Multi-source Survival analysis

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Motivation

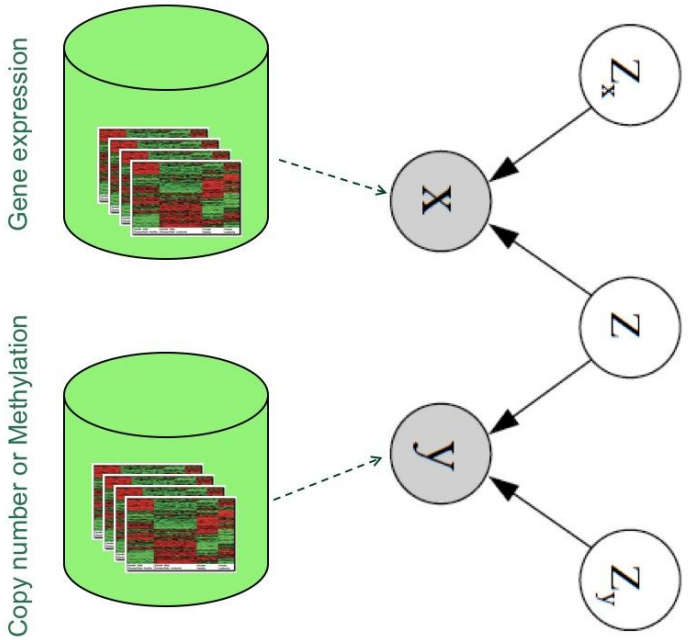
- How can we increase the reliability of putative driver genes involved in tumor progression and drug resistance?
- Combination of many different molecular mechanisms disrupt cellular pathways and characterize a cancer
- Modeling these requires genome scale multi-source approaches (which is one of the main contributions of this work)
- Specifically our aim is to identify potential regions (or biomarkers) that effectively stratify patients in low and high survival groups.

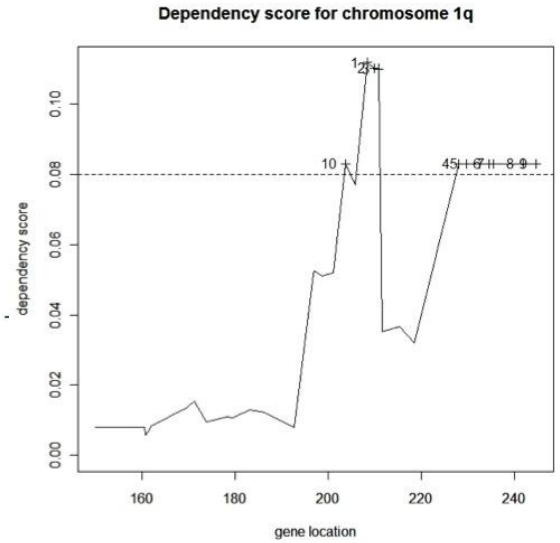
Multi-source survival analysis

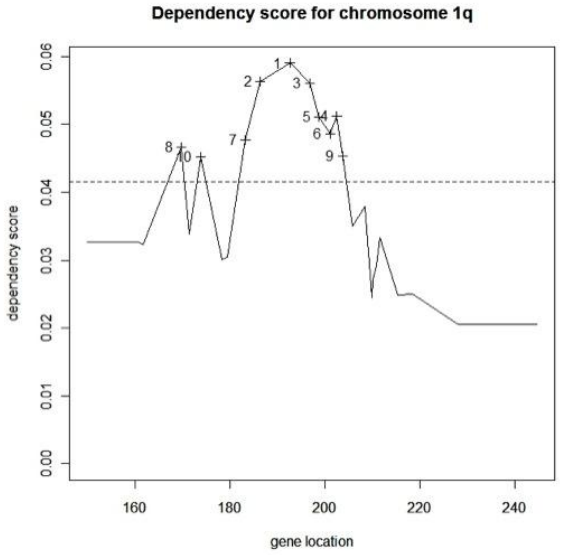
Identify chromosomal regions that have high dependencies among gene-expression, methylation and copy number changes,

Then form patients groups from the regions

Finally check weather the identified genomic aberrations have survival association.







$$\mathbf{x} \sim \mathbf{W}_x\mathbf{z} + \boldsymbol{\varepsilon}_x$$
$$\mathbf{y} \sim \mathbf{W}_y\mathbf{z} + \boldsymbol{\varepsilon}_y$$
$$\mathbf{W}_y = \mathbf{T}\mathbf{W}_x$$

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Results: Survival Associated Regions (qvals < 0.05)

	Dataset used		Biomarker	Genes in the region										Enrichment Test (qvals) Clinical factors			
														White	Female	Male	Age > 60
KM	cgh - exp		10p13	MCM10	SEC61A2	OPTN	CDC123	OLAH	RPP38	PRPF18	PTER	CAMK1D	HSPA14	1	0.18644	1	1
			10q22.1	UNC5B	CHST3	SUPV3L1	HKDC1	HK1	DDX21	SGPL1	COL13A1	SLC29A3	KIAA1279	0.2544	0.37807	1	9E-05
			10q22.1	HNRNPH3	UNC5B	SUPV3L1	HKDC1	HK1	DDX21	SGPL1	COL13A1	SLC29A3	KIAA1279	1	1	1	1
			10q26.13	SEC23IP	PLEKHA1	BCCIP	WDR11	PTPRE	TACC2	BUB3	FAM175B	ACADSB	INPP5F	1	1	1	0.8119
	mehty-exp		21q22.2	DOPEY2	ETS2	CBR1	MORC3	SLC37A1	PKNOX1	CRYAA	TTC3	MX2	SH3BGR	1	1	1	1
Cox	cgh-methy	& exp	9p24.3	SMARCA2	DNAJA1	TYRP1	SH3GL2	TEK	IFNA8	SNAPC3	NUDT2	KCNV2	PDCD1LG2	1	1	0.37807	1

Code available at: http://research.ics.tkk.fi/mi/software/daSAr/

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