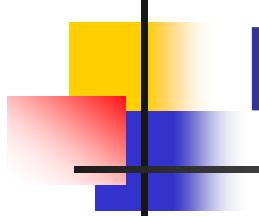
Uniport/IPI
IPI

human/animal
human

ID

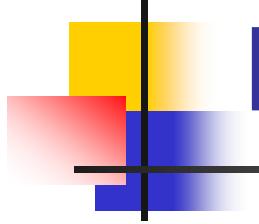
submit

[中文版|ENGLISH](#)



Data statistics-human

- 131 papers (40 proteomics studies)
- 273 proteins
- 40 diseases
- 443 records (including 5 negative results)
- 387 biomarkers



Data statistics-animal model

- 21 papers (14 on rat, 7 on mouse)
 - 169 proteins
 - 19 diseases
 - 230 records
-
- 约1/3的动物蛋白具有人的直系同源蛋白



network analysis of human data

Human disease-protein network

40 disease nodes

272 protein nodes

387 edges

Ave.edges per disease node

9.7

Ave edges per biomarker
node

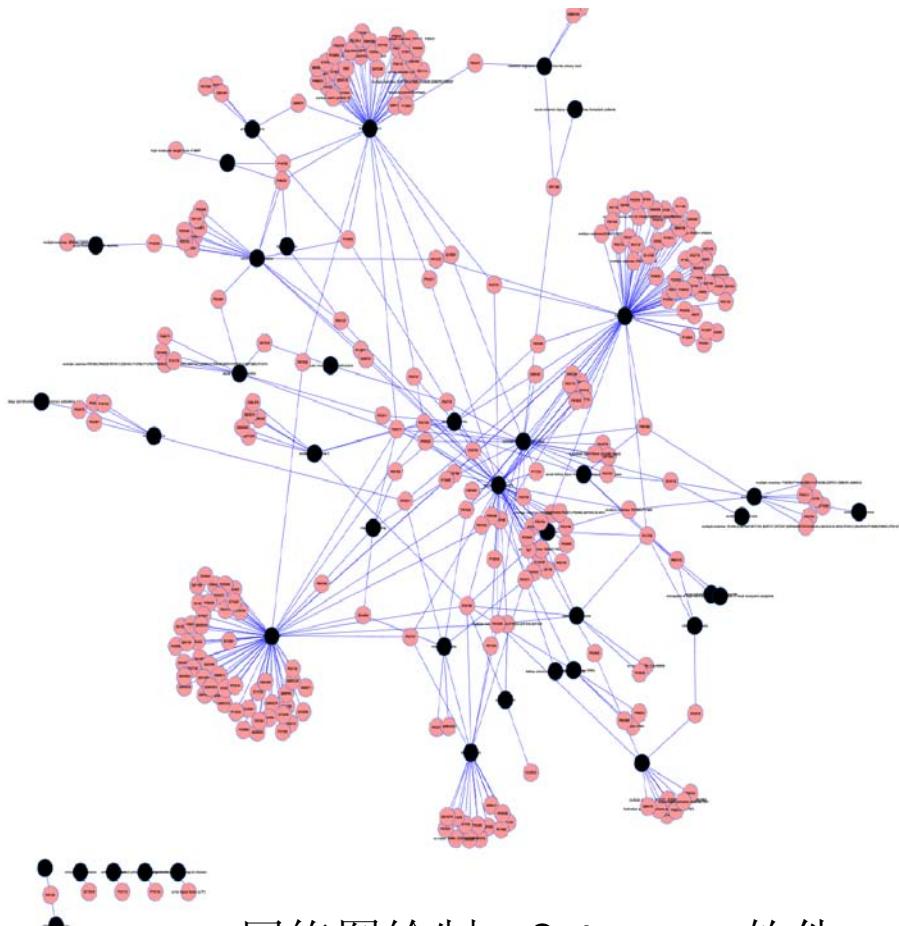
1.4

Cluster coefficient

0.025

Number of compartments

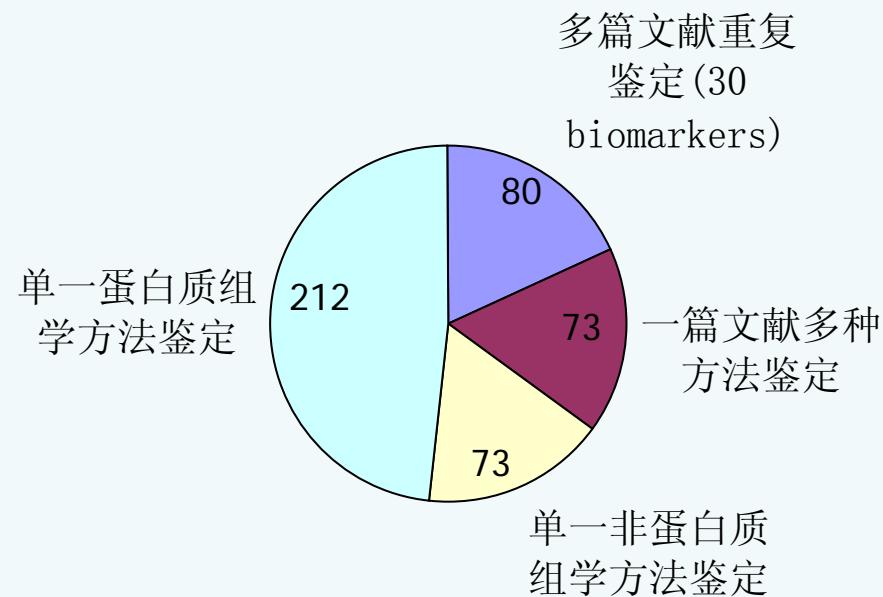
6



网络图绘制: Cytoscape软件

Data confidence-human

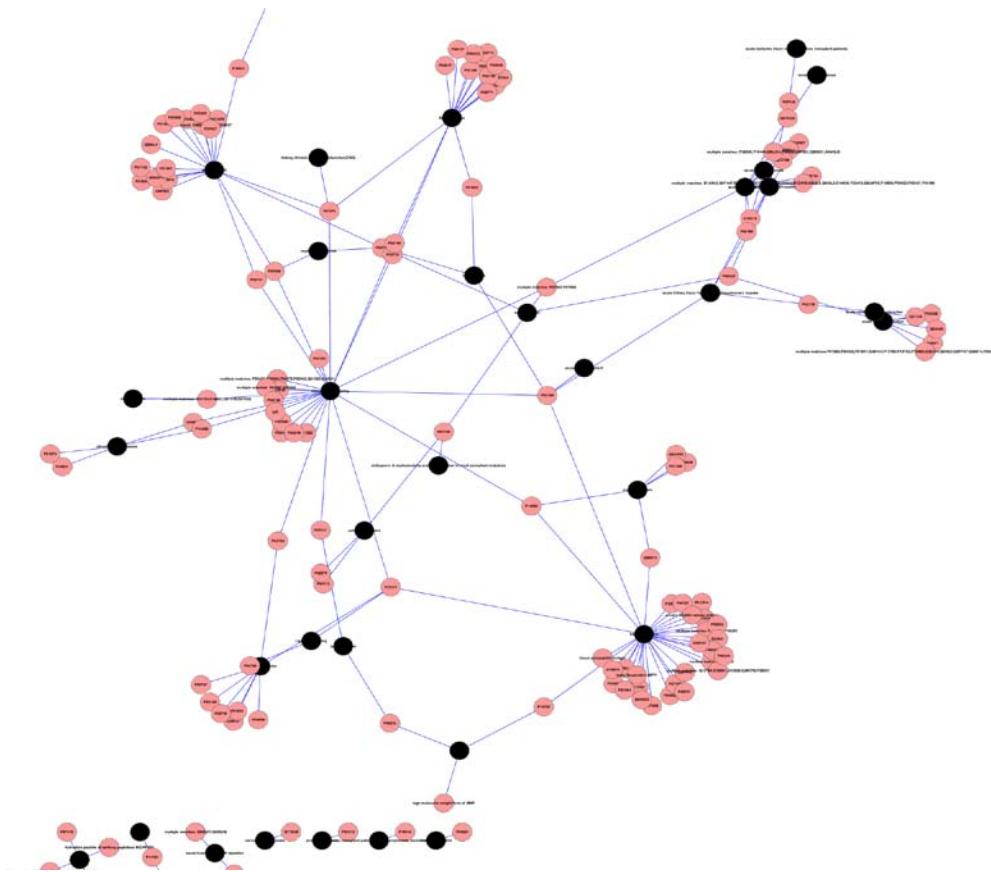
438 human records



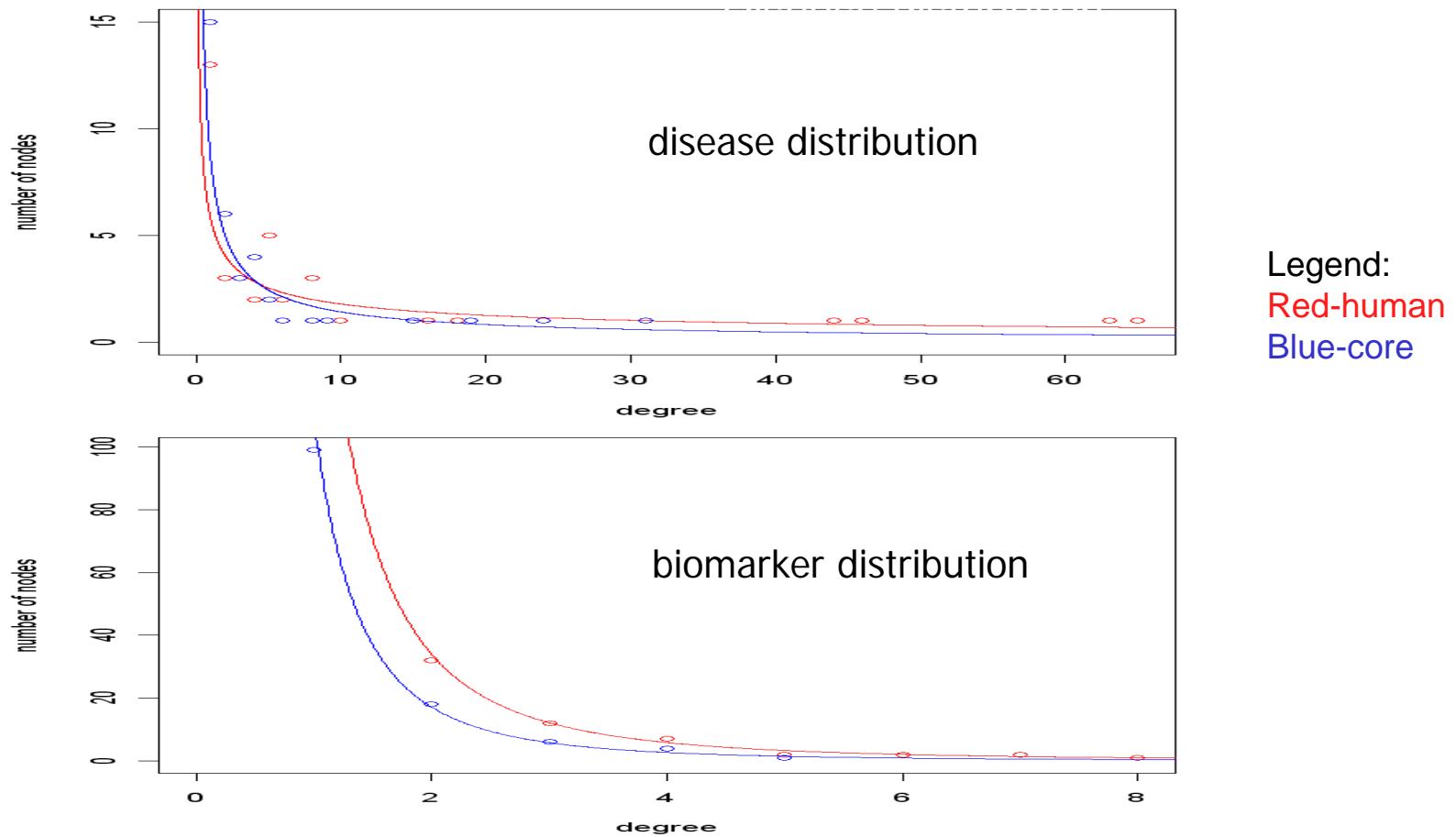
Human_core dataset

37 disease nodes
128 protein nodes
174 edges

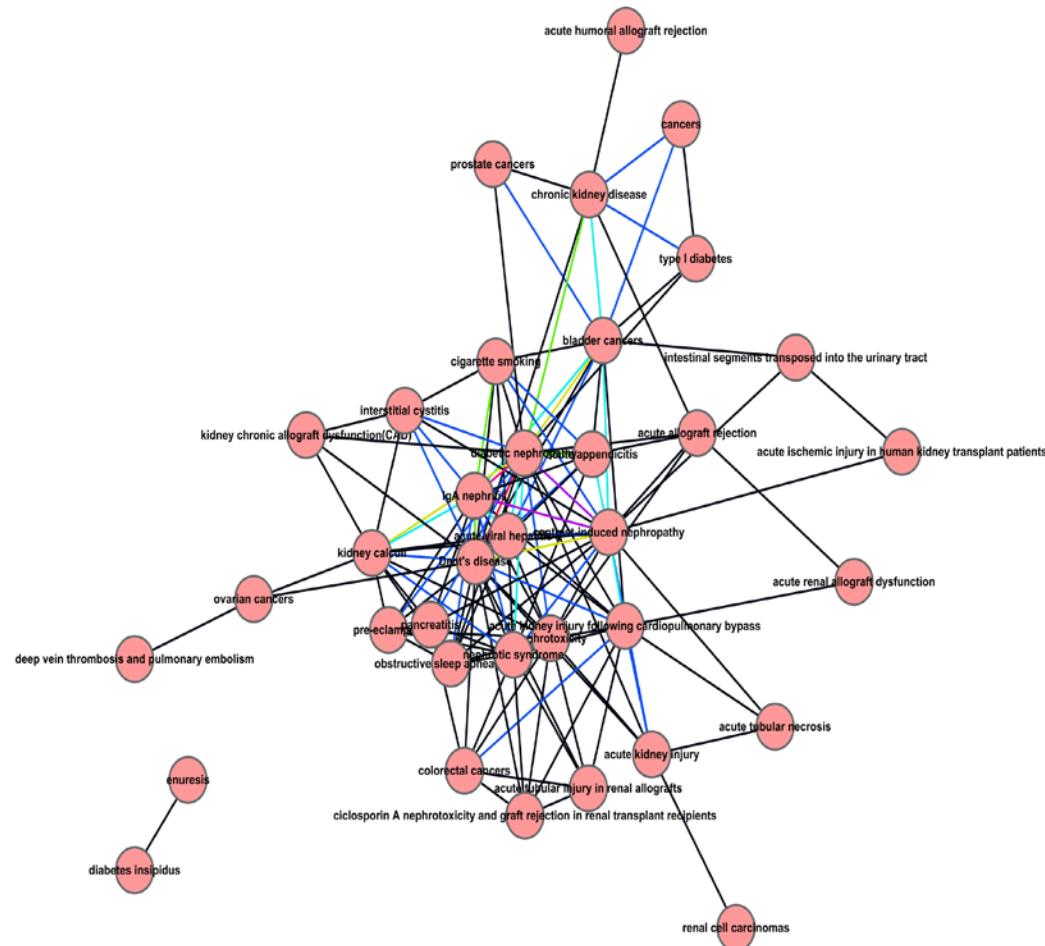
Ave.edges per disease node
4.7
Ave edges per biomarker
node
1.4
Cluster coefficient
0.027
Number of compartments
10



Node distribution

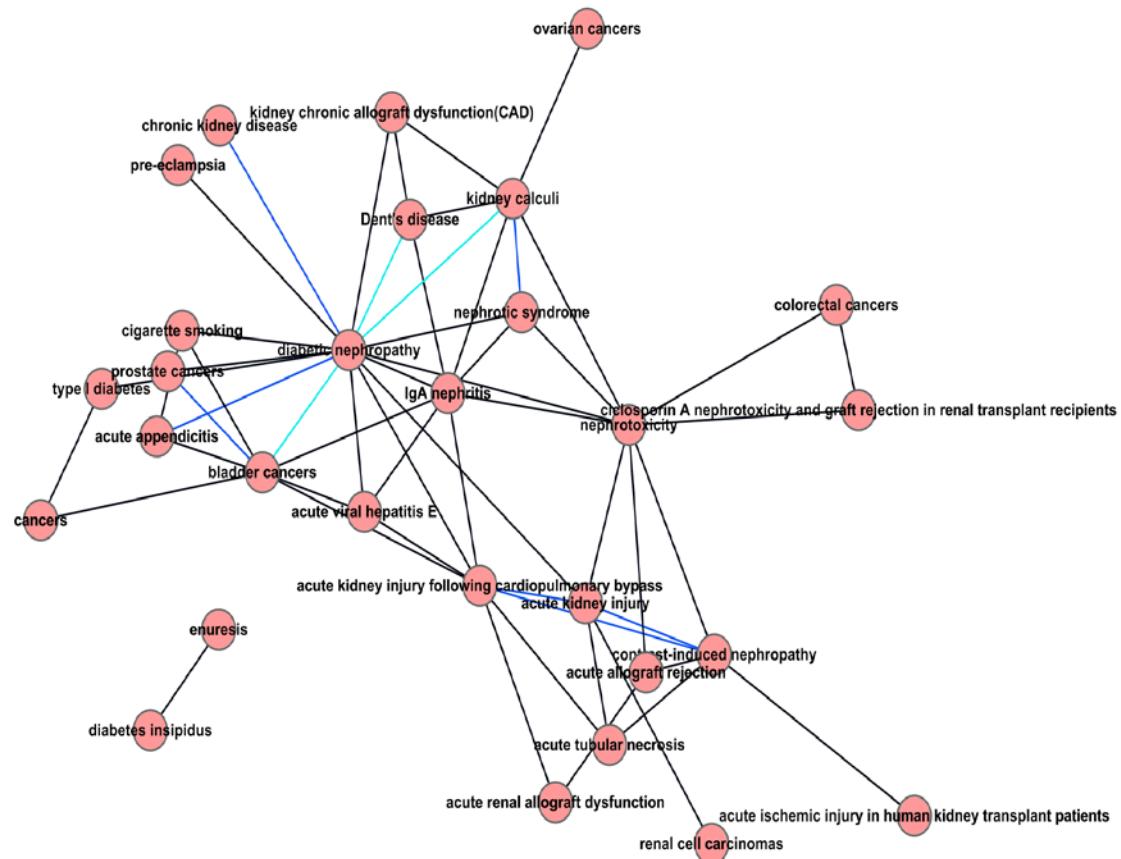


Human disease-disease network



36 nodes
137 edges
Clustering coefficient
0.59
Ave. degree
7.6
Mean shortest path
2.02

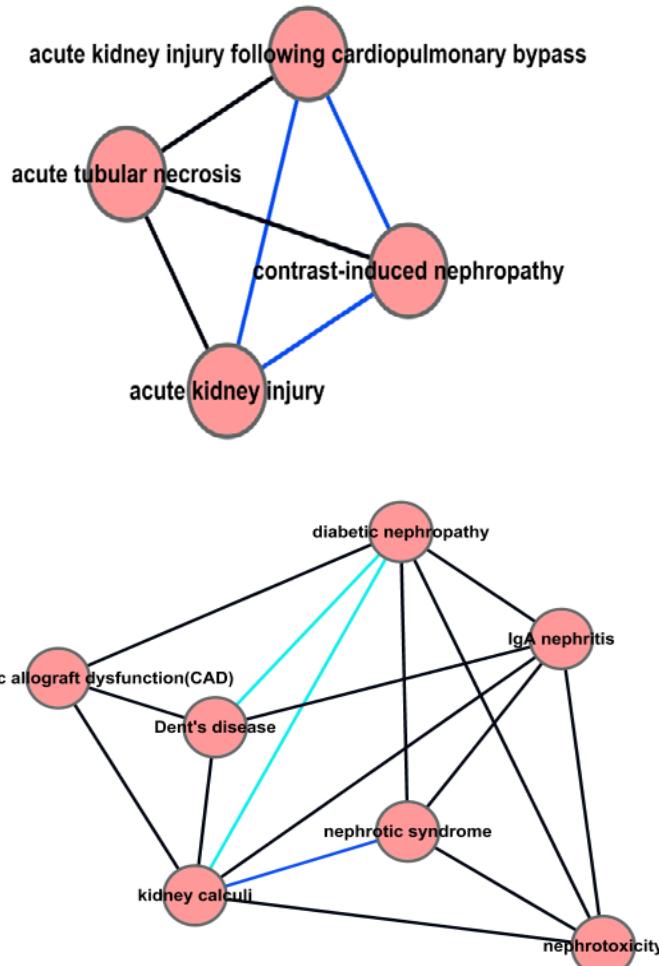
Human_core dataset



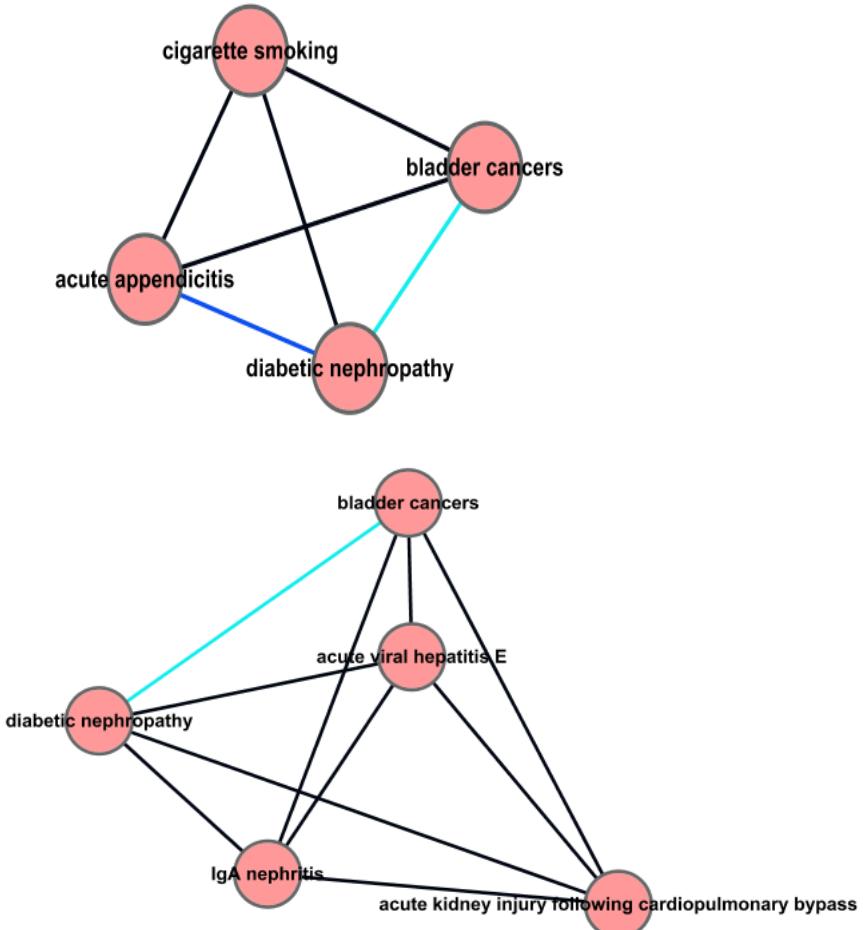
29 nodes
57 edges
Clustering coefficient
0.23
Ave. degree
3.9
Mean shortest path
1.64

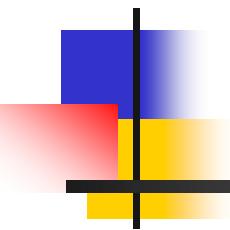
Densely connected communities in the human_core network (4-clique clustering by CFinder)

左：相似的疾病聚类在一起

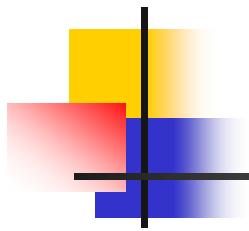


右：不同的疾病聚类在一起





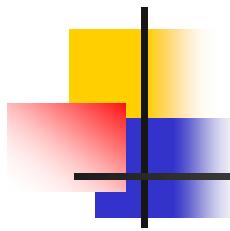
通过建立数据库，回答疾病标志物研究中的一些问题：



问题一：蛋白质组学研究的重复性如何？

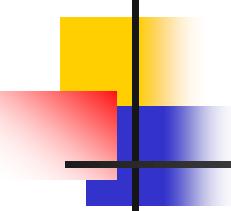
	疾病	文献	文献两两组合	共同鉴定的标志物	
human	8	26	64	6对文献， 10个标志物	平均两次实验共鉴定到41个候选标志物，才有1个共同鉴定的
animal	2	4	2	1对文献， 10个标志物	两疾病的标志物数分别为 (11, 24) 和 (16, 2)

不同样品处理和蛋白鉴定方法对病人样品的研究的重合率极低



问题二：动物模型 vs 病人样本

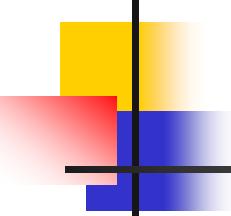
- 实验动物间的个体差异较小，动物模型可以方便的监测病程变化，进行各种干预，具有不可替代的优点。
- 从进化角度讲，uniprot数据库中，仅有1/3左右的大鼠蛋白具有人的直系同源蛋白。
- 从蛋白序列相似性来看，也仅有1/3左右的大鼠蛋白与人类蛋白的相似性>90%。



问题二：动物模型 vs 病人样本

	human	animal	Co-identified biomarker
Interstitial cystitis	5	11	1
Diabetic nephrology	41	2	1
Acute kidney injury	12	13	0

考虑到同是人类样品，两次蛋白质组实验的重合率都极低，
没有证据说明动物模型和病人样品之间的差距很大



问题三：标志物的疾病特异性

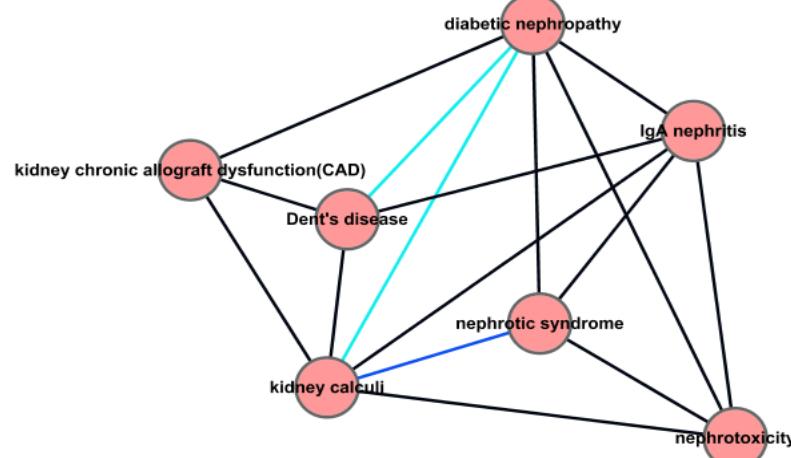
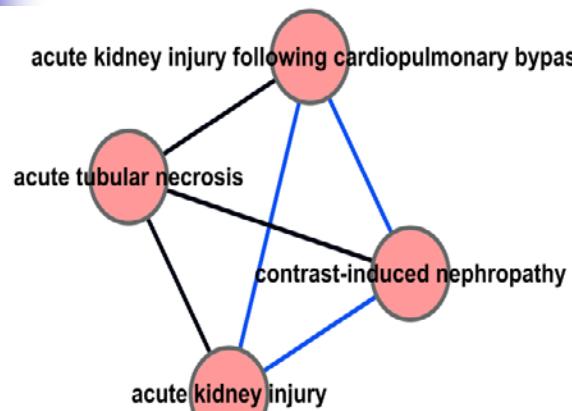
- 272个人类蛋白中57个蛋白至少与两个以上疾病相关，其中34(45)个是血浆蛋白

不具备疾病特异性的标志物（前三位）

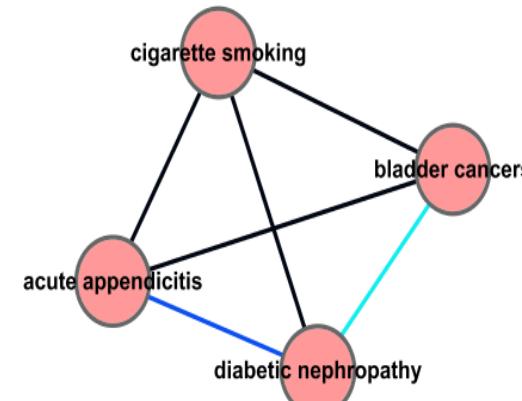
protein	Plasma	Related diseases
albumin	yes	acute viral hepatitis E,obstructive sleep apnea (OSA),pre-eclampsia,diabetic nephropathy,IgA nephritis,kidney stones,nephrotic syndrome,nephrotoxicity
Zinc-alpha-2-glycoprotein	yes	acute appendicitis,acute viral hepatitis E,bladder cancers,cigarette smoking, contrast-induced nephropathy,diabetic nephropathy,IgA nephritis
Alpha-1-microglobulin	yes	acute viral hepatitis E,bladder cancers, contrast-induced nephropathy,diabetic nephropathy,IgA nephritis, acute kidney injury following cardiopulmonary bypass

Densely connected communities in the human_core network (4-clique clustering by CFinder)

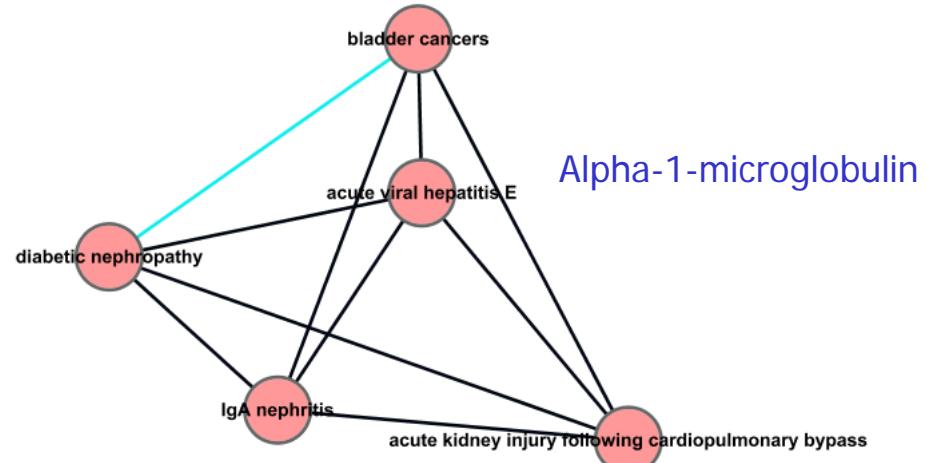
左：相似的疾病聚类在一起

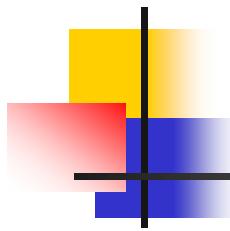


右：不同的疾病聚类在一起



Zinc-alpha-2-glycoprotein

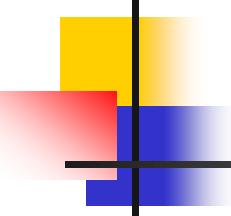




问题三：标志物的疾病特异性

未鉴定到特异性标志物的疾病

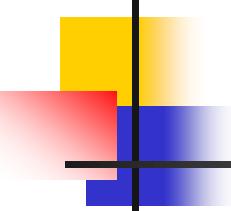
disease	papers	biomarkers
ciclosporin A nephrotoxicity and graft rejection in renal transplant recipients	1	1
kidney chronic allograft dysfunction(CAD)	1	1
nephrotoxicity	2	4
deep vein thrombosis and pulmonary embolism	1	1
diabetes insipidus	1	1
type I diabetes	2	2
cigarette smoking	1	5
renal cell carcinomas	1	1
colorectal cancers	1	3
enuresis	1	1



问题三：标志物的疾病特异性

多篇文献重复鉴定的疾病特异性标志物

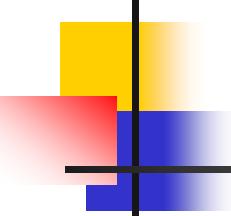
protein name	plasma	papers	disease
prostate-specific antigen (PSA)		4	prostate cancers
trypsinogen activation peptide(TAP)		6	pancreatitis
Trypsinogen-2		5	pancreatitis
survivin		2	bladder cancers
nuclear matrix protein 22		6	bladder cancers
UBC		2	bladder cancers
Keratin, type I cytoskeletal 19		5	bladder cancers
BLCA-4		3	bladder cancers
Haptoglobin precursor		2	diabetic nephropathy
CTGF		2	diabetic nephropathy
Ceruloplasmin	yes	2	diabetic nephropathy



问题四：发现疾病/标志物参与的生命过程

- 通过比较标志物关联的多种疾病，发现疾病/标志物参与的共同的生命过程
- 下表中的4个蛋白，相关的疾病都是慢性肾脏病和癌症，可推测它们涉及的是衰老的过程

protein	disease
vascular endothelial growth factor (VEGF)	bladder cancers, chronic kidney disease, diabetic nephropathy, prostate cancers
transforming growth factor beta1	chronic kidney disease, diabetic nephropathy, type I diabetes
matrix metalloproteinase-2 (MMP-2)	bladder cancers, cancers, chronic kidney disease, type I diabetes
matrix metalloproteinase-9 (MMP-9)	bladder cancers, cancers, chronic kidney disease



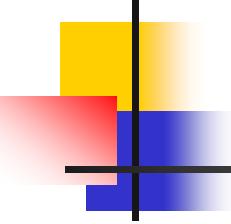
问题五：肾脏病的鉴别诊断

数据库中只在肾小管疾病中有变化的蛋白

Hemopexin	Apolipoprotein A1
N-acetyl-beta-(D)-glucosaminidase	Plasma retinol-binding protein precursor
Polymeric-immunoglobulin receptor	Apolipoprotein A-IV
TNF	Complement factor B
Vitamin D binding protein (VDBP)	Polymeric-immunoglobulin receptor

另两个普遍承认的肾小管损伤标志物还和其它的疾病相关

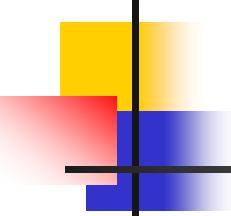
beta2-microglobulin	colorectal cancer
uromodulin	interstitial cystitis



问题五：肾脏病的鉴别诊断

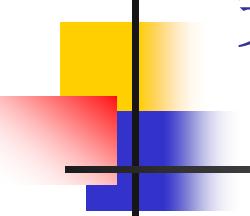
多种肾小球疾病的鉴别诊断 (animal model)

	total biomarkers	specific biomarkers
focal segmental glomerulosclerosis	58	46
membranoproliferative glomerulonephritis	4	4
mesangiocapillary glomerulonephritis	34	24
nephrotoxic serum nephritis	2	1
membranous nephritis	46	33



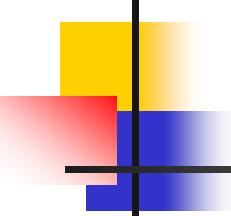
总结——尿蛋白标志物研究现状

- 蛋白质组实验的重复性很低
- 已经发现了一些特异的标志物，正在向临床应用转化
- 绝大部分标志物都只被鉴定一次，可信度不高
- 很多高丰度的血浆蛋白都不是特异性的标志物
- 一些疾病研究较少，肾小球疾病缺乏病人样本



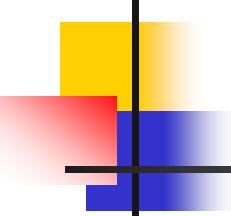
数据库的生命力

- 以上的一切分析都是建立在现有数据的结果上的
- 随着质谱技术和蛋白质组学方法的发展，数据会被逐渐更新，分析的结果也会随之产生变化
- 这种利用数据库研究生物标志物特异性的方法，利用数据库研究疾病关联的生物过程的方法将保持着生命力。



对未来研究的展望

- 建立统一的样品处理、鉴定、定量平台，使不同实验室间的数据具有可比性
- 找到更多的高可信度的疾病特异标志物
- 在大样本集上验证候选标志物的特异性和灵敏度，计算表达量随病程变化的曲线，制定诊断的标准



谢谢

