

Contents

Glossary	xii
Acronyms	xiii
1 Introduction	1
1.1 Cancer Research in the Post-Genomic Era	1
1.1.1 Cancer as a Global Health Concern	2
1.1.1.1 The Genetics and Molecular Biology of Cancers	3
1.1.2 The Human Genome Revolution	6
1.1.2.1 The First Human Genome Sequence	6
1.1.2.2 Impact of Genomics	7
1.1.3 Technologies to Enable Genetics Research	7
1.1.3.1 DNA Sequencing and Genotyping Technologies	7
1.1.3.2 Microarrays and Quantitative Technologies	8
1.1.3.3 Massively Parallel “Next Generation” Sequencing . . .	9
1.1.3.3.1 Molecular Profiling with Genomics Technology .	11
1.1.3.3.2 Sequencing Technologies	11
1.1.3.4 Bioinformatics as Interdisciplinary Genomic Analysis .	12
1.1.4 Follow-up Large-Scale Genomics Projects	13
1.1.5 Cancer Genomes	14
1.1.5.1 The Cancer Genome Atlas Project	15
1.1.5.1.1 Findings from Cancer Genomes	15
1.1.5.1.2 Genomic Comparisons Across Cancer Tissues .	17
1.1.5.1.3 Cancer Genomic Data Resources	18
1.1.6 Genomic Cancer Medicine	18
1.1.6.1 Cancer Genes and Driver Mutations	18
1.1.6.2 Personalised or Precision Cancer Medicine	19
1.1.6.2.1 Molecular Diagnostics and Pan-Cancer Medicine	20
1.1.6.3 Targeted Therapeutics and Pharmacogenomics	21
1.1.6.3.1 Targeting Oncogenic Driver Mutations	21
1.1.6.4 Systems and Network Biology	22
1.1.6.4.1 Network Medicine, and Polypharmacology . . .	24
1.2 A Synthetic Lethal Approach to Cancer Medicine	25
1.2.1 Synthetic Lethal Genetic Interactions	26
1.2.2 Synthetic Lethal Concepts in Genetics	26
1.2.3 Studies of Synthetic Lethality	27

1.2.3.1	Synthetic Lethal Pathways and Networks	28
1.2.3.1.1	Evolution of Synthetic Lethality	29
1.2.4	Synthetic Lethal Concepts in Cancer	29
1.2.5	Clinical Impact of Synthetic Lethality in Cancer	31
1.2.6	High-throughput Screening for Synthetic Lethality	33
1.2.6.1	Synthetic Lethal Screens	34
1.2.7	Computational Prediction of Synthetic Lethality	37
1.2.7.1	Bioinformatics Approaches to Genetic Interactions . .	37
1.2.7.2	Comparative Genomics	38
1.2.7.3	Analysis and Modelling of Protein Data	41
1.2.7.4	Differential Gene Expression	43
1.2.7.5	Data Mining and Machine Learning	44
1.2.7.6	Bimodality	47
1.2.7.7	Rationale for Further Development	48
1.3	E-cadherin as a Synthetic Lethal Target	48
1.3.1	The <i>CDH1</i> gene and it's Biological Functions	48
1.3.1.1	Cytoskeleton	49
1.3.1.2	Extracellular and Tumour Micro-Environment	49
1.3.1.3	Cell-Cell Adhesion and Signalling	49
1.3.2	<i>CDH1</i> as a Tumour (and Invasion) Suppressor	50
1.3.2.1	Breast Cancers and Invasion	50
1.3.3	Hereditary Diffuse Gastric Cancer and Lobular Breast Cancer .	50
1.3.4	Somatic Mutations	52
1.3.4.1	Mutation Rate	52
1.3.4.2	Co-occurring Mutations	52
1.3.5	Models of <i>CDH1</i> loss in cell lines	53
1.4	Summary and Research Direction of Thesis	54
2	Methods and Resources	58
2.1	Bioinformatics Resources for Genomics Research	58
2.1.1	Public Data and Software Packages	58
2.1.1.1	Cancer Genome Atlas Data	59
2.1.1.2	Reactome and Annotation Data	60
2.2	Data Handling	60
2.2.1	Normalisation	60
2.2.2	Sample Triage	61
2.2.3	Metagenes and the Singular Value Decomposition	63
2.2.3.1	Candidate Triage and Integration with Screen Data . .	63
2.3	Techniques	64
2.3.1	Statistical Procedures and Tests	64
2.3.2	Gene Set Over-representation Analysis	65
2.3.3	Clustering	65
2.3.4	Heatmap	66
2.3.5	Modeling and Simulations	66
2.3.5.1	Receiver Operating Characteristic (Performance) . . .	67
2.3.6	Resampling Analysis	67

2.4	Pathway Structure Methods	68
2.4.1	Network and Graph Analysis	68
2.4.2	Sourcing Graph Structure Data	69
2.4.3	Constructing Pathway Subgraphs	70
2.4.4	Network Analysis Metrics	70
2.5	Implementation	71
2.5.1	Computational Resources and Linux Utilities	71
2.5.2	R Language and Packages	72
2.5.3	High Performance and Parallel Computing	75
3	Methods Developed During Thesis	77
3.1	A Synthetic Lethal Detection Methodology	77
3.2	Synthetic Lethal Simulation and Modelling	80
3.2.1	A Model of Synthetic Lethality in Expression Data	80
3.2.2	Simulation Procedure	84
3.3	Detecting Simulated Synthetic Lethal Partners	87
3.3.1	Binomial Simulation of Synthetic lethality	87
3.3.2	Multivariate Normal Simulation of Synthetic lethality	89
3.3.2.1	Multivariate Normal Simulation with Correlated Genes	92
3.3.2.2	Specificity with Query-Correlated Pathways	99
3.3.2.3	Importance of Directional Testing	99
3.4	Graph Structure Methods	101
3.4.1	Upstream and Downstream Gene Detection	101
3.4.1.1	Permutation Analysis for Statistical Significance	102
3.4.1.2	Hierarchy Based on Biological Context	103
3.4.2	Simulating Gene Expression from Graph Structures	104
3.5	Customised Functions and Packages Developed	108
3.5.1	Synthetic Lethal Interaction Prediction Tool	108
3.5.2	Data Visualisation	109
3.5.3	Extensions to the iGraph Package	112
3.5.3.1	Sampling Simulated Data from Graph Structures	112
3.5.3.2	Plotting Directed Graph Structures	112
3.5.3.3	Computing Information Centrality	113
3.5.3.4	Testing Pathway Structure with Permutation Testing	113
3.5.3.5	Metapackage to Install iGraph Functions	114
4	Synthetic Lethal Analysis of Gene Expression Data	115
4.1	Synthetic Lethal Genes in Breast Cancer	116
4.1.1	Synthetic Lethal Pathways in Breast Cancer	118
4.1.2	Expression Profiles of Synthetic Lethal Partners	119
4.1.2.1	Subgroup Pathway Analysis	122
4.2	Comparing Synthetic Lethal Gene Candidates	125
4.2.1	Primary siRNA Screen Candidates	125
4.2.2	Comparison with Correlation	126
4.2.3	Comparison with Primary Screen Viability	128
4.2.4	Comparison with Secondary siRNA Screen Validation	129

4.2.5	Comparison to Primary Screen at Pathway Level	131
4.2.5.1	Resampling Genes for Pathway Enrichment	133
4.2.6	Integrating Synthetic Lethal Pathways and Screens	136
4.3	Metagene Analysis	138
4.3.1	Pathway Expression	139
4.3.2	Somatic Mutation	141
4.3.3	Synthetic Lethal Pathway Metagenes	145
4.3.4	Synthetic Lethality in Breast Cancer	146
4.4	Replication in Stomach Cancer	147
4.5	Discussion	147
4.5.1	Strengths of the SLIPT Methodology	147
4.5.2	Synthetic Lethal Pathways for E-cadherin	148
4.5.3	Replication and Validation	150
4.5.3.1	Integration with siRNA Screening	150
4.5.3.2	Replication across Tissues and Cell lines	151
4.6	Summary	151
5	Synthetic Lethal Pathway Structure	155
5.1	Synthetic Lethal Genes in Reactome Pathways	156
5.1.1	The PI3K/AKT Pathway	156
5.1.2	The Extracellular Matrix	158
5.1.3	G Protein Coupled Receptors	161
5.1.4	Gene Regulation and Translation	162
5.2	Network Analysis of Synthetic Lethal Genes	163
5.2.1	Gene Connectivity and Vertex Degree	163
5.2.2	Gene Importance and Centrality	165
5.2.2.1	Information Centrality	165
5.2.2.2	PageRank Centrality	167
5.3	Relationships between Synthetic Lethal Genes	168
5.3.1	Hierarchical Pathway Structure	168
5.3.1.1	Contextual Hierarchy of PI3K	168
5.3.1.2	Testing Contextual Hierarchy of Synthetic Lethal Genes	169
5.3.2	Upstream or Downstream Synthetic Lethality	172
5.3.2.1	Measuring Structure of Candidates within PI3K	172
5.3.2.2	Resampling for Synthetic Lethal Pathway Structure . .	174
5.4	Discussion	176
5.5	Summary	178
6	Simulation and Modeling of Synthetic Lethal Pathways	181
6.1	Comparing methods	182
6.1.1	Performance of SLIPT and χ^2 across Quantiles	183
6.1.1.1	Correlated Query Genes affects Specificity	186
6.1.2	Alternative Synthetic Lethal Detection Strategies	188
6.1.2.1	Correlation for Synthetic Lethal Detection	188
6.1.2.2	Testing for Bimodality with BiSEp	190
6.2	Simulations with Graph Structures	192

6.2.1	Performance over a Graph Structure	193
6.2.1.1	Simple Graph Structures	193
6.2.1.2	Constructed Graph Structures	195
6.2.2	Performance with Inhibitions	199
6.2.3	Synthetic Lethality across Graph Structures	205
6.2.4	Performance within a Simulated Human Genome	209
6.3	Simulations over pathway-based graphs	215
6.3.1	Pathway Structures in a Simulated Human Genome	217
6.4	Discussion	220
6.4.1	Simulation Procedure	220
6.4.2	Design and Performance of SLIPT	221
6.4.3	Simulations from Graph Structures	223
6.5	Summary	224
7	Discussion	227
7.1	Synthetic Lethality and <i>CDH1</i> Biology	227
7.1.1	Established Functions of <i>CDH1</i>	228
7.1.2	The Molecular Role of <i>CDH1</i> in Cancer	228
7.2	Significance	229
7.2.1	Synthetic Lethality in the Genomic Era	229
7.2.2	Clinical Interventions based on Synthetic Lethality	231
7.3	Evaluating the Synthetic Lethality Prediction Tool	232
7.3.1	Strength of the Synthetic Lethality Prediction Tool	232
7.3.2	Limitations of the Synthetic Lethality Prediction Tool	232
7.3.3	Comparisons to Alternative Methods	232
7.3.3.1	Combined with Experimental Screening	232
7.3.3.2	Differences to Computational Methods	232
7.4	Future Directions	232
7.4.1	Refinements Synthetic Lethality Prediction Methods	234
7.4.1.1	Wider Use of Synthetic Lethality Prediction	234
7.4.2	Validation of Synthetic Lethal Genes and Pathways	234
7.4.2.1	Pre-clinical and Clinical Testing	234
7.4.3	Application to Further Genes and Pathways	234
8	Conclusion	235
	References	239
A	Sample Quality	265
A.1	Sample Correlation	265
A.2	Replicate Samples in TCGA Breast	268
B	Software Used for Thesis	272

C	Mutation Analysis in Breast Cancer	281
C.1	Synthetic Lethal Genes and Pathways	281
C.2	Synthetic Lethal Expression Profiles	284
C.3	Comparison to Primary Screen	287
C.3.1	Resampling Analysis	289
C.4	Compare SLIPT genes	291
C.5	Metagene Analysis	293
C.6	Expression of Somatic Mutations	294
C.7	Metagene Expression Profiles	297
D	Intrinsic Subtyping	300
E	Stomach Expression Analysis	302
E.1	Synthetic Lethal Genes and Pathways	302
E.2	Synthetic Lethal Expression Profiles	305
E.3	Comparison to Primary Screen	308
E.3.1	Resampling Analysis	310
E.4	Metagene Analysis	312
F	Synthetic Lethal Genes in Pathways	313
G	Pathway Connectivity for Mutation SLIPT	321
H	Information Centrality for Gene Essentiality	325
I	Pathway Structure for Mutation SLIPT	328

List of Figures

1.1	Synthetic genetic interactions	27
1.2	Synthetic lethality in cancer	30
2.1	Read count density	62
2.2	Read count sample mean	62
3.1	Framework for synthetic lethal prediction	78
3.2	Synthetic lethal prediction adapted for mutation	79
3.3	A model of synthetic lethal gene expression	81
3.4	Modeling synthetic lethal gene expression	82
3.5	Synthetic lethality with multiple genes	83
3.6	Simulating gene function	85
3.7	Simulating synthetic lethal gene function	85
3.8	Simulating synthetic lethal gene expression	86
3.9	Performance of binomial simulations	88
3.10	Comparison of statistical performance	88
3.11	Performance of multivariate normal simulations	90
3.12	Simulating expression with correlated gene blocks	93
3.13	Simulating expression with correlated gene blocks	94
3.14	Synthetic lethal prediction across simulations	95
3.15	Performance with correlations	96
3.16	Comparison of statistical performance with correlation structure	97
3.17	Performance with query correlations	98
3.18	Statistical evaluation of directional criteria	99
3.19	Performance of directional criteria	100
3.20	Simulated graph structures	104
3.21	Simulating expression from a graph structure	106
3.22	Simulating expression from graph structure with inhibitions	107
3.23	Demonstration of violin plots with custom features	110
3.24	Demonstration of annotated heatmap	110
3.25	Simulating graph structures	113
4.1	Synthetic lethal expression profiles of analysed samples	121
4.2	Comparison of SLIPT to siRNA	125
4.3	Compare SLIPT and siRNA genes with correlation	126
4.4	Compare SLIPT and siRNA genes with correlation	127
4.5	Compare SLIPT and siRNA genes with viability	128

4.6	Compare SLIPT genes with siRNA viability	129
4.7	Resampled intersection of SLIPT and siRNA candidates	133
4.8	Pathway metagene expression profiles	140
4.9	Expression profiles for constituent genes of PI3K	142
4.10	Expression profiles for estrogen receptor related genes	143
4.11	Somatic mutation against the PI3K metagene	144
5.1	Synthetic Lethality in the PI3K Cascade	157
5.2	Synthetic Lethality in the Elastic Fibre Formation Pathway	159
5.3	Synthetic Lethality in the Fibrin Clot Formation	161
5.4	Synthetic Lethality and Vertex Degree	164
5.5	Synthetic Lethality and Centrality	166
5.6	Synthetic Lethality and PageRank	168
5.7	Hierarchical Structure of PI3K	169
5.8	Hierarchy Score in PI3K against Synthetic Lethality in PI3K	170
5.9	Structure of Synthetic Lethality in PI3K	172
5.10	Structure of Synthetic Lethality Resampling in PI3K	173
6.1	Performance of χ^2 and SLIPT across quantiles	184
6.2	Performance of χ^2 and SLIPT across quantiles with more genes	185
6.3	Performance of χ^2 and SLIPT across quantiles with query correlation	186
6.4	Performance of χ^2 and SLIPT across quantiles with query correlation and more genes	187
6.5	Performance of negative correlation and SLIPT	189
6.6	Performance of simulations on a simple graph	194
6.7	Performance of simulations is similar in simple graphs	195
6.8	Performance of simulations on a constructed graph	196
6.9	Performance of simulations on a large graph	198
6.10	Performance of simulations on a simple graph with inhibition	200
6.11	Performance is higher on a simple inhibiting graph	201
6.12	Performance of simulations on a constructed graph with inhibition	203
6.13	Performance is affected by inhibition in graphs	204
6.14	Detection of Synthetic Lethality within a Graph Structure	206
6.15	Detection of Synthetic Lethality within a Graph Structure with Inhibitions	208
6.16	Performance of simulations including a simple graph	210
6.17	Performance on a simple graph improves with more genes	211
6.18	Performance on an inhibiting graph with more genes	212
6.19	Performance on an inhibiting graph improves with more genes	214
6.20	Performance of simulations on the PI3K cascade	216
6.21	Performance of simulations including the PI3K cascade	218
6.22	Performance on pathways improves with more genes	219
A.1	Correlation profiles of removed samples	266
A.2	Correlation analysis and sample removal	267
A.3	Replicate excluded samples	268
A.4	Replicate samples with all remaining	269

A.5	Replicate samples with some excluded	270
C.1	Synthetic lethal expression profiles of analysed samples	285
C.2	Comparison of mtSLIPT to siRNA	287
C.3	Compare mtSLIPT and siRNA genes with correlation	291
C.4	Compare mtSLIPT and siRNA genes with correlation	291
C.5	Compare mtSLIPT and siRNA genes with siRNA viability	292
C.6	Somatic mutation against PIK3CA metagene	294
C.7	Somatic mutation against PI3K protein	295
C.8	Somatic mutation against AKT protein	296
C.9	Pathway metagene expression profiles	297
C.10	Expression profiles for p53 related genes	298
C.11	Expression profiles for BRCA related genes	299
E.1	Synthetic lethal expression profiles of stomach samples	307
E.2	Comparison of SLIPT in stomach to siRNA	308
F.1	Synthetic Lethality in the PI3K/AKT Pathway	313
F.2	Synthetic Lethality in the PI3K/AKT Pathway in Cancer	314
F.3	Synthetic Lethality in the Extracellular Matrix	315
F.4	Synthetic Lethality in the GPCRs	316
F.5	Synthetic Lethality in the GPCR Downstream	317
F.6	Synthetic Lethality in the Translation Elongation	318
F.7	Synthetic Lethality in the Nonsense-mediated Decay	319
F.8	Synthetic Lethality in the 3' UTR	320
G.1	Synthetic Lethality and Vertex Degree	321
G.2	Synthetic Lethality and Centrality	322
G.3	Synthetic Lethality and PageRank	323
H.1	Information centrality distribution	327
I.1	Synthetic Lethality and Heirarchy Score in PI3K	328
I.2	Heirarchy Score in PI3K against Synthetic Lethality in PI3K	329
I.3	Structure of Synthetic Lethality in PI3K	329
I.4	Structure of Synthetic Lethality Resampling	330

List of Tables

1.1	Methods for Predicting Genetic Interactions	38
1.2	Methods for Predicting Synthetic Lethality in Cancer	39
1.3	Methods used by Wu <i>et al.</i> (2014)	40
2.1	Excluded Samples by Batch and Clinical Characteristics.	61
2.2	Computers used during Thesis	72
2.3	Linux Utilities and Applications used during Thesis	72
2.4	R Installations used during Thesis	73
2.5	R Packages used during Thesis	73
2.6	R Packages Developed during Thesis	75
4.1	Candidate synthetic lethal gene partners of <i>CDH1</i> from SLIPT	117
4.2	Pathways for <i>CDH1</i> partners from SLIPT	119
4.3	Pathway composition for clusters of <i>CDH1</i> partners from SLIPT	123
4.4	Analysis of variance (ANOVA) for Synthetic Lethality and Correlation with <i>CDH1</i>	127
4.5	Comparing SLIPT genes against secondary siRNA screen in breast cancer	130
4.6	Pathway composition for <i>CDH1</i> partners from SLIPT and siRNA screen- ing	132
4.7	Pathways for <i>CDH1</i> partners from SLIPT	135
4.8	Pathways for <i>CDH1</i> partners from SLIPT and siRNA primary screen .	137
4.9	Candidate synthetic lethal metagenes against <i>CDH1</i> from SLIPT	146
5.1	ANOVA for Synthetic Lethality and Vertex Degree	163
5.2	ANOVA for Synthetic Lethality and Information Centrality	167
5.3	ANOVA for Synthetic Lethality and PageRank Centrality	167
5.4	ANOVA for Synthetic Lethality and PI3K Hierarchy	171
5.5	Resampling for pathway structure of synthetic lethal detection methods	175
B.1	R Packages used during Thesis	272
C.1	Candidate synthetic lethal gene partners of <i>CDH1</i> from mtSLIPT	282
C.2	Pathways for <i>CDH1</i> partners from mtSLIPT	283
C.3	Pathway composition for clusters of <i>CDH1</i> partners from mtSLIPT . .	286
C.4	Pathway composition for <i>CDH1</i> partners from mtSLIPT and siRNA . .	288
C.5	Pathways for <i>CDH1</i> partners from mtSLIPT	289
C.6	Pathways for <i>CDH1</i> partners from mtSLIPT and siRNA primary screen	290
C.7	Candidate synthetic lethal metagenes against <i>CDH1</i> from mtSLIPT . .	293

D.1	Comparison of Intrinsic Subtypes	300
E.1	Synthetic lethal gene partners of <i>CDH1</i> from SLIPT in stomach cancer	303
E.2	Pathways for <i>CDH1</i> partners from SLIPT in stomach cancer	304
E.3	Pathway composition for clusters of <i>CDH1</i> partners in stomach SLIPT	306
E.4	Pathway composition for <i>CDH1</i> partners from SLIPT and siRNA screening	309
E.5	Pathways for <i>CDH1</i> partners from SLIPT in stomach cancer	310
E.6	Pathways for <i>CDH1</i> partners from SLIPT in stomach and siRNA screen	311
E.7	Candidate synthetic lethal metagenes against <i>CDH1</i> from SLIPT in stomach cancer	312
G.1	ANOVA for Synthetic Lethality and Vertex Degree	324
G.2	ANOVA for Synthetic Lethality and Information Centrality	324
G.3	ANOVA for Synthetic Lethality and PageRank Centrality	324
H.1	Information centrality for genes and molecules in the Reactome network	326
I.1	ANOVA for Synthetic Lethality and PI3K Hierarchy	328
I.2	Resampling for pathway structure of synthetic lethal detection methods	330

Glossary

synthetic lethal Genetic interactions where inactivation of multiple genes is inviable (or deleterious) when they are viable if inactivated separately.

Acronyms

AMP	Adenosine monophosphate.
AMPK	AMP-activated protein kinase.
ANOVA	Analysis of Variance.
BioPAX	Biological Pathway Exchange.
BMP	Bone morphogenic protein.
CXCR	Chemokine receptors.
EMT	Epithelial-mesenchymal transition.
GPCR	G protein coupled receptor.
JAK	Janus kinase.
NMD	Nonsense-mediated decay.
PDE	Phosphodiesterase.
PI3K	Phosphoinositide 3-kinase.
PIP ₂	Phosphatidylinositol (4,5)-bisphosphate.
PIP ₃	Phosphatidylinositol (3,4,5)-trisphosphate.
RGS	G-protein signalling.
RHO	Ras Homolog Family.
RNA	Ribonucleic acid.
siRNA	Short interfering ribonucleic acid.
SLIPT	Synthetic lethal interaction prediction tool.
TCGA	The Cancer Genome Atlas (genomics project).
TGF β	Transforming growth factor β .
UTR	Untranslated region (of mRNA).
WNT	Wingless-related integration site.

Chapter 5

Synthetic Lethal Pathway Structure

Having identified key pathways implicated in synthetic lethal genetic interactions with *CDH1* (in Chapter 4), these were investigated for the underlying synthetic lethal genes within them and their relationships to pathway structure in Reactome pathways. This chapter will focus on the pathway structure of biological pathways detected across analyses in Chapter 4.

The synthetic lethal genes identified were further examined within the context of biological pathways. Specifically, investigations were performed synthetic lethal candidates detected by each approach exhibited difference with respect to network metrics of pathway structure of connectivity and importance in the network (as described in Sections 2.4.4 and 3.5.3). The relationships between synthetic lethal candidates detected by either approach was also considered to detect whether genes detected by Synthetic Lethal Interaction Prediction Tool (SLIPT) were upstream or downstream of genes detected by short interfering ribonucleic acid (siRNA). These directional relationships were tested by resampling (as described in Sections 3.4.1 and 3.4.1.1) and comparisons to the pathway hierarchical score based on biological context (as derived in Section 3.4.1.2).

The pathway relationships between SLIPT and siRNA synthetic lethal gene candidate partners for *CDH1* were examined within the biological pathways identified previously (in Chapter 4). Together these investigations into structural relationships demonstrate how a combination of network biology and statistical techniques can be performed with genes identified by a Bioinformatics analysis.

5.1 Synthetic Lethal Genes in Reactome Pathways

The graph structure for Reactome pathways was obtained from Pathway Commons via Biological pathway exchange (BioPAX) (as described in Section 2.4.2). The pathways describe the (directional) relationships between biomolecules, including genes which encode proteins in biological pathways. These relationships include cell signalling (e.g., kinase phosphorylation cascades), gene regulation (e.g., transcription factors, chromatin modifiers, ribonucleic acid (RNA) binding proteins), and metabolism (e.g., the product of an enzyme being the substrate of another). Together these relationships describe the known functional pathways in a human cell with a reasonable resolution, from a curated database supported by publications documenting pathway relationships.

Pathway structures from the Reactome network (as described in Section 2.4.3) were used to derive the graph structure of each biological pathway. The synthetic lethal candidate genes for notable pathways discussed in Chapter 4, including candidate synthetic lethal pathways of *CDH1*, were examined to show the SLIPT and siRNA candidates within these pathways. The synthetic lethal genes considered here are those candidates detected by SLIPT (as described in Section 3.1) in The Cancer Genome Atlas (TCGA) breast cancer expression and mutation data (TCGA, 2012) in comparison to the candidate gene partners from the siRNA screening in breast cell lines (Telford *et al.*, 2015).

5.1.1 The PI3K/AKT Pathway

The phosphoinositide 3-kinase (PI3K) cascade signalling pathway exhibited unexpected results with metagene analyses (as discussed in Section 4.3). This pathway is also of interest because mediating signals between the G protein coupled receptors and regulation of protein translation have both been strongly implicated to be synthetic lethal pathways with loss of *CDH1* function (in Chapter 4). These pathways have are all subject to dysregulation in cancer (Courtney *et al.*, 2010; Dorsam and Gutkind, 2007; Gao and Roux, 2015). Thus the PI3K cascade will be examined along with the most supported synthetic lethal pathways (as identified in Chapter 4).

The phosphoinositide 3-kinase (PI3K) pathway is also an ideal pathway in which to test pathway structure because it has an established direction of signal transduction from extracellular stimuli (and membrane bound receptors) to the inner mechanisms of the cell, namely, the regulation of protein translation. The production of proteins is necessary for the growth of the cell so it is reasonable to suggest that these processes may be subject to (non-oncogene) addiction in some cancer cells which rely upon

them for sustained protein production and cell growth. This is also supported by the oncogenes *PIK3CA* and *AKT1* being involved with the PI3K cascade and related PI3K/AKT pathway which may be subject to oncogene addiction when these proto-oncogenes are activated.

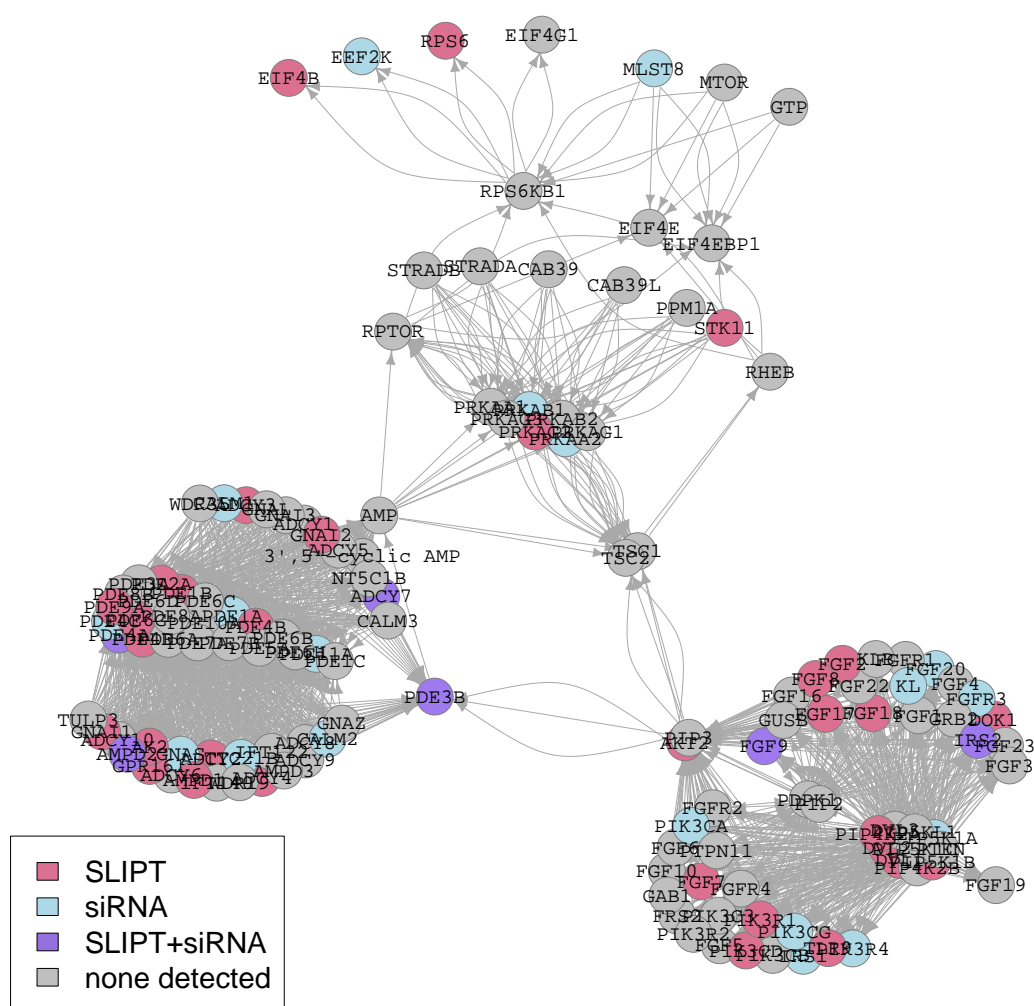


Figure 5.1: **Synthetic Lethality in the PI3K Cascade.** The Reactome PI3K Cascade pathway with synthetic lethal candidates coloured as shown in the legend.

The PI3K cascade was not supported across SLIPT in TCGA breast expression data and the siRNA primary screen by over-representation (in Section 4.2.5) or resampling (in Section 4.2.5.1) but genes were detectable by either approach (as shown in Figure 5.1). While few genes were identified by both approaches, these include genes

that are highly connected in the PI3K cascade and are hubs to information transmission such as *FGF9*, *PDE3B*, and *PDE4A*. The key upstream genes *PIK3CA* and *PIK3CG* were detected by siRNA whereas the downstream *PIK3R1* and *AKT2* genes were detected by SLIPT. Gene detected by either method were also prevalent in the PI3K, phosphodiesterase (PDE), and AMP-activated protein kinase (AMPK) modules, in addition to the downstream translation factors and ribosomal genes (*EIF4B*, *EEF2K*, and *RPS6*). Together these suggest that there may further be structure between the SLIPT and siRNA candidate partners of *CDH1* in pathways as illustrated by PI3K. As such, pathway structure will be investigated to detect differences in the upstream and downstream gene candidates of those detected by either method. Pathway structure may account for the disparity between SLIPT and siRNA genes, even in pathways such as PI3K where they did not significantly intersect. For instance, SLIPT gene partners may be downstream of siRNA candidates rather than replicating them directly.

This disparity between SLIPT and siRNA gene candidate synthetic lethal partners of *CDH1*, that is a high number of genes detected by either approach with few detected by both, was replicated in the related PI3K/AKT pathway and the “PI3K/AKT in cancer” pathway (shown in Appendix Figures F.1 and F.2). With many synthetic lethal candidates at the upstream core of these pathway networks and the downstream extremities. It is particularly notable that the many genes important in cell signalling and gene regulation were detected by either synthetic lethal detection approach. These include *AKT1*, *AKT2*, and *AKT3*, the Calmodulin signalling genes *CALM1* and *CAMK4*, and the forkhead family transcription factors *FOXO1* (a tumour suppressor) and *FOXO4* and inhibitor of epithelial-mesenchymal transition (EMT).

5.1.2 The Extracellular Matrix

The extracellular pathways “elastic fibre formation” and “fibrin clot formation” (shown in Figures 5.2 and 5.3 respectively) were both supported across analyses (in Chapter 4. Significant over-representation and resampling the intersection between SLIPT (for TCGA breast cancer) and siRNA gene candidates which showed that both approaches identified these pathways.

Particularly for elastic fibres (Figure 5.2), the vast majority of genes were detected by either approach in addition to a significant proportion of genes detected by both approaches (as determined in Section 4.2.5). The genes detected by both approaches also appeared to have a non-random distribution in the network with *TFGB1*, *ITGB8*, and *MFAP2* exhibiting high connectivity, and having a central role in their respective path-

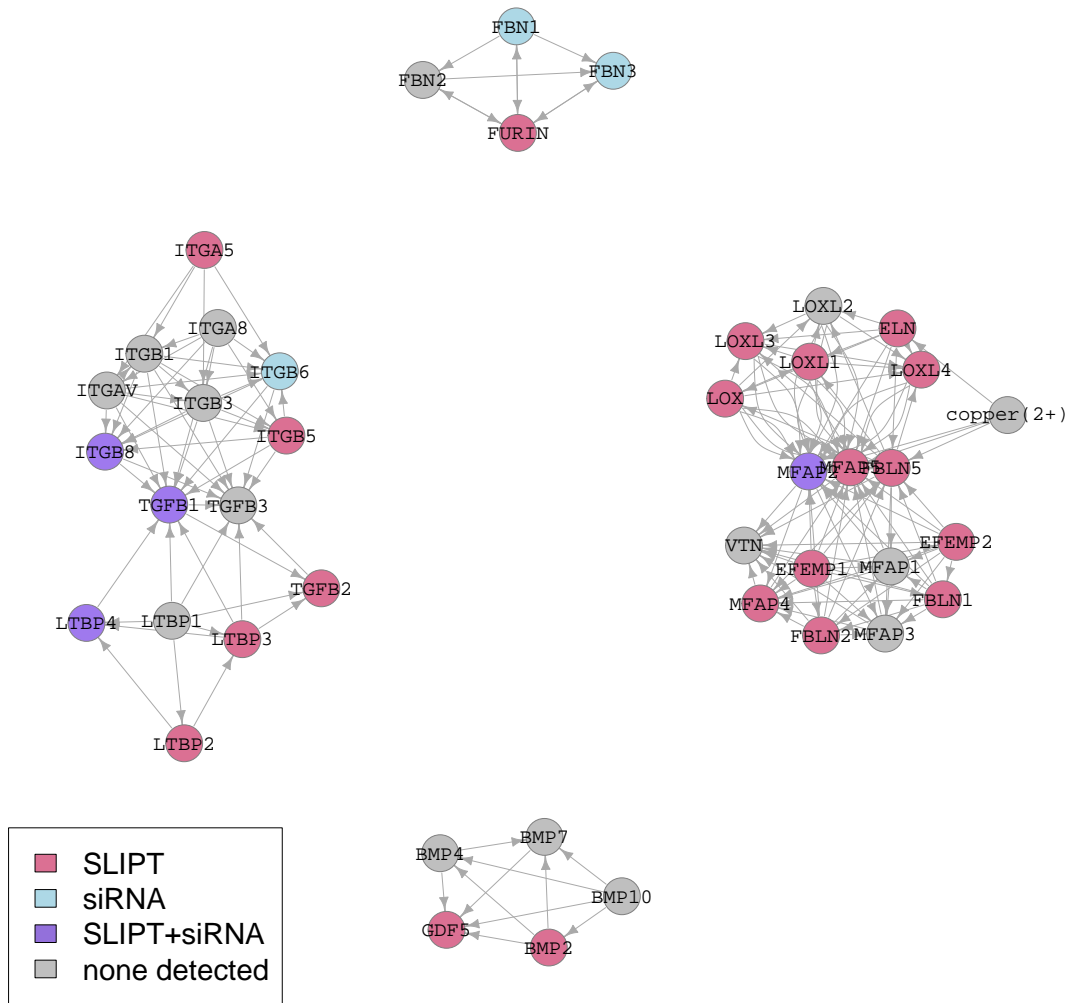


Figure 5.2: **Synthetic Lethality in the Elastic Fibre Formation Pathway.** The Reactome Elastic Fibre Formation pathway with synthetic lethal candidates coloured as shown in the legend.

way modules. In addition to a structural role in the extracellular matrix and connective tissue (including the tumour microenvironment), these proteins including Furin, transforming growth factor β ($TGF\beta$), and the bone morphogenic proteins (BMPs), are also involved in responses to endocrine signals and interacting with the cellular receptors for signalling pathways. Therefore it is plausible that *CDH1* deficient tumours will be subject to non-oncogene addiction to the extracellular environment and growth signals arising from this pathway. The pathway structure is also worth further investigation

into whether the genes detected by siRNA or both approaches are downstream of those detected by SLIPT, in addition to whether they have higher connectivity or centrality than other genes in the pathway.

Genes detected as synthetic lethal partners of *CDH1* by SLIPT or siRNA screening were also common in the Fibrin clot formation pathway (shown in Figure 5.3). This is consistent with the established pleiotropic role of *CDH1* in regulating fibrin clotting. It is also notable that the genes detected by either method appear to be highly connected such as *C1QBP*, *KNG1*, *F8*, *F10*, *F12*, *F13A*, and *PROC* (including many of the coagulation factors). Synthetic lethal candidates also include *SERPINE2* and *PRCP*, which only affect downstream genes, in addition to *PROCR* and *VWF*, which are only affected by upstream genes.

Many of these genes are involved in the larger Extracellular Matrix pathway (shown in Appendix Figure F.3), including many of the synthetic lethal candidates discussed for elastic fibres. The number of SLIPT candidate genes outnumbers those identified by siRNA, as expected from an isolated cell model. However, the endocrine response genes (e.g., *TGFB1* and *LTBP4*) which are potentially artifacts of the cell line growth process were replicated with SLIPT analysis in patient tumours (TCGA breast cancer data). There is also additional support for synthetic lethal genes such as *ITGB2*, *MFAP2*, and *SPARC* being highly connected network hubs of the pathway. The complexity of the extracellular matrix pathway lends credence to the need for formal network analysis approaches to interpret the pathway structure of synthetic lethal candidates. Furthermore statistical approaches are needed to determine whether structural relationships are unlikely to be observed between synthetic lethal candidates by sampling error.

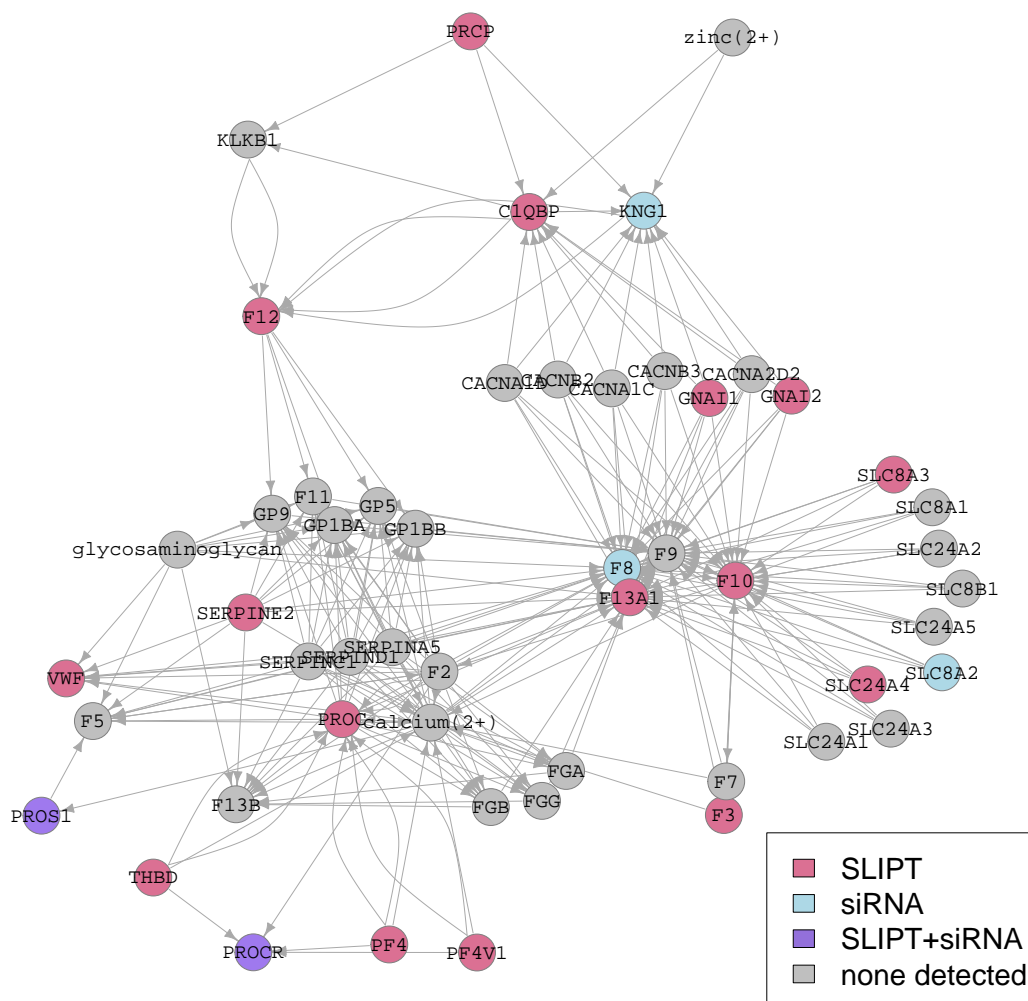


Figure 5.3: **Synthetic Lethality in the Fibrin Clot Formation.** The Reactome Fibrin Clot Formation pathway with synthetic lethal candidates coloured as shown in the legend.

5.1.3 G Protein Coupled Receptors

G protein coupled receptor (GPCR) pathways are highly complex (as shown in Appendix Figures F.4 and F.5). Many of these were synthetic lethal candidates by either SLIPT or siRNA screening, with many detected with both approaches, consistent with these pathways being supported by prior analyses (in Sections 4.2.5 and 4.2.5.1). Synthetic lethal candidates include the PDE and Calmodulin genes (as discussed in Section 5.1.3) in addition to others such as the regulators of G-protein signalling (RGS),

chemokine receptors (CXCR), Janus kinase (JAK), and the Ras homolog family (RHO) genes. These are important regulatory signalling pathways necessary for cellular growth and cancer proliferation. Thus the GPCR pathways (and downstream PI3K/AKT signals) are a potentially actionable vulnerability against *CDH1* deficient cancers, particularly since many existing drug targets exist among these signalling pathways, some of which have been experimentally validated (Kelly *et al.*, 2017b; Telford *et al.*, 2015). However, the complexity of GPCR networks containing hundreds of genes requires the relationships between SLIPT and experimental candidates to be tested with a network based statistical approach, although a statistically significant intersection of these approaches has been established (in Sections 4.2.5 and 4.2.5.1).

5.1.4 Gene Regulation and Translation

While very few synthetic lethal genes were detected in translational pathways in an experimental screen against *CDH1* Telford *et al.* (2015), these were highly over-represented in translational elongation (as shown in Appendix Figure F.6). These SLIPT genes include many ribosomal proteins and the regulatory “elongation factors” which may be subject to responses in the upstream signalling pathways. This observation lends support to the notion of pathway structure among synthetic lethal candidates detected by SLIPT in comparison with siRNA. The computational approach with SLIPT displays the ability to detect downstream genes in the core translational processes which experimental screening did not identify. The experimental screening may similarly detect upstream regulatory genes less sensitive inactivation, that is genes which are less likely to be indiscriminately lethal to both genotypes at high doses of inactivation.

Many of these SLIPT candidate genes are also among the nonsense-mediated decay (NMD) pathway (shown in Appendix Figure F.7) or 3' untranslated region (UTR) mediated translational regulation (shown in Appendix Figure F.8). While genes in these pathways were also supported by experimental screening with siRNA, there was clear pathway structure. In particular, *UPF1* was detected in the siRNA screen and is the focal downstream gene for the entire NMD pathway showing that (in this case) siRNA genes are downstream effectors of those detected by SLIPT. 3' UTR mediated translational regulation has a similar structure with two modules connected solely by *RPL13A*, giving an example of SLIPT candidates genes with high connectivity, although there were many ribosomal proteins detected by SLIPT. However *EIF3K*, a regulatory elongation factor (not essential to ribosomal function) that was detected by SLIPT, was replicated with siRNA screening, while the majority of the elongation

factors were not detected by either approach. Regulatory genes, being more amenable to experimental validation, also support further investigation into pathway structure. The SLIPT candidates may support experimental candidates by in biological pathways by detecting downstream genes which may not be detectable by experimental screening with high dose inhibitors. This difference between the approaches may explain the greater number of SLIPT candidate partners of *CDH1* than those experimentally identified.

5.2 Network Analysis of Synthetic Lethal Genes

Genes detected as synthetic lethal partners of *CDH1* with the SLIPT computational approach and the siRNA screen (Telford *et al.*, 2015) were compared across network metrics in the example of the PI3K cascade pathway (where the genes differed considerably between synthetic lethal detection methods). These were used to test whether network metrics differed between groups of genes detected by either or both approaches. These analyses serve to both test whether synthetic lethal gene candidates had higher connectivity or importance in a network and whether either detection approach is biased towards genes with different network properties.

5.2.1 Gene Connectivity and Vertex Degree

Vertex degree (the number of connections) for each gene is a fundamental property of a network. The vast majority of genes had a relatively modest number of connections, each with only a few genes in the PI3K pathway (shown in Figure 5.4) having pathway relationships with a high number of genes, consistent with the scale-free property of biological networks (Barabási and Oltvai, 2004). There were few differences in the number of connections between gene groups (by synthetic lethal detection), although genes detected by siRNA included those with the fewest connections. The median connectivity of genes detected by both approaches was marginally higher.

Table 5.1: Analysis of variance (ANOVA) for Synthetic Lethality and Vertex Degree

	DF	Sum Squares	Mean Squares	F-value	p-value
siRNA	1	15	15.50	0.0134	0.9082
SLIPT	1	506	506.01	0.4378	0.5105
siRNA×SLIPT	1	0	0.05	0.0000	0.9947

Analysis of variance for vertex degree against synthetic lethal detection approaches (with an interaction term)

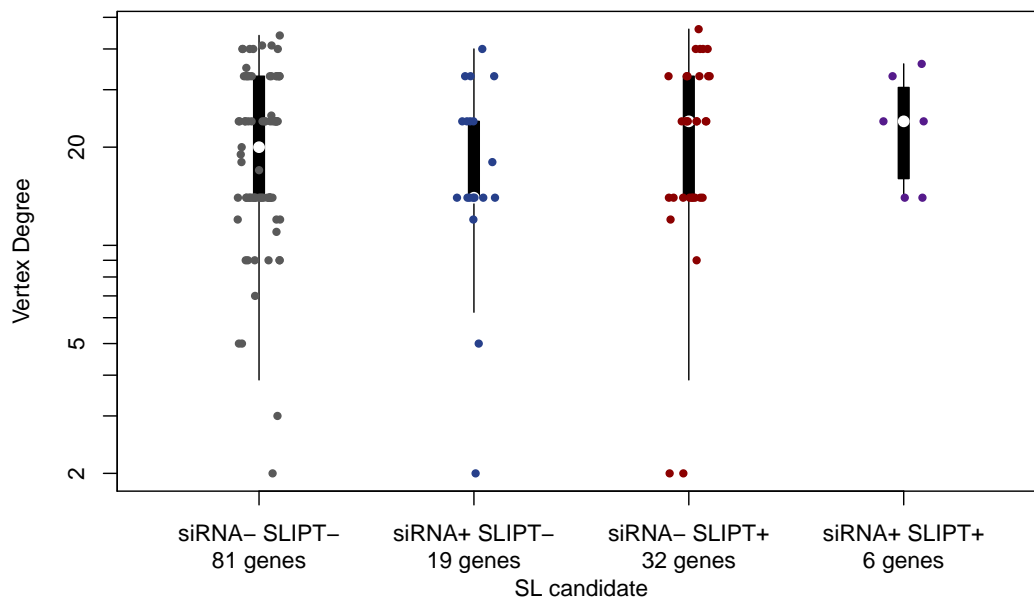


Figure 5.4: **Synthetic Lethality and Vertex Degree.** The number of connected genes (vertex degree) was compared (on a log-scale) across genes detected by SLIPT and siRNA screening in the Reactome PI3K cascade pathway. There were very few differences in vertex degree between the groups, although genes detected by siRNA included those with the fewest connections.

The results for the PI3K pathway were very similar when testing synthetic lethality against *CDH1* mutation (mtSLIPT). In this case, there is also indication that mtSLIPT-specific genes may have higher connectivity than those detected by siRNA screening (shown in Appendix Figure G.1).

However, these apparent differences in vertex degree may be due to fewer genes being detected by either approach. There was no statistically significant effect of either computational or experimental synthetic lethal detection method on vertex degree, as determined by ANOVA (shown by Table 5.1 and Appendix Table G.1). Thus synthetic lethal detection does not discriminate among genes by their connectivity in a pathway network, nor is either approach constrained to detecting highly connected genes. Both approaches have been demonstrated to detect genes with many and very few connections.

5.2.2 Gene Importance and Centrality

5.2.2.1 Information Centrality

Information centrality is a measure of the importance of nodes in a network by how vital they are to the transmission of information throughout the network. This applies well to biological pathways, particularly gene regulation and cell signalling. The nodes with the highest information centrality are not necessarily the most connected, as they may also include nodes which pass signals between highly connected network hubs. Information centrality therefore provides a distinct metric for the connectivity of a gene in a pathway, which has the added benefit of being directly related to the disruption of pathway function were it to be inactivated or removed.

Information centrality has also been suggested to indicate essentiality of genes or proteins (Kranthi *et al.*, 2013). The information centrality for each gene was computed across the entire Reactome network (as discussed in Appendix H). Reactome contains substrates and cofactors in addition to genes and proteins. In support of centrality as a measure of essentiality or importance to the network, a number nodes with the highest centrality (shown in and Appendix Table H.1) were essential nutrients, including Mg^{2+} , Ca^{2+} , Zn^{2+} , and Fe.

Genes important in development of epithelial tissues and breast cancer were also detected with relatively high information centrality (as shown by the distribution across the Reactome network in Appendix Figure H.1). Interleukin 8 (encoded by *IL8*) is a chemokine important in epithelial cells, the innate immune system, and binding GPCRs. *GATA4* is an embryonic transcription factor involved in heart development, EMT, and has been shown to be recurrently mutated in breast cancer (TCGA, 2012). β -catenin (encoded by the proto-oncogene *CTNNB1*) is a regulatory protein which binds E-cadherin, being involved in cell-cell adhesion and Wntless-related integration site (WNT) signalling. Together these show that information centrality identifies nodes of importance to biological functions in pathway networks, including those relevant to *CDH1* deficient breast cancers.

Within the PI3K pathway, genes detected by siRNA did not include those with lower centrality (shown in Figure 5.5), although the median information centrality across gene groups detected by either synthetic lethal approach did not differ. The genes with the highest information centrality included the synthetic candidates *PDE3B* (detected by SLIPT and siRNA) and *AKT2* (detected by SLIPT) which were markedly higher than most other genes in the pathway which is consistent with their known bio-

logical role in PI3K/AKT signalling and the pathway structure (shown in Figure 5.1). Other biomolecules with high centrality included the *RPS6KB1* and *RPTOR* genes, adenosine monophosphate (AMP), phosphatidylinositol (4,5)-bisphosphate (PIP₂), and phosphatidylinositol (3,4,5)-trisphosphate (PIP₃).

These findings were replicated (shown in Appendix Figure G.2) when testing synthetic lethality against *CDH1* mutation (mtSLIPT). The differences in network centrality between gene groups detected by either method were not statistically significant as determined by ANOVA (shown by Table 5.2 and Appendix Table G.2). Thus neither method was unable to detect synthetic lethal genes with particular centrality constraints, although they were also not detecting genes with higher centrality than expected by chance.

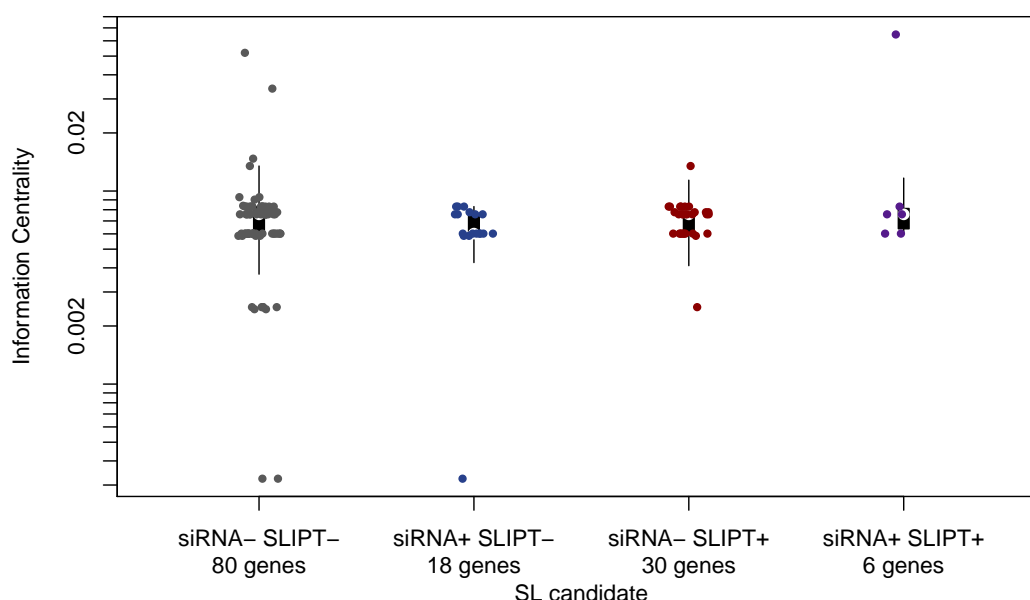


Figure 5.5: **Synthetic Lethality and Centrality.** The information centrality was compared (on a log-scale across genes detected by SLIPT and siRNA screening in the Reactome PI3K cascade pathway. Genes detected by SLIPT or siRNA did not have higher connectivity than other genes. The gene with the highest centrality was detected by both approaches.

Table 5.2: ANOVA for Synthetic Lethality and Information Centrality

	DF	Sum Squares	Mean Squares	F-value	p-value
siRNA	1	0.000256	0.0002561	0.1854	0.6682
SLIPT	1	0.003827	0.0038275	2.7717	0.1008
siRNA×SLIPT	1	0.000804	0.0008036	0.5820	0.4483

Analysis of variance for information centrality against synthetic lethal detection approaches (with an interaction term)

5.2.2.2 PageRank Centrality

PageRank centrality is another network analysis procedure to infer a hierarchy of gene importance from a network using connections and structure (Brin and Page, 1998). In contrast to the information centrality approach of removing nodes, PageRank uses the eigenvalue properties of the adjacency matrix to rank genes according to the number of connections and paths they are involved in.

This distinction is immediately clear within the PI3K pathway (shown in Figure 5.6), which differs considerably from the information centrality scores. Genes detected by SLIPT span the complete range of PageRank centrality values for this pathway which was replicated when testing synthetic lethality against *CDH1* mutation (shown in Appendix Figure G.3). However, the genes detected by both SLIPT and siRNA screening have a higher median PageRank centrality, although the differences in PageRank centrality between these methods were not statistically significant as determined by ANOVA (shown by Table 5.3 and Appendix Table G.3).

Table 5.3: ANOVA for Synthetic Lethality and PageRank Centrality

	DF	Sum Squares	Mean Squares	F-value	p-value
siRNA	1	0.0002038	2.0385×10^{-4}	1.1423	0.2892
SLIPT	1	0.0000208	2.0752×10^{-5}	0.1163	0.7342
siRNA×SLIPT	1	0.0000137	1.3743×10^{-5}	0.0770	0.7823

Analysis of variance for PageRank centrality against synthetic lethal detection approaches (with an interaction term)

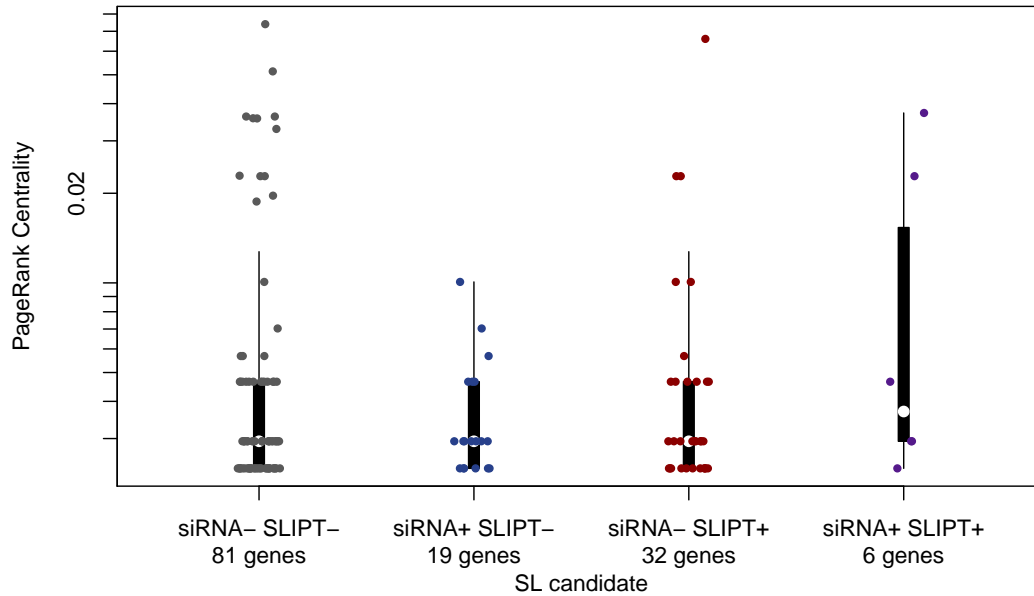


Figure 5.6: **Synthetic Lethality and PageRank.** The PageRank centrality was compared (on a log-scale across genes detected by mtSLIPT and siRNA screening in the Reactome PI3K cascade pathway. Genes detected by siRNA had a more restricted range of centrality values (which may be constrained experimental detection in a cell line model) than other genes not detected by either approach, although these groups also had fewer genes and a higher median.

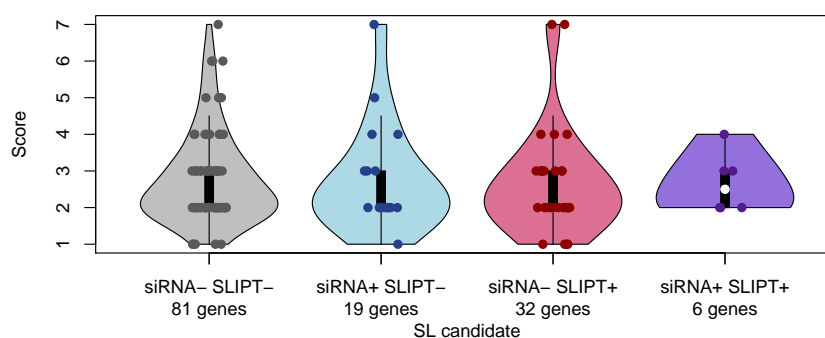
5.3 Relationships between Synthetic Lethal Genes

5.3.1 Hierarchical Pathway Structure

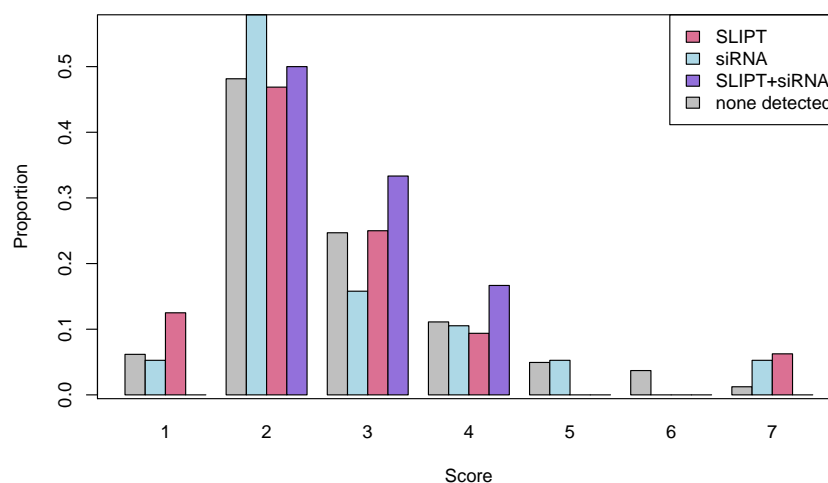
5.3.1.1 Contextual Hierarchy of PI3K

A contextual hierarchy of genes in the PI3K pathway was performed (as described in in Secion 3.4.1.2) to assign scores for their relative order in the pathway. In the case of PI3K (shown in Figure 5.7), this orders genes from the upstream genes which respond to signals from extracellular stimuli, to the downstream genes which transmit these to the gene expression (translation) responses of the cell. The directionality of this pathway is evident in transmitting signals from the PI3K complex, via AKT, PDE, and mTOR to the ribosomal regulatory proteins. This hierarchical procedure enables testing whether the biological context of a gene in a pathway is relevant to detection as

detected by either method (as shown by Figure 5.8a) did not differ, each being distributed throughout the pathway. When adjusted for being more numerous, there was little indication that SLIPT candidate genes are more frequently upstream or downstream of siRNA candidate genes (as shown by Figure 5.8b) and were more frequent at moderate hierarchies which contained more genes. Synthetic lethal candidates from both methods were less frequently detected in the downstream effectors of the pathway



(a) Hierarchical Distance Score



(b) Proportion of Genes

Figure 5.8: **Hierarchy Score in PI3K against Synthetic Lethality in PI3K.** The hierarchical distance scores were similarly distributed across SLIPT and siRNA genes. The number of SLIPT and siRNA genes against the hierarchical distance scores showing no significant tendency for either method to either of the pathway upstream or downstream extremities.

(e.g., the mTOR complex), although core pathway genes (e.g., *AKT2* and *PDE3B*) were detectable as synthetic lethal candidates (as discussed for Figures 5.1 and 5.6).

Similarly, when testing synthetic lethality against *CDH1* mutation (mtSLIPT), the hierarchical score for the PI3K pathway did not differ between mtSLIPT-specific and siRNA-specific gene candidates (as shown by Appendix Figure I.1). The median among genes detected by both approaches was marginally elevated such that these genes may be further downstream in the pathway than other synthetic lethal candidate partners of *CDH1*. There were fewer genes overall with higher scores (shown in Appendix Figure I.2). While these were more frequently detected by both SLIPT and siRNA, there was no significant effect variation in pathway hierarchy (shown by ANOVA in Table 5.4 and Appendix Table I.1) accounted for by SLIPT or siRNA detection in the PI3K pathway (as shown in Figure 5.1). Thus these hierarchical scores may be observed by sampling variation and there is no indication that SLIPT or siRNA detection differs along the direction of the pathway. Genes detected by either method are no more or less common among upstream or downstream of the pathway.

Table 5.4: ANOVA for Synthetic Lethality and PI3K Hierarchy

	DF	Sum Squares	Mean Squares	F-value	p-value
siRNA	1	0.001	0.00066	0.0004	0.9842
SLIPT	1	0.456	0.45605	0.2740	0.6016
siRNA×SLIPT	1	0.019	0.01878	0.0113	0.9156

Analysis of variance for PI3K hierarchy score against synthetic lethal detection approaches (with an interaction term)

[remove this paragraph and Figures 5.9 and I.3?]

Furthermore the pathway hierarchical scores did not exhibit different more or less SLIPT than siRNA genes above or below given threshold. Since the ideal threshold to detect pathway structure is unclear, an exploratory analysis was performed, with χ^2 -test for the SLIPT or siRNA candidate genes upstream or downstream of each gene. It is unsurprising that these χ^2 tests were highest when the gene used as a threshold was in the middle of the pathway (as shown in Figure 5.9). However, there was no statistically significant support for pathway structure by this approach, as none of the χ^2 values were high enough to detect pathway structure between SLIPT and siRNA gene candidates. Nor was structure detectable for mtSLIPT testing synthetic lethality against *CDH1* mutation (as shown in Appendix Figure I.3).

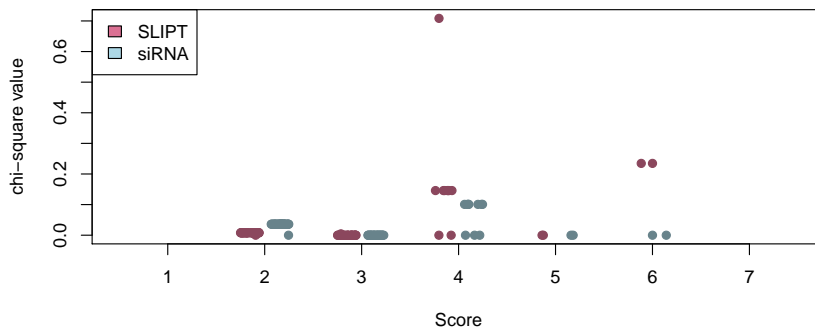


Figure 5.9: **Structure of Synthetic Lethality in PI3K.** The number of SLIPT and siRNA genes upstream or downstream of each gene in the Reactome PI3K pathway were tested (by the χ^2 -test). These are plotted as a split jitter stripchart against the hierarchical distance scores showing no significant tendency for either method to either of the pathway upstream or downstream extremities.

5.3.2 Upstream or Downstream Synthetic Lethality

This approach does not ascertain whether SLIPT and siRNA candidate partners of *CDH1* are upstream or downstream of one and other within a pathway such as the PI3K cascade. The hierarchical approach is designed to detect differences in pathway location between gene groups. An alternative pathway structure method has been devised to use network structures to identify directional relationships between individual SLIPT and siRNA genes. This pathway structure methodology will be applied (as described in Section 3.4.1) to detect the direction of shortest paths between SLIPT and siRNA gene candidates. This will be used to demonstrate the methodology on the PI3K pathway, to develop a statistical test for pathway structure between SLIPT and siRNA gene candidate using resampling (as described in Section 3.4.1.1, and to apply this test for pathway structure among synthetic lethal gene candidates to the pathways identified in Chapter 4 and discussed in Section 5.1.

5.3.2.1 Measuring Structure of Candidates within PI3K

Shortest paths in a pathway network were used to devise a strategy to detect pathway structure between SLIPT and siRNA gene candidate partners of *CDH1* (as described in Section 3.4.1). Thus we can determine whether individual SLIPT genes have upstream or downstream siRNA candidates (scored as “up” or “down” events respectively). This

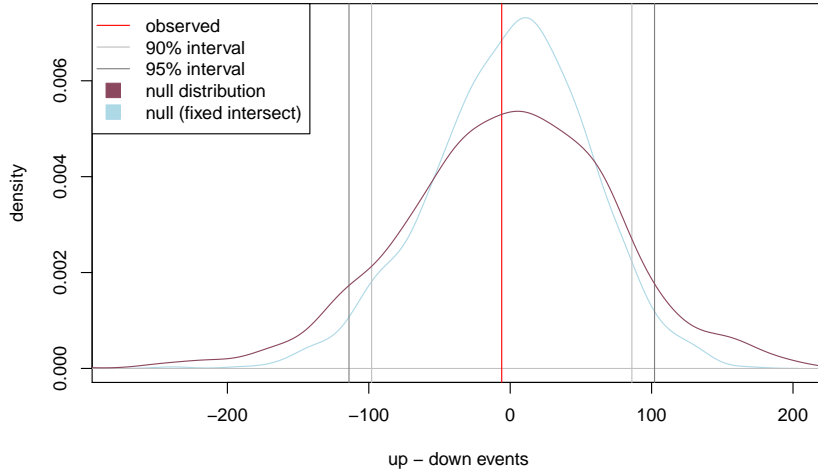


Figure 5.10: **Structure of Synthetic Lethality Resampling in PI3K.** A null distribution with 10,000 iterations of the number of siRNA genes upstream or downstream of SLIPT genes (depicted as the difference of these) in the PI3K pathway. To assess significance, the observed events (with shortest paths) were compared to the 90% and 95% intervals for the null distribution (shown in violet). Genes detected by both methods were fixed to the same number as observed for the alternative null distribution (shown in blue), although the observed number of events (red) was not significant in either case. In both cases, these genes detected by both approaches were included in computing the number of shortest paths (in either direction) between SLIPT and siRNA genes.

procedure enables the detection of directional relationships between SLIPT and siRNA gene candidates (in contrast to the hierarchical approach).

The total number of gene candidate pairs in either direction can be compared within a pathway network to assess the overall directional relationships in a pathway. This directionality is detectable by the difference between the number SLIPT candidate genes with upstream and downstream siRNA gene partners. However, this measure alone is not sufficient to determine whether there is evidence of pathway structure between SLIPT and siRNA gene candidate partners of *CDH1* in a pathway network. Although it does serve to measure the magnitude (and direction) of the consensus of directional relationships (upstream and downstream) between SLIPT and siRNA gene candidate partners. This measure of pathway structure can be used for testing for statistical significance of pathway structure by resampling, using a permutation procedure to test whether these relationships are detectable among randomly selected

gene groups rather than the detected SLIPT and siRNA gene candidate partners (as described in Sections 2.3.6 and 3.4.1.1).

This resampling procedure was performed for the PI3K network (as shown in Figure 5.1) which generated a null distribution for the difference in the number of “up events” and “down events” for this Pathway. Resampling yields a distribution to detect whether genes detected by SLIPT had significantly more upstream or downstream siRNA candidates. While there was modest indication that glssiRNA genes were downstream of SLIPT candidate genes, resampling for the PI3K pathway (as shown in Figure 5.10) did not detect a significant number of siRNA genes upstream or downstream.

In contrast, when testing synthetic lethality against *CDH1* mutation (mtSLIPT) there was modest indication that glssiRNA genes were upstream of SLIPT candidate genes. However, resampling (as shown in Appendix Figure I.4) was also unable to detect a significant number of siRNA genes upstream or downstream of mtSLIPT candidates. Fixing the number of genes detected by both approaches (as shown by the blue line in Figure 5.10 and Appendix Figure I.4) did not alter the findings of this approach. Nor did excluding these jointly detected genes, although these were included in the analysis since they can disproportionately count towards siRNA genes being upstream (or downstream) of SLIPT genes since they have different proportions of gene detected by either approach upstream (or downstream) of them. Furthermore, expanding the range of shortest paths to consider links in related pathways (using the “metapathways” constructed in Section 2.4.3) also had little effect on the null distribution generated, despite increasing the computational demands of the procedure.

5.3.2.2 Resampling for Synthetic Lethal Pathway Structure

The permutation procedure (as described in Section 3.4.1.1) that was performed in Section 5.3.2.1 for the PI3K cascade was also applied to other pathways identified in Chapter 4 and discussed in Section 5.1. These include extracellular matrix (with constituent elastic fibre and fibrin pathways), cell signalling (by PI3K/AKT and GPCRs), and translational pathways (with NMD and 3'UTR regulation). The resampling results across these pathways (as shown in Table 5.5) had limited support for association between pathway structure and detection of synthetic lethal genes, with the majority of these being non-significant as shown for PI3K (in Appendix Figure I.4). However, the distribution for these pathways will differ depending on their structure, the number of genes they consist of, and the proportion of synthetic lethal candidates among them (including a higher frequency of genes detected by both methods pathways identified

in Sections 4.2.5.1 and ??). This resampling is an appropriate procedure to use to detect structural relationships across pathways as it does not assume an underlying test statistic distribution.

Pathway structure was supported for the NMD pathway (which is consistent with siRNA being downstream in Appendix Figure F.7). However, this observation rests upon a single gene and was not replicated when testing synthetic lethality (mtSLIPT) against *CDH1* mutation (as shown in Appendix Table I.2) nor was it supported by the related 3'UTR regulation and translational elongation pathways.

Table 5.5: Resampling for pathway structure of synthetic lethal detection methods

Pathway	Graph		States		Observed				Permutation p-value	
	Nodes	Edges	SLIPT	siRNA	Up	Down	Up-Down	Up/Down	Up-Down	Down-Up
PI3K Cascade	138	1495	38	25	122	128	-6	0.953	0.5326	0.4606
PI3K/AKT Signalling in Cancer	275	12882	98	44	779	679	100	1.147	0.3255	0.6734
G_{αi} Signalling	292	22003	95	58	836	1546	-710	0.541	0.9971	0.0029
GPCR downstream	1270	142071	312	160	9755	9261	494	1.053	0.3692	0.6305
Elastic fibre formation	42	175	24	7	1	2	-1	0.500	0.5461	0.3865
Extracellular matrix	299	3677	127	29	547	455	92	1.202	0.3351	0.6636
Formation of Fibrin	52	243	18	5	12	17	-5	0.706	0.6198	0.3564
Nonsense-Mediated Decay	103	102	74	2	0	74	-74	0	1.0000	< 0.0001
3' -UTR-mediated translational regulation	107	2860	77	1	0	0	0		0.4902	0.5027
Eukaryotic Translation Elongation	92	3746	76	0	0	0	0		0.4943	0.4933

Pathways in the Reactome network tested for structural relationships between SLIPT and siRNA genes by resampling. The raw p-value (computed without adjusting for multiple comparisons over pathways) is given for the difference in upstream and downstream paths from SLIPT to siRNA gene candidate partners of *CDH1* with significant pathways highlighted in bold. Sampling was performed only in the target pathway and shortest paths were computed within it. Loops or paths in either direction that could not be resolved were excluded from the analysis. The gene detected by both SLIPT and siRNA (or resampling for them) were included in the analysis and the number of these were fixed to the number observed.

There does not appear to be a consensus on the directionality of SLIPT and siRNA candidates across pathways as distinct pathways showed stronger tendency for siRNA genes to be either upstream or downstream. Even related pathways such as PI3K and PI3K/AKT signalling showed directional events in opposite directions. The strongest pathway (among those tested) with support for directional pathways structure is G_{αi} signalling which showed significant downstream siRNA genes for both SLIPT and mtSLIPT from a large number of shortest paths (in Table 5.5 and Appendix Table I.2). This would indicate that SLIPT detects upstream regulators of genes experimentally validated by siRNA. However, these results are borderline significant (with raw permutation p-values) and are unlikely to be detected after adjusting for multiple comparisons across the 10 pathways presented here (nor in the 1652 Reactome pathways used previously in Chapter 4).

Therefore, there is insufficient evidence to determine whether there is pathway structure, gene detected upstream or downstream by either method, between the SLIPT and siRNA candidates in many of the synthetic lethal pathways (identified in Chapter 4). In particular, directional structure among synthetic lethal candidates for *CDH1* was not strongly supported in signalling pathways upon which the rationale for pathway structure hypotheses were based on. Despite the design of a robust resampling approach to test relationships between gene groups, this did not detect many structural relationships between SLIPT and siRNA gene candidates, although it may apply more broadly to gene networks. Furthermore, the pathway relationships are unlikely to be statistically supported by resampling when testing across the search space of Reactome pathways and adjusting for multiple comparisons. While there is statistically significant over-representation of many of these pathways in gene detected by both SLIPT and siRNA (as described in Chapter 4), these did not show pathway structure, nor does pathway structure account for the discrepancy between SLIPT and siRNA gene candidates which did not significantly intersect such as the PI3K cascade.

5.4 Discussion

These investigations used a functional pathway network that encapsulates protein complexes and functional modules. The Reactome network (Croft *et al.*, 2014) uses curated experimentally identified pathways to determine relationships between genes and does not have the limitation of relying solely on protein binding or text-mining which are prone to false positives. While it is not documented whether these relationships are activating or inhibitory, the Reactome network (Croft *et al.*, 2014) is sufficient to test pathway relationships with directional information.

Synthetic lethal genes and pathways (for *CDH1* loss in cancer) were identified across gene expression and mutation datasets in Chapter 4. These pathway structure investigations extend those investigations into synthetic lethal gene candidates including exploring the discrepancy between SLIPT and siRNA candidates genes in a pathway such as PI3K in which they did not significantly intersect. Pathways with replicated synthetic lethal genes across these detection methods, breast and stomach cancer data, and patient and cell line data were also investigated including pathways from the extracellular microenvironment to core translational pathway and the signalling pathways which mediate between them.

Synthetic lethal gene candidates in the context of pathway structures can also be interpreted to provide additional mechanisms and support for belonging to a synthetic

lethal pathway. Gene candidates with known mechanisms are ideal for triage of targets specific to *CDH1* deficient tumours and for further experimental validation in preclinical models. This chapter presents computational methods to use pathway structure in an attempt to detect genes with importance in a pathway and reconcile the differences between SLIPT and siRNA candidates genes with pathway relationships (e.g., one group being downstream of the other).

Many genes were detected by either method and the differences between the computational and experimental screening approaches could feasibly lead to differences in which genes within a synthetic lethal pathway are identified. Genes detected by synthetic lethal detection strategies included those biological importance within synthetic lethal pathways, those which are actionable drug targets, and those with functional implications for the biological growth mechanisms or vulnerabilities of *CDH1* deficient tumours. It appeared that genes detected by both approaches were highly connected (or of importance) in the network structure or some pathways and that there may be some structure with SLIPT and siRNA upstream or downstream of each other. However, the complexity of biological pathways meant that relationships between gene candidates are difficult to discern without formal mathematical and computational approaches so these were used to analyse large biological networks.

Network analysis techniques were therefore applied to formalise and quantify the connectivity and importance (centrality) of genes within pathways (using PI3K as an example). However, these network techniques were unable to identify distinct differences in the network properties of genes detected as synthetic lethal candidates by computational or experimental methods. These network metrics support the application of synthetic detection across pathways (and the findings using pathways as gene sets in Chapter 4) as neither synthetic lethal detection approach was biased towards genes of higher importance or connectivity and neither approach was insensitive to genes of lower importance or connectivity. SLIPT is therefore not biased towards genes with more crucial role in the pathway as inferred by pathway connectivity and centrality measures and detects genes irrespective of pathway structure.

Similarly, a network hierarchy based on biological context (ordered from receiving extracellular stimuli to affecting downstream gene expression and cell growth) was devised to test whether PI3K genes of a particular upstream or downstream level were more frequently detected as synthetic lethal candidates. However, this approach was unable to ascertain whether genes detected by either method were further upstream or

downstream in the pathway and there was no statistical evidence that either method differed in which levels of this structure were detected.

A measure of pathway structure between individual SLIPT and siRNA genes within a pathway was also devised using the direction of shortest paths in a directed graph structure. This is amenable to detecting the consensus directionality of the pathway across pairs of genes detected by either method. The pathway structure methodology developed here is generally applicable to comparison of node groups (allowing overlapping) including genes in biological pathways and their detection by different methodologies. While the pathway structure measure alone is not able to detect structural relationships between gene groups (such SLIPT and siRNA gene candidates), it is amenable to resampling to determine whether these relationships are statistically significant.

5.5 Summary

Together these analyses of biological pathways, network metrics, and statistical procedures devised specifically for purpose were applied to Reactome pathway structures to test whether structural relationships exist between synthetic lethal candidates. Of particular interest was whether these relationships relate to the differences between the computational (SLIPT) and experimental (siRNA) synthetic lethal candidate partners of *CDH1* (in the pathways discussed in Chapter 4).

While biologically relevant relationships were observed in specific pathways, there were not detectable structural relationships between SLIPT and siRNA gene candidates. These candidates did not exhibit significant differences in network connectivity or centrality measures. Network analyses were also unable to ascertain whether the candidates detected by either method stratified into upstream and downstream genes on the pathway and they likely do not.

A statistical resampling procedure was applied to shortest paths to test whether pairs of SLIPT and siRNA gene candidates were more likely to be upstream or downstream of each other. This approach detected very few structural relationships in the synthetic lethal pathways identified in Chapter 4. Overall, support for pathway structure between SLIPT and siRNA gene candidates is weak and the direction is inconsistent between pathways. Therefore pathway structure does not account for the differences between the SLIPT and siRNA gene candidates, although this does support the validity of gene set analyses in Chapter 4 and the synthetic lethal pathways identified.

Furthermore, the resampling procedure demonstrated in this Chapter is more widely applicable to gene states in network structures and may be further utility in the analysis of biological pathway or networks. This approach was able to quantify structural relationships that were otherwise difficult to interpret and to conclusively exclude many potential relationships. In this respect, the network resampling methodology may also be applicable to triage of experimental validation.

Aims

- Synthetic Lethal Genes within a Biological Pathway Structure
- Importance and Connectivity of Synthetic Lethal Genes within Pathway Networks
- Upstream and Downstream Relationships between SLIPT and siRNA Candidates

Summary

- Synthetic Lethal genes were explored within a graph structures for key pathways identified previously
- In some cases these graph structures appeared to have relationships between synthetic lethal genes
- However, no existing network metrics of importance and connectivity with the networks were elevated significantly for Synthetic Lethal genes
- Nor was there significant evidence of upstream and downstream relationships between SLIPT and siRNA Candidates in a shortest path permutation analysis

References

- Aarts, M., Bajrami, I., Herrera-Abreu, M.T., Elliott, R., Brough, R., Ashworth, A., Lord, C.J., and Turner, N.C. (2015) Functional genetic screen identifies increased sensitivity to weel inhibition in cells with defects in fanconi anemia and hr pathways. *Mol Cancer Ther*, **14**(4): 865–76.
- Abeshouse, A., Ahn, J., Akbani, R., Ally, A., Amin, S., Andry, C.D., Annala, M., Aprikian, A., Armenia, J., Arora, A., *et al.* (2015) The Molecular Taxonomy of Primary Prostate Cancer. *Cell*, **163**(4): 1011–1025.
- Adamski, M.G., Gumann, P., and Baird, A.E. (2014) A method for quantitative analysis of standard and high-throughput qPCR expression data based on input sample quantity. *PLoS ONE*, **9**(8): e103917.
- Adler, D. (2005) *vioplot: Violin plot*. R package version 0.2.
- Agarwal, S., Deane, C.M., Porter, M.A., and Jones, N.S. (2010) Revisiting date and party hubs: Novel approaches to role assignment in protein interaction networks. *PLoS Comput Biol*, **6**(6): e1000817.
- Agrawal, N., Akbani, R., Aksoy, B.A., Ally, A., Arachchi, H., Asa, S.L., Auman, J.T., Balasundaram, M., Balu, S., Baylin, S.B., *et al.* (2014) Integrated genomic characterization of papillary thyroid carcinoma. *Cell*, **159**(3): 676–690.
- Akbani, R., Akdemir, K.C., Aksoy, B.A., Albert, M., Ally, A., Amin, S.B., Arachchi, H., Arora, A., Auman, J.T., Ayala, B., *et al.* (2015) Genomic Classification of Cutaneous Melanoma. *Cell*, **161**(7): 1681–1696.
- Akobeng, A.K. (2007) Understanding diagnostic tests 3: receiver operating characteristic curves. *Acta Paediatrica*, **96**(5): 644–647.
- American Cancer Society (2017) Genetics and cancer. <https://www.cancer.org/cancer/cancer-causes/genetics.html>. Accessed: 22/03/2017.

- American Society for Clinical Oncology (ASCO) (2017) The genetics of cancer. <http://www.cancer.net/navigating-cancer-care/cancer-basics/genetics/genetics-cancer>. Accessed: 22/03/2017.
- Anjomshoaa, A., Lin, Y.H., Black, M.A., McCall, J.L., Humar, B., Song, S., Fukuzawa, R., Yoon, H.S., Holzmann, B., Friederichs, J., *et al.* (2008) Reduced expression of a gene proliferation signature is associated with enhanced malignancy in colon cancer. *Br J Cancer*, **99**(6): 966–973.
- Araki, H., Knapp, C., Tsai, P., and Print, C. (2012) GeneSetDB: A comprehensive meta-database, statistical and visualisation framework for gene set analysis. *FEBS Open Bio*, **2**: 76–82.
- Ashburner, M., Ball, C.A., Blake, J.A., Botstein, D., Butler, H., Cherry, J.M., Davis, A.P., Dolinski, K., Dwight, S.S., Eppig, J.T., *et al.* (2000) Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. *Nat Genet*, **25**(1): 25–29.
- Ashworth, A. (2008) A synthetic lethal therapeutic approach: poly(adp) ribose polymerase inhibitors for the treatment of cancers deficient in dna double-strand break repair. *J Clin Oncol*, **26**(22): 3785–90.
- Audeh, M.W., Carmichael, J., Penson, R.T., Friedlander, M., Powell, B., Bell-McGuinn, K.M., Scott, C., Weitzel, J.N., Oaknin, A., Loman, N., *et al.* (2010) Oral poly(adp-ribose) polymerase inhibitor olaparib in patients with *BRCA1* or *BRCA2* mutations and recurrent ovarian cancer: a proof-of-concept trial. *Lancet*, **376**(9737): 245–51.
- Babyak, M.A. (2004) What you see may not be what you get: a brief, nontechnical introduction to overfitting in regression-type models. *Psychosom Med*, **66**(3): 411–21.
- Bamford, S., Dawson, E., Forbes, S., Clements, J., Pettett, R., Dogan, A., Flanagan, A., Teague, J., Futreal, P.A., Stratton, M.R., *et al.* (2004) The COSMIC (Catalogue of Somatic Mutations in Cancer) database and website. *Br J Cancer*, **91**(2): 355–358.
- Barabási, A.L. and Albert, R. (1999) Emergence of scaling in random networks. *Science*, **286**(5439): 509–12.

- Barabási, A.L., Gulbahce, N., and Loscalzo, J. (2011) Network medicine: a network-based approach to human disease. *Nat Rev Genet*, **12**(1): 56–68.
- Barabási, A.L. and Oltvai, Z.N. (2004) Network biology: understanding the cell’s functional organization. *Nat Rev Genet*, **5**(2): 101–13.
- Barrat, A. and Weigt, M. (2000) On the properties of small-world network models. *The European Physical Journal B - Condensed Matter and Complex Systems*, **13**(3): 547–560.
- Barretina, J., Caponigro, G., Stransky, N., Venkatesan, K., Margolin, A.A., Kim, S., Wilson, C.J., Lehar, J., Kryukov, G.V., Sonkin, D., *et al.* (2012) The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. *Nature*, **483**(7391): 603–607.
- Barry, W.T. (2016) *safe: Significance Analysis of Function and Expression*. R package version 3.14.0.
- Baryshnikova, A., Costanzo, M., Dixon, S., Vizeacoumar, F.J., Myers, C.L., Andrews, B., and Boone, C. (2010a) Synthetic genetic array (sga) analysis in *saccharomyces cerevisiae* and *schizosaccharomyces pombe*. *Methods Enzymol*, **470**: 145–79.
- Baryshnikova, A., Costanzo, M., Kim, Y., Ding, H., Koh, J., Toufighi, K., Youn, J.Y., Ou, J., San Luis, B.J., Bandyopadhyay, S., *et al.* (2010b) Quantitative analysis of fitness and genetic interactions in yeast on a genome scale. *Nat Meth*, **7**(12): 1017–1024.
- Bass, A.J., Thorsson, V., Shmulevich, I., Reynolds, S.M., Miller, M., Bernard, B., Hinoue, T., Laird, P.W., Curtis, C., Shen, H., *et al.* (2014) Comprehensive molecular characterization of gastric adenocarcinoma. *Nature*, **513**(7517): 202–209.
- Bates, D. and Maechler, M. (2016) *Matrix: Sparse and Dense Matrix Classes and Methods*. R package version 1.2-7.1.
- Bateson, W. and Mendel, G. (1909) *Mendel’s principles of heredity*, by W. Bateson. University Press, Cambridge [Eng.].
- Beck, T.F., Mullikin, J.C., and Biesecker, L.G. (2016) Systematic Evaluation of Sanger Validation of Next-Generation Sequencing Variants. *Clin Chem*, **62**(4): 647–654.

- Becker, K.F., Atkinson, M.J., Reich, U., Becker, I., Nekarda, H., Siewert, J.R., and Hfler, H. (1994) E-cadherin gene mutations provide clues to diffuse type gastric carcinomas. *Cancer Research*, **54**(14): 3845–3852.
- Bell, D., Berchuck, A., Birrer, M., Chien, J., Cramer, D., Dao, F., Dhir, R., DiSaia, P., Gabra, H., Glenn, P., *et al.* (2011) Integrated genomic analyses of ovarian carcinoma. *Nature*, **474**(7353): 609–615.
- Benjamini, Y. and Hochberg, Y. (1995) Controlling the false discovery rate: A practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society Series B (Methodological)*, **57**(1): 289–300.
- Berx, G., Cleton-Jansen, A.M., Nollet, F., de Leeuw, W.J., van de Vijver, M., Cornelisse, C., and van Roy, F. (1995) E-cadherin is a tumour/invasion suppressor gene mutated in human lobular breast cancers. *EMBO J*, **14**(24): 6107–15.
- Berx, G., Cleton-Jansen, A.M., Strumane, K., de Leeuw, W.J., Nollet, F., van Roy, F., and Cornelisse, C. (1996) E-cadherin is inactivated in a majority of invasive human lobular breast cancers by truncation mutations throughout its extracellular domain. *Oncogene*, **13**(9): 1919–25.
- Berx, G. and van Roy, F. (2009) Involvement of members of the cadherin superfamily in cancer. *Cold Spring Harb Perspect Biol*, **1**: a003129.
- Bitler, B.G., Aird, K.M., Garipov, A., Li, H., Amatangelo, M., Kossenkov, A.V., Schultz, D.C., Liu, Q., Shih Ie, M., Conejo-Garcia, J.R., *et al.* (2015) Synthetic lethality by targeting ezh2 methyltransferase activity in arid1a-mutated cancers. *Nat Med*, **21**(3): 231–8.
- Blake, J.A., Christie, K.R., Dolan, M.E., Drabkin, H.J., Hill, D.P., Ni, L., Sitnikov, D., Burgess, S., Buza, T., Gresham, C., *et al.* (2015) Gene Ontology Consortium: going forward. *Nucleic Acids Res*, **43**(Database issue): D1049–1056.
- Boettcher, M., Lawson, A., Ladenburger, V., Fredebohm, J., Wolf, J., Hoheisel, J.D., Frezza, C., and Shlomi, T. (2014) High throughput synthetic lethality screen reveals a tumorigenic role of adenylate cyclase in fumarate hydratase-deficient cancer cells. *BMC Genomics*, **15**: 158.
- Boone, C., Bussey, H., and Andrews, B.J. (2007) Exploring genetic interactions and networks with yeast. *Nat Rev Genet*, **8**(6): 437–49.

- Borgatti, S.P. (2005) Centrality and network flow. *Social Networks*, **27**(1): 55 – 71.
- Boucher, B. and Jenna, S. (2013) Genetic interaction networks: better understand to better predict. *Front Genet*, **4**: 290.
- Breiman, L. (2001) Random forests. *Machine Learning*, **45**(1): 5–32.
- Brin, S. and Page, L. (1998) The anatomy of a large-scale hypertextual web search engine. *Computer Networks and ISDN Systems*, **30**(1): 107 – 117.
- Bryant, H.E., Schultz, N., Thomas, H.D., Parker, K.M., Flower, D., Lopez, E., Kyle, S., Meuth, M., Curtin, N.J., and Helleday, T. (2005) Specific killing of *BRCA2*-deficient tumours with inhibitors of polyadprribose polymerase. *Nature*, **434**(7035): 913–7.
- Burk, R.D., Chen, Z., Saller, C., Tarvin, K., Carvalho, A.L., Scapulatempo-Neto, C., Silveira, H.C., Fregnani, J.H., Creighton, C.J., Anderson, M.L., *et al.* (2017) Integrated genomic and molecular characterization of cervical cancer. *Nature*, **543**(7645): 378–384.
- Bussey, H., Andrews, B., and Boone, C. (2006) From worm genetic networks to complex human diseases. *Nat Genet*, **38**(8): 862–3.
- Butland, G., Babu, M., Diaz-Mejia, J.J., Bohdana, F., Phanse, S., Gold, B., Yang, W., Li, J., Gagarinova, A.G., Pogoutse, O., *et al.* (2008) esga: E. coli synthetic genetic array analysis. *Nat Methods*, **5**(9): 789–95.
- Cancer Research UK (2017) Family history and cancer genes. <http://www.cancerresearchuk.org/about-cancer/causes-of-cancer/inherited-cancer-genes-and-increased-cancer-risk/family-history-and-inherited-cancer-genes>. Accessed: 22/03/2017.
- cBioPortal for Cancer Genomics (cBioPortal) (2017) cBioPortal for Cancer Genomics. <http://www.cbioportal.org/>. Accessed: 26/03/2017.
- Cerami, E.G., Gross, B.E., Demir, E., Rodchenkov, I., Babur, O., Anwar, N., Schultz, N., Bader, G.D., and Sander, C. (2011) Pathway Commons, a web resource for biological pathway data. *Nucleic Acids Res*, **39**(Database issue): D685–690.
- Chen, A., Beetham, H., Black, M.A., Priya, R., Telford, B.J., Guest, J., Wiggins, G.A.R., Godwin, T.D., Yap, A.S., and Guilford, P.J. (2014) E-cadherin loss alters

- cytoskeletal organization and adhesion in non-malignant breast cells but is insufficient to induce an epithelial-mesenchymal transition. *BMC Cancer*, **14**(1): 552.
- Chen, K., Yang, D., Li, X., Sun, B., Song, F., Cao, W., Brat, D.J., Gao, Z., Li, H., Liang, H., *et al.* (2015) Mutational landscape of gastric adenocarcinoma in Chinese: implications for prognosis and therapy. *Proc Natl Acad Sci USA*, **112**(4): 1107–1112.
- Chen, S. and Parmigiani, G. (2007) Meta-analysis of BRCA1 and BRCA2 penetrance. *J Clin Oncol*, **25**(11): 1329–1333.
- Chen, X. and Tompa, M. (2010) Comparative assessment of methods for aligning multiple genome sequences. *Nat Biotechnol*, **28**(6): 567–572.
- Cherniack, A.D., Shen, H., Walter, V., Stewart, C., Murray, B.A., Bowlby, R., Hu, X., Ling, S., Soslow, R.A., Broaddus, R.R., *et al.* (2017) Integrated Molecular Characterization of Uterine Carcinosarcoma. *Cancer Cell*, **31**(3): 411–423.
- Chipman, K. and Singh, A. (2009) Predicting genetic interactions with random walks on biological networks. *BMC Bioinformatics*, **10**(1): 17.
- Christofori, G. and Semb, H. (1999) The role of the cell-adhesion molecule E-cadherin as a tumour-suppressor gene. *Trends in Biochemical Sciences*, **24**(2): 73 – 76.
- Ciriello, G., Gatza, M.L., Beck, A.H., Wilkerson, M.D., Rhie, S.K., Pastore, A., Zhang, H., McLellan, M., Yau, C., Kandoth, C., *et al.* (2015) Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. *Cell*, **163**(2): 506–519.
- Clark, M.J. (2004) Endogenous Regulator of G Protein Signaling Proteins Suppress G o-Dependent μ -Opioid Agonist-Mediated Adenylyl Cyclase Supersensitization. *Journal of Pharmacology and Experimental Therapeutics*, **310**(1): 215–222.
- Clough, E. and Barrett, T. (2016) The Gene Expression Omnibus Database. *Methods Mol Biol*, **1418**: 93–110.
- Collingridge, D.S. (2013) A primer on quantitized data analysis and permutation testing. *Journal of Mixed Methods Research*, **7**(1): 81–97.
- Collins, F.S. and Barker, A.D. (2007) Mapping the cancer genome. Pinpointing the genes involved in cancer will help chart a new course across the complex landscape of human malignancies. *Sci Am*, **296**(3): 50–57.

- Collins, F.S., Morgan, M., and Patrinos, A. (2003) The Human Genome Project: lessons from large-scale biology. *Science*, **300**(5617): 286–290.
- Collisson, E., Campbell, J., Brooks, A., Berger, A., Lee, W., Chmielecki, J., Beer, D., Cope, L., Creighton, C., Danilova, L., *et al.* (2014) Comprehensive molecular profiling of lung adenocarcinoma. *Nature*, **511**(7511): 543–550.
- Corcoran, R.B., Ebi, H., Turke, A.B., Coffee, E.M., Nishino, M., Cogdill, A.P., Brown, R.D., Della Pelle, P., Dias-Santagata, D., Hung, K.E., *et al.* (2012) Egfr-mediated re-activation of mapk signaling contributes to insensitivity of *BRAF*-mutant colorectal cancers to raf inhibition with vemurafenib. *Cancer Discovery*, **2**(3): 227–235.
- Costanzo, M., Baryshnikova, A., Bellay, J., Kim, Y., Spear, E.D., Sevier, C.S., Ding, H., Koh, J.L., Toufighi, K., Mostafavi, S., *et al.* (2010) The genetic landscape of a cell. *Science*, **327**(5964): 425–31.
- Costanzo, M., Baryshnikova, A., Myers, C.L., Andrews, B., and Boone, C. (2011) Charting the genetic interaction map of a cell. *Curr Opin Biotechnol*, **22**(1): 66–74.
- Courtney, K.D., Corcoran, R.B., and Engelman, J.A. (2010) The PI3K pathway as drug target in human cancer. *J Clin Oncol*, **28**(6): 1075–1083.
- Creighton, C.J., Morgan, M., Gunaratne, P.H., Wheeler, D.A., Gibbs, R.A., Robertson, A., Chu, A., Beroukhim, R., Cibulskis, K., Signoretti, S., *et al.* (2013) Comprehensive molecular characterization of clear cell renal cell carcinoma. *Nature*, **499**(7456): 43–49.
- Croft, D., Mundo, A.F., Haw, R., Milacic, M., Weiser, J., Wu, G., Caudy, M., Garapati, P., Gillespie, M., Kamdar, M.R., *et al.* (2014) The Reactome pathway knowledge-base. *Nucleic Acids Res*, **42**(database issue): D472D477.
- Crunkhorn, S. (2014) Cancer: Predicting synthetic lethal interactions. *Nat Rev Drug Discov*, **13**(11): 812.
- Csardi, G. and Nepusz, T. (2006) The igraph software package for complex network research. *InterJournal*, **Complex Systems**: 1695.
- Curtis, C., Shah, S.P., Chin, S.F., Turashvili, G., Rueda, O.M., Dunning, M.J., Speed, D., Lynch, A.G., Samarajiwa, S., Yuan, Y., *et al.* (2012) The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. *Nature*, **486**(7403): 346–352.

- Dai, X., Li, T., Bai, Z., Yang, Y., Liu, X., Zhan, J., and Shi, B. (2015) Breast cancer intrinsic subtype classification, clinical use and future trends. *Am J Cancer Res*, **5**(10): 2929–2943.
- Davierwala, A.P., Haynes, J., Li, Z., Brost, R.L., Robinson, M.D., Yu, L., Mnaimneh, S., Ding, H., Zhu, H., Chen, Y., *et al.* (2005) The synthetic genetic interaction spectrum of essential genes. *Nat Genet*, **37**(10): 1147–1152.
- De Leeuw, W.J., Berx, G., Vos, C.B., Peterse, J.L., Van de Vijver, M.J., Litvinov, S., Van Roy, F., Cornelisse, C.J., and Cleton-Jansen, A.M. (1997) Simultaneous loss of E-cadherin and catenins in invasive lobular breast cancer and lobular carcinoma in situ. *J Pathol*, **183**(4): 404–11.
- Demir, E., Babur, O., Rodchenkov, I., Aksoy, B.A., Fukuda, K.I., Gross, B., Sumer, O.S., Bader, G.D., and Sander, C. (2013) Using biological pathway data with Paxtools. *PLoS Comput Biol*, **9**(9): e1003194.
- Deshpande, R., Asiedu, M.K., Klebig, M., Sutor, S., Kuzmin, E., Nelson, J., Piotrowski, J., Shin, S.H., Yoshida, M., Costanzo, M., *et al.* (2013) A comparative genomic approach for identifying synthetic lethal interactions in human cancer. *Cancer Res*, **73**(20): 6128–36.
- Dickson, D. (1999) Wellcome funds cancer database. *Nature*, **401**(6755): 729.
- Dienstmann, R. and Tabernero, J. (2011) *BRAF* as a target for cancer therapy. *Anti-cancer Agents Med Chem*, **11**(3): 285–95.
- Dijkstra, E.W. (1959) A note on two problems in connexion with graphs. *Numerische Mathematik*, **1**(1): 269–271.
- Dixon, S.J., Andrews, B.J., and Boone, C. (2009) Exploring the conservation of synthetic lethal genetic interaction networks. *Commun Integr Biol*, **2**(2): 78–81.
- Dixon, S.J., Fedyshyn, Y., Koh, J.L., Prasad, T.S., Chahwan, C., Chua, G., Toufighi, K., Baryshnikova, A., Hayles, J., Hoe, K.L., *et al.* (2008) Significant conservation of synthetic lethal genetic interaction networks between distantly related eukaryotes. *Proc Natl Acad Sci U S A*, **105**(43): 16653–8.
- Dorogovtsev, S.N. and Mendes, J.F. (2003) *Evolution of networks: From biological nets to the Internet and WWW*. Oxford University Press, USA.

- Dorsam, R.T. and Gutkind, J.S. (2007) G-protein-coupled receptors and cancer. *Nat Rev Cancer*, **7**(2): 79–94.
- Erdős, P. and Rényi, A. (1959) On random graphs I. *Publ Math Debrecen*, **6**: 290–297.
- Erdős, P. and Rényi, A. (1960) On the evolution of random graphs. In *Publ. Math. Inst. Hung. Acad. Sci*, volume 5, 17–61.
- Eroles, P., Bosch, A., Perez-Fidalgo, J.A., and Lluch, A. (2012) Molecular biology in breast cancer: intrinsic subtypes and signaling pathways. *Cancer Treat Rev*, **38**(6): 698–707.
- Ezkurdia, I., Juan, D., Rodriguez, J.M., Frankish, A., Diekhans, M., Harrow, J., Vazquez, J., Valencia, A., and Tress, M.L. (2014) Multiple evidence strands suggest that there may be as few as 19 000 human protein-coding genes. *Human Molecular Genetics*, **23**(22): 5866.
- Farmer, H., McCabe, N., Lord, C.J., Tutt, A.N., Johnson, D.A., Richardson, T.B., Santarosa, M., Dillon, K.J., Hickson, I., Knights, C., *et al.* (2005) Targeting the dna repair defect in BRCA mutant cells as a therapeutic strategy. *Nature*, **434**(7035): 917–21.
- Fawcett, T. (2006) An introduction to ROC analysis. *Pattern Recognition Letters*, **27**(8): 861 – 874. {ROC} Analysis in Pattern Recognition.
- Fece de la Cruz, F., Gapp, B.V., and Nijman, S.M. (2015) Synthetic lethal vulnerabilities of cancer. *Annu Rev Pharmacol Toxicol*, **55**: 513–531.
- Ferlay, J., Soerjomataram, I., Dikshit, R., Eser, S., Mathers, C., Rebelo, M., Parkin, D.M., Forman, D., and Bray, F. (2015) Cancer incidence and mortality worldwide: sources, methods and major patterns in GLOBOCAN 2012. *Int J Cancer*, **136**(5): E359–386.
- Fisher, R.A. (1919) Xv.the correlation between relatives on the supposition of mendelian inheritance. *Earth and Environmental Science Transactions of the Royal Society of Edinburgh*, **52**(02): 399–433.
- Fong, P.C., Boss, D.S., Yap, T.A., Tutt, A., Wu, P., Mergui-Roelvink, M., Mortimer, P., Swaisland, H., Lau, A., O’Connor, M.J., *et al.* (2009) Inhibition of poly(adp-ribose) polymerase in tumors from BRCA mutation carriers. *N Engl J Med*, **361**(2): 123–34.

- Fong, P.C., Yap, T.A., Boss, D.S., Carden, C.P., Mergui-Roelvink, M., Gourley, C., De Greve, J., Lubinski, J., Shanley, S., Messiou, C., *et al.* (2010) Poly(adp)-ribose polymerase inhibition: frequent durable responses in BRCA carrier ovarian cancer correlating with platinum-free interval. *J Clin Oncol*, **28**(15): 2512–9.
- Forbes, S.A., Beare, D., Gunasekaran, P., Leung, K., Bindal, N., Boutselakis, H., Ding, M., Bamford, S., Cole, C., Ward, S., *et al.* (2015) COSMIC: exploring the world’s knowledge of somatic mutations in human cancer. *Nucleic Acids Res*, **43**(Database issue): D805–811.
- Fraser, A. (2004) Towards full employment: using RNAi to find roles for the redundant. *Oncogene*, **23**(51): 8346–52.
- Futreal, P.A., Coin, L., Marshall, M., Down, T., Hubbard, T., Wooster, R., Rahman, N., and Stratton, M.R. (2004) A census of human cancer genes. *Nat Rev Cancer*, **4**(3): 177–183.
- Futreal, P.A., Kasprzyk, A., Birney, E., Mullikin, J.C., Wooster, R., and Stratton, M.R. (2001) Cancer and genomics. *Nature*, **409**(6822): 850–852.
- Gao, B. and Roux, P.P. (2015) Translational control by oncogenic signaling pathways. *Biochimica et Biophysica Acta*, **1849**(7): 753–65.
- Gatza, M.L., Kung, H.N., Blackwell, K.L., Dewhirst, M.W., Marks, J.R., and Chi, J.T. (2011) Analysis of tumor environmental response and oncogenic pathway activation identifies distinct basal and luminal features in HER2-related breast tumor subtypes. *Breast Cancer Res*, **13**(3): R62.
- Gatza, M.L., Lucas, J.E., Barry, W.T., Kim, J.W., Wang, Q., Crawford, M.D., Datto, M.B., Kelley, M., Mathey-Prevot, B., Potti, A., *et al.* (2010) A pathway-based classification of human breast cancer. *Proc Natl Acad Sci USA*, **107**(15): 6994–6999.
- Gatza, M.L., Silva, G.O., Parker, J.S., Fan, C., and Perou, C.M. (2014) An integrated genomics approach identifies drivers of proliferation in luminal-subtype human breast cancer. *Nat Genet*, **46**(10): 1051–1059.
- Gentleman, R.C., Carey, V.J., Bates, D.M., Bolstad, B., Dettling, M., Dudoit, S., Ellis, B., Gautier, L., Ge, Y., Gentry, J., *et al.* (2004) Bioconductor: open software development for computational biology and bioinformatics. *Genome Biol*, **5**(10): R80.

- Genz, A. and Bretz, F. (2009) Computation of multivariate normal and t probabilities. In *Lecture Notes in Statistics*, volume 195. Springer-Verlag, Heidelberg.
- Genz, A., Bretz, F., Miwa, T., Mi, X., Leisch, F., Scheipl, F., and Hothorn, T. (2016) *mvtnorm: Multivariate Normal and t Distributions*. R package version 1.0-5. URL.
- Gilbert, W. and Maxam, A. (1973) The nucleotide sequence of the lac operator. *Proceedings of the National Academy of Sciences*, **70**(12): 3581–3584.
- Git, A., Dvinge, H., Salmon-Divon, M., Osborne, M., Kutter, C., Hadfield, J., Bertone, P., and Caldas, C. (2010) Systematic comparison of microarray profiling, real-time PCR, and next-generation sequencing technologies for measuring differential microRNA expression. *RNA*, **16**(5): 991–1006.
- Globus (Globus) (2017) Research data management simplified. <https://www.globus.org/>. Accessed: 25/03/2017.
- Graziano, F., Humar, B., and Guilford, P. (2003) The role of the E-cadherin gene (*CDH1*) in diffuse gastric cancer susceptibility: from the laboratory to clinical practice. *Annals of Oncology*, **14**(12): 1705–1713.
- Güell, O., Sagus, F., and Serrano, M. (2014) Essential plasticity and redundancy of metabolism unveiled by synthetic lethality analysis. *PLoS Comput Biol*, **10**(5): e1003637.
- Guilford, P. (1999) E-cadherin downregulation in cancer: fuel on the fire? *Molecular Medicine Today*, **5**(4): 172 – 177.
- Guilford, P., Hopkins, J., Harraway, J., McLeod, M., McLeod, N., Harawira, P., Taite, H., Scoular, R., Miller, A., and Reeve, A.E. (1998) E-cadherin germline mutations in familial gastric cancer. *Nature*, **392**(6674): 402–5.
- Guilford, P., Humar, B., and Blair, V. (2010) Hereditary diffuse gastric cancer: translation of *CDH1* germline mutations into clinical practice. *Gastric Cancer*, **13**(1): 1–10.
- Guilford, P.J., Hopkins, J.B., Grady, W.M., Markowitz, S.D., Willis, J., Lynch, H., Rajput, A., Wiesner, G.L., Lindor, N.M., Burgart, L.J., *et al.* (1999) E-cadherin germline mutations define an inherited cancer syndrome dominated by diffuse gastric cancer. *Hum Mutat*, **14**(3): 249–55.

- Guo, J., Liu, H., and Zheng, J. (2016) SynLethDB: synthetic lethality database toward discovery of selective and sensitive anticancer drug targets. *Nucleic Acids Res*, **44**(D1): D1011–1017.
- Hajian-Tilaki, K. (2013) Receiver Operating Characteristic (ROC) Curve Analysis for Medical Diagnostic Test Evaluation. *Caspian J Intern Med*, **4**(2): 627–635.
- Hall, M., Frank, E., Holmes, G., Pfahringer, B., Reutemann, P., and Witten, I.H. (2009) The weka data mining software: an update. *SIGKDD Explor Newsl*, **11**(1): 10–18.
- Hammerman, P.S., Lawrence, M.S., Voet, D., Jing, R., Cibulskis, K., Sivachenko, A., Stojanov, P., McKenna, A., Lander, E.S., Gabriel, S., *et al.* (2012) Comprehensive genomic characterization of squamous cell lung cancers. *Nature*, **489**(7417): 519–525.
- Han, J.D.J., Bertin, N., Hao, T., Goldberg, D.S., Berriz, G.F., Zhang, L.V., Dupuy, D., Walhout, A.J.M., Cusick, M.E., Roth, F.P., *et al.* (2004) Evidence for dynamically organized modularity in the yeast protein-protein interaction network. *Nature*, **430**(6995): 88–93.
- Hanahan, D. and Weinberg, R.A. (2000) The hallmarks of cancer. *Cell*, **100**(1): 57–70.
- Hanahan, D. and Weinberg, R.A. (2011) Hallmarks of cancer: the next generation. *Cell*, **144**(5): 646–674.
- Hanna, S. (2003) Cancer incidence in new zealand (2003-2007). In D. Forman, D. Bray F Brewster, C. Gombe Mbalawa, B. Kohler, M. Piñeros, E. Steliarova-Foucher, R. Swaminathan, and J. Ferlay (editors), *Cancer Incidence in Five Continents*, volume X, 902–907. International Agency for Research on Cancer, Lyon, France. Electronic version <http://ci5.iarc.fr> Accessed 22/03/2017.
- Heiskanen, M., Bian, X., Swan, D., and Basu, A. (2014) caArray microarray database in the cancer biomedical informatics gridTM (caBIGTM). *Cancer Research*, **67**(9 Supplement): 3712–3712.
- Heiskanen, M.A. and Aittokallio, T. (2012) Mining high-throughput screens for cancer drug targets-lessons from yeast chemical-genomic profiling and synthetic lethality. *Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery*, **2**(3): 263–272.

- Hell, P. (1976) Graphs with given neighbourhoods i. problèmes combinatorics at theorie des graphes. *Proc Coil Int CNRS, Orsay*, **260**: 219–223.
- Herschkowitz, J.I., Simin, K., Weigman, V.J., Mikaelian, I., Usary, J., Hu, Z., Rasmussen, K.E., Jones, L.P., Assefnia, S., Chandrasekharan, S., *et al.* (2007) Identification of conserved gene expression features between murine mammary carcinoma models and human breast tumors. *Genome Biol*, **8**(5): R76.
- Hillenmeyer, M.E. (2008) The chemical genomic portrait of yeast: uncovering a phenotype for all genes. *Science*, **320**: 362–365.
- Hoadley, K.A., Yau, C., Wolf, D.M., Cherniack, A.D., Tamborero, D., Ng, S., Leiserson, M.D., Niu, B., McLellan, M.D., Uzunangelov, V., *et al.* (2014) Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. *Cell*, **158**(4): 929–944.
- Hoehndorf, R., Hardy, N.W., Osumi-Sutherland, D., Tweedie, S., Schofield, P.N., and Gkoutos, G.V. (2013) Systematic analysis of experimental phenotype data reveals gene functions. *PLoS ONE*, **8**(4): e60847.
- Holm, S. (1979) A simple sequentially rejective multiple test procedure. *Scandinavian Journal of Statistics*, **6**(2): 65–70.
- Holme, P. and Kim, B.J. (2002) Growing scale-free networks with tunable clustering. *Physical Review E*, **65**(2): 026107.
- Hopkins, A.L. (2008) Network pharmacology: the next paradigm in drug discovery. *Nat Chem Biol*, **4**(11): 682–690.
- Hu, Z., Fan, C., Oh, D.S., Marron, J.S., He, X., Qaqish, B.F., Livasy, C., Carey, L.A., Reynolds, E., Dressler, L., *et al.* (2006) The molecular portraits of breast tumors are conserved across microarray platforms. *BMC Genomics*, **7**: 96.
- Huang, E., Cheng, S., Dressman, H., Pittman, J., Tsou, M., Horng, C., Bild, A., Iversen, E., Liao, M., Chen, C., *et al.* (2003) Gene expression predictors of breast cancer outcomes. *Lancet*, **361**: 1590–1596.
- Illumina, Inc (Illumina) (2017) Sequencing and array-based solutions for genetic research. <https://www.illumina.com/>. Accessed: 26/03/2017.

- International HapMap 3 Consortium (HapMap) (2003) The International HapMap Project. *Nature*, **426**(6968): 789–796.
- International Human Genome Sequencing Consortium (IHGSC) (2004) Finishing the euchromatic sequence of the human genome. *Nature*, **431**(7011): 931–945.
- Jerby-Arnon, L., Pfetzer, N., Waldman, Y., McGarry, L., James, D., Shanks, E., Seashore-Ludlow, B., Weinstock, A., Geiger, T., Clemons, P., *et al.* (2014) Predicting cancer-specific vulnerability via data-driven detection of synthetic lethality. *Cell*, **158**(5): 1199–1209.
- Joachims, T. (1999) Making large-scale support vector machine learning practical. In S. Bernhard, I. Kopr, J.C.B. Christopher, and J.S. Alexander (editors), *Advances in kernel methods*, 169–184. MIT Press.
- Ju, Z., Liu, W., Roebuck, P.L., Siwak, D.R., Zhang, N., Lu, Y., Davies, M.A., Akbani, R., Weinstein, J.N., Mills, G.B., *et al.* (2015) Development of a robust classifier for quality control of reverse-phase protein arrays. *Bioinformatics*, **31**(6): 912.
- Kaelin, Jr, W. (2005) The concept of synthetic lethality in the context of anticancer therapy. *Nat Rev Cancer*, **5**(9): 689–98.
- Kaelin, Jr, W. (2009) Synthetic lethality: a framework for the development of wiser cancer therapeutics. *Genome Med*, **1**: 99.
- Kakiuchi, M., Nishizawa, T., Ueda, H., Gotoh, K., Tanaka, A., Hayashi, A., Yamamoto, S., Tatsuno, K., Katoh, H., Watanabe, Y., *et al.* (2014) Recurrent gain-of-function mutations of RHOA in diffuse-type gastric carcinoma. *Nat Genet*, **46**(6): 583–587.
- Kamada, T. and Kawai, S. (1989) An algorithm for drawing general undirected graphs. *Information Processing Letters*, **31**(1): 7–15.
- Kandoth, C., Schultz, N., Cherniack, A.D., Akbani, R., Liu, Y., Shen, H., Robertson, A.G., Pashtan, I., Shen, R., Benz, C.C., *et al.* (2013) Integrated genomic characterization of endometrial carcinoma. *Nature*, **497**(7447): 67–73.
- Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., *et al.* (2001) Functional annotation of a full-length mouse cDNA collection. *Nature*, **409**(6821): 685–690.

- Kelley, R. and Ideker, T. (2005) Systematic interpretation of genetic interactions using protein networks. *Nat Biotech*, **23**(5): 561–566.
- Kelly, S., Chen, A., Guilford, P., and Black, M. (2017a) Synthetic lethal interaction prediction of target pathways in E-cadherin deficient breast cancers. Submitted to *BMC Genomics*.
- Kelly, S.T. (2013) *Statistical Predictions of Synthetic Lethal Interactions in Cancer*. Dissertation, University of Otago.
- Kelly, S.T., Single, A.B., Telford, B.J., Beetham, H.G., Godwin, T.D., Chen, A., Black, M.A., and Guilford, P.J. (2017b) Towards HDGC chemoprevention: vulnerabilities in E-cadherin-negative cells identified by genome-wide interrogation of isogenic cell lines and whole tumors. Submitted to *Cancer Prev Res*.
- Kozlov, K.N., Gursky, V.V., Kulakovskiy, I.V., and Samsonova, M.G. (2015) Sequence-based model of gap gene regulation network. *BMC Genomics*, **15**(Suppl 12): S6.
- Kranthi, S., Rao, S., and Manimaran, P. (2013) Identification of synthetic lethal pairs in biological systems through network information centrality. *Mol BioSyst*, **9**(8): 2163–2167.
- Lander, E.S. (2011) Initial impact of the sequencing of the human genome. *Nature*, **470**(7333): 187–197.
- Lander, E.S., Linton, L.M., Birren, B., Nusbaum, C., Zody, M.C., Baldwin, J., Devon, K., Dewar, K., Doyle, M., FitzHugh, W., *et al.* (2001) Initial sequencing and analysis of the human genome. *Nature*, **409**(6822): 860–921.
- Langmead, B., Trapnell, C., Pop, M., and Salzberg, S.L. (2009) Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biol*, **10**(3): R25.
- Latora, V. and Marchiori, M. (2001) Efficient behavior of small-world networks. *Phys Rev Lett*, **87**: 198701.
- Laufer, C., Fischer, B., Billmann, M., Huber, W., and Boutros, M. (2013) Mapping genetic interactions in human cancer cells with RNAi and multiparametric phenotyping. *Nat Methods*, **10**(5): 427–31.

- Law, C.W., Chen, Y., Shi, W., and Smyth, G.K. (2014) voom: precision weights unlock linear model analysis tools for RNA-seq read counts. *Genome Biol*, **15**(2): R29.
- Lawrence, M.S., Sougnez, C., Lichtenstein, L., Cibulskis, K., Lander, E., Gabriel, S.B., Getz, G., Ally, A., Balasundaram, M., Birol, I., *et al.* (2015) Comprehensive genomic characterization of head and neck squamous cell carcinomas. *Nature*, **517**(7536): 576–582.
- Le Meur, N. and Gentleman, R. (2008) Modeling synthetic lethality. *Genome Biol*, **9**(9): R135.
- Le Meur, N., Jiang, Z., Liu, T., Mar, J., and Gentleman, R.C. (2014) Slgi: Synthetic lethal genetic interaction. r package version 1.26.0.
- Lee, A.Y., Perreault, R., Harel, S., Boulier, E.L., Suderman, M., Hallett, M., and Jenna, S. (2010a) Searching for signaling balance through the identification of genetic interactors of the rab guanine-nucleotide dissociation inhibitor gdi-1. *PLoS ONE*, **5**(5): e10624.
- Lee, I., Lehner, B., Vavouri, T., Shin, J., Fraser, A.G., and Marcotte, E.M. (2010b) Predicting genetic modifier loci using functional gene networks. *Genome Research*, **20**(8): 1143–1153.
- Lee, I. and Marcotte, E.M. (2009) Effects of functional bias on supervised learning of a gene network model. *Methods Mol Biol*, **541**: 463–75.
- Lee, M.J., Ye, A.S., Gardino, A.K., Heijink, A.M., Sorger, P.K., MacBeath, G., and Yaffe, M.B. (2012) Sequential application of anticancer drugs enhances cell death by rewiring apoptotic signaling networks. *Cell*, **149**(4): 780–94.
- Lehner, B., Crombie, C., Tischler, J., Fortunato, A., and Fraser, A.G. (2006) Systematic mapping of genetic interactions in *caenorhabditis elegans* identifies common modifiers of diverse signaling pathways. *Nat Genet*, **38**(8): 896–903.
- Li, X.J., Mishra, S.K., Wu, M., Zhang, F., and Zheng, J. (2014) Syn-lethality: An integrative knowledge base of synthetic lethality towards discovery of selective anticancer therapies. *Biomed Res Int*, **2014**: 196034.
- Linehan, W.M., Spellman, P.T., Ricketts, C.J., Creighton, C.J., Fei, S.S., Davis, C., Wheeler, D.A., Murray, B.A., Schmidt, L., Vocke, C.D., *et al.* (2016) Comprehen-

- sive Molecular Characterization of Papillary Renal-Cell Carcinoma. *N Engl J Med*, **374**(2): 135–145.
- Lokody, I. (2014) Computational modelling: A computational crystal ball. *Nature Reviews Cancer*, **14**(10): 649–649.
- Lord, C.J., Tutt, A.N., and Ashworth, A. (2015) Synthetic lethality and cancer therapy: lessons learned from the development of PARP inhibitors. *Annu Rev Med*, **66**: 455–470.
- Lu, X., Kensche, P.R., Huynen, M.A., and Notebaart, R.A. (2013) Genome evolution predicts genetic interactions in protein complexes and reveals cancer drug targets. *Nat Commun*, **4**: 2124.
- Lu, X., Megchelenbrink, W., Notebaart, R.A., and Huynen, M.A. (2015) Predicting human genetic interactions from cancer genome evolution. *PLoS One*, **10**(5): e0125795.
- Lum, P.Y., Armour, C.D., Stepaniants, S.B., Cavet, G., Wolf, M.K., Butler, J.S., Hinshaw, J.C., Garnier, P., Prestwich, G.D., Leonardson, A., *et al.* (2004) Discovering modes of action for therapeutic compounds using a genome-wide screen of yeast heterozygotes. *Cell*, **116**(1): 121–137.
- Luo, J., Solimini, N.L., and Elledge, S.J. (2009) Principles of Cancer Therapy: Oncogene and Non-oncogene Addiction. *Cell*, **136**(5): 823–837.
- Machado, J., Olivera, C., Carvalh, R., Soares, P., Berx, G., Caldas, C., Sercuca, R., Carneiro, F., and Sorbrinho-Simoes, M. (2001) E-cadherin gene (*CDH1*) promoter methylation as the second hit in sporadic diffuse gastric carcinoma. *Oncogene*, **20**: 1525–1528.
- Masciari, S., Larsson, N., Senz, J., Boyd, N., Kaurah, P., Kandel, M.J., Harris, L.N., Pinheiro, H.C., Troussard, A., Miron, P., *et al.* (2007) Germline E-cadherin mutations in familial lobular breast cancer. *J Med Genet*, **44**(11): 726–31.
- Mattison, J., van der Weyden, L., Hubbard, T., and Adams, D.J. (2009) Cancer gene discovery in mouse and man. *Biochim Biophys Acta*, **1796**(2): 140–161.
- Maxam, A.M. and Gilbert, W. (1977) A new method for sequencing DNA. *Proceedings of the National Academy of Science*, **74**(2): 560–564.

- McCourt, C.M., McArt, D.G., Mills, K., Catherwood, M.A., Maxwell, P., Waugh, D.J., Hamilton, P., O’Sullivan, J.M., and Salto-Tellez, M. (2013) Validation of next generation sequencing technologies in comparison to current diagnostic gold standards for BRAF, EGFR and KRAS mutational analysis. *PLoS ONE*, **8**(7): e69604.
- McLachlan, J., George, A., and Banerjee, S. (2016) The current status of parp inhibitors in ovarian cancer. *Tumori*, **102**(5): 433–440.
- McLendon, R., Friedman, A., Bigner, D., Van Meir, E.G., Brat, D.J., Mastrogianakis, G.M., Olson, J.J., Mikkelsen, T., Lehman, N., Aldape, K., *et al.* (2008) Comprehensive genomic characterization defines human glioblastoma genes and core pathways. *Nature*, **455**(7216): 1061–1068.
- Miles, D.W. (2001) Update on HER-2 as a target for cancer therapy: herceptin in the clinical setting. *Breast Cancer Res*, **3**(6): 380–384.
- Mortazavi, A., Williams, B.A., McCue, K., Schaeffer, L., and Wold, B. (2008) Mapping and quantifying mammalian transcriptomes by RNA-Seq. *Nat Methods*, **5**(7): 621–628.
- Muzny, D.M., Bainbridge, M.N., Chang, K., Dinh, H.H., Drummond, J.A., Fowler, G., Kovar, C.L., Lewis, L.R., Morgan, M.B., Newsham, I.F., *et al.* (2012) Comprehensive molecular characterization of human colon and rectal cancer. *Nature*, **487**(7407): 330–337.
- Nagalla, S., Chou, J.W., Willingham, M.C., Ruiz, J., Vaughn, J.P., Dubey, P., Lash, T.L., Hamilton-Dutoit, S.J., Bergh, J., Sotiriou, C., *et al.* (2013) Interactions between immunity, proliferation and molecular subtype in breast cancer prognosis. *Genome Biol*, **14**(4): R34.
- Neeley, E.S., Kornblau, S.M., Coombes, K.R., and Baggerly, K.A. (2009) Variable slope normalization of reverse phase protein arrays. *Bioinformatics*, **25**(11): 1384.
- Novomestky, F. (2012) *matrixcalc: Collection of functions for matrix calculations*. R package version 1.0-3.
- Oliveira, C., Senz, J., Kaurah, P., Pinheiro, H., Sanges, R., Haegert, A., Corso, G., Schouten, J., Fitzgerald, R., Vogelsang, H., *et al.* (2009) Germline *CDH1* deletions in hereditary diffuse gastric cancer families. *Human Molecular Genetics*, **18**(9): 1545–1555.

- Oliveira, C., Seruca, R., Hoogerbrugge, N., Ligtenberg, M., and Carneiro, F. (2013) Clinical utility gene card for: Hereditary diffuse gastric cancer (HDGC). *Eur J Hum Genet*, **21**(8).
- Pandey, G., Zhang, B., Chang, A.N., Myers, C.L., Zhu, J., Kumar, V., and Schadt, E.E. (2010) An integrative multi-network and multi-classifier approach to predict genetic interactions. *PLoS Comput Biol*, **6**(9).
- Parker, J., Mullins, M., Cheung, M., Leung, S., Voduc, D., Vickery, T., Davies, S., Fauron, C., He, X., Hu, Z., *et al.* (2009) Supervised risk predictor of breast cancer based on intrinsic subtypes. *Journal of Clinical Oncology*, **27**(8): 1160–1167.
- Peltonen, L. and McKusick, V.A. (2001) Genomics and medicine. Dissecting human disease in the postgenomic era. *Science*, **291**(5507): 1224–1229.
- Pereira, B., Chin, S.F., Rueda, O.M., Vollan, H.K., Provenzano, E., Bardwell, H.A., Pugh, M., Jones, L., Russell, R., Sammut, S.J., *et al.* (2016) Erratum: The somatic mutation profiles of 2,433 breast cancers refine their genomic and transcriptomic landscapes. *Nat Commun*, **7**: 11908.
- Perou, C.M., Sørlie, T., Eisen, M.B., van de Rijn, M., Jeffrey, S.S., Rees, C.A., Pollack, J.R., Ross, D.T., Johnsen, H., Akslen, L.A., *et al.* (2000) Molecular portraits of human breast tumours. *Nature*, **406**(6797): 747–752.
- Pleasance, E.D., Cheetham, R.K., Stephens, P.J., McBride, D.J., Humphray, S.J., Greenman, C.D., Varela, I., Lin, M.L., Ordonez, G.R., Bignell, G.R., *et al.* (2010) A comprehensive catalogue of somatic mutations from a human cancer genome. *Nature*, **463**(7278): 191–196.
- Polyak, K. and Weinberg, R.A. (2009) Transitions between epithelial and mesenchymal states: acquisition of malignant and stem cell traits. *Nat Rev Cancer*, **9**(4): 265–73.
- Prahallad, A., Sun, C., Huang, S., Di Nicolantonio, F., Salazar, R., Zecchin, D., Beijersbergen, R.L., Bardelli, A., and Bernards, R. (2012) Unresponsiveness of colon cancer to *BRAF*(v600e) inhibition through feedback activation of egfr. *Nature*, **483**(7387): 100–3.
- R Core Team (2016) *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria. R version 3.3.2.

- Ravnan, M.C. and Matalaka, M.S. (2012) Vemurafenib in patients with *BRAF* v600e mutation-positive advanced melanoma. *Clin Ther*, **34**(7): 1474–86.
- Ritchie, M.E., Phipson, B., Wu, D., Hu, Y., Law, C.W., Shi, W., and Smyth, G.K. (2015) limma powers differential expression analyses for RNA-sequencing and microarray studies. *Nucleic Acids Research*, **43**(7): e47.
- Robin, J.D., Ludlow, A.T., LaRanger, R., Wright, W.E., and Shay, J.W. (2016) Comparison of DNA Quantification Methods for Next Generation Sequencing. *Sci Rep*, **6**: 24067.
- Robinson, M.D. and Oshlack, A. (2010) A scaling normalization method for differential expression analysis of RNA-seq data. *Genome Biol*, **11**(3): R25.
- Roguev, A., Bandyopadhyay, S., Zofall, M., Zhang, K., Fischer, T., Collins, S.R., Qu, H., Shales, M., Park, H.O., Hayles, J., *et al.* (2008) Conservation and rewiring of functional modules revealed by an epistasis map in fission yeast. *Science*, **322**(5900): 405–10.
- Rung, J. and Brazma, A. (2013) Reuse of public genome-wide gene expression data. *Nat Rev Genet*, **14**(2): 89–99.
- Rustici, G., Kolesnikov, N., Brandizi, M., Burdett, T., Dylag, M., Emam, I., Farne, A., Hastings, E., Ison, J., Keays, M., *et al.* (2013) ArrayExpress update—trends in database growth and links to data analysis tools. *Nucleic Acids Res*, **41**(Database issue): D987–990.
- Ryan, C., Lord, C., and Ashworth, A. (2014) Daisy: Picking synthetic lethals from cancer genomes. *Cancer Cell*, **26**(3): 306–308.
- Sander, J.D. and Joung, J.K. (2014) Crispr-cas systems for editing, regulating and targeting genomes. *Nat Biotechnol*, **32**(4): 347–55.
- Sanger, F. and Coulson, A. (1975) A rapid method for determining sequences in dna by primed synthesis with dna polymerase. *Journal of Molecular Biology*, **94**(3): 441 – 448.
- Scheuer, L., Kauff, N., Robson, M., Kelly, B., Barakat, R., Satagopan, J., Ellis, N., Hensley, M., Boyd, J., Borgen, P., *et al.* (2002) Outcome of preventive surgery and screening for breast and ovarian cancer in BRCA mutation carriers. *J Clin Oncol*, **20**(5): 1260–1268.

- Semb, H. and Christofori, G. (1998) The tumor-suppressor function of E-cadherin. *Am J Hum Genet*, **63**(6): 1588–93.
- Sing, T., Sander, O., Beerenwinkel, N., and Lengauer, T. (2005) Rocr: visualizing classifier performance in r. *Bioinformatics*, **21**(20): 7881.
- Slurm development team (Slurm) (2017) Slurm workload manager. <https://slurm.schedmd.com/>. Accessed: 25/03/2017.
- Sørlie, T., Perou, C.M., Tibshirani, R., Aas, T., Geisler, S., Johnsen, H., Hastie, T., Eisen, M.B., van de Rijn, M., Jeffrey, S.S., *et al.* (2001) Gene expression patterns of breast carcinomas distinguish tumor subclasses with clinical implications. *Proc Natl Acad Sci USA*, **98**(19): 10869–10874.
- Stajich, J.E. and Lapp, H. (2006) Open source tools and toolkits for bioinformatics: significance, and where are we? *Brief Bioinformatics*, **7**(3): 287–296.
- Stratton, M.R., Campbell, P.J., and Futreal, P.A. (2009) The cancer genome. *Nature*, **458**(7239): 719–724.
- Ström, C. and Helleday, T. (2012) Strategies for the use of poly(adenosine diphosphate ribose) polymerase (parp) inhibitors in cancer therapy. *Biomolecules*, **2**(4): 635–649.
- Sun, C., Wang, L., Huang, S., Heynen, G.J.J.E., Prahallad, A., Robert, C., Haanen, J., Blank, C., Wesseling, J., Willems, S.M., *et al.* (2014) Reversible and adaptive resistance to *BRAF*(v600e) inhibition in melanoma. *Nature*, **508**(7494): 118–122.
- Taylor, I.W., Linding, R., Warde-Farley, D., Liu, Y., Pesquita, C., Faria, D., Bull, S., Pawson, T., Morris, Q., and Wrana, J.L. (2009) Dynamic modularity in protein interaction networks predicts breast cancer outcome. *Nat Biotechnol*, **27**(2): 199–204.
- Telford, B.J., Chen, A., Beetham, H., Frick, J., Brew, T.P., Gould, C.M., Single, A., Godwin, T., Simpson, K.J., and Guilford, P. (2015) Synthetic lethal screens identify vulnerabilities in gpcr signalling and cytoskeletal organization in E-cadherin-deficient cells. *Mol Cancer Ther*, **14**(5): 1213–1223.
- The 1000 Genomes Project Consortium (1000 Genomes) (2010) A map of human genome variation from population-scale sequencing. *Nature*, **467**(7319): 1061–1073.

- The Cancer Genome Atlas Research Network (TCGA) (2012) Comprehensive molecular portraits of human breast tumours. *Nature*, **490**(7418): 61–70.
- The Cancer Genome Atlas Research Network (TCGA) (2017a) The Cancer Genome Atlas Project. <https://cancergenome.nih.gov/>. Accessed: 26/03/2017.
- The Cancer Genome Atlas Research Network (TCGA) (2017b) The Cancer Genome Atlas Project Data Portal. <https://tcga-data.nci.nih.gov/>. Accessed: 06/02/2017 (via cBioPortal).
- The Cancer Society of New Zealand (Cancer Society of NZ) (2017) What is cancer? <https://otago-southland.cancernz.org.nz/en/cancer-information/other-links/what-is-cancer-3/>. Accessed: 22/03/2017.
- The Catalogue Of Somatic Mutations In Cancer (COSMIC) (2016) Cosmic: The catalogue of somatic mutations in cancer. <http://cancer.sanger.ac.uk/cosmic>. Release 79 (23/08/2016), Accessed: 05/02/2017.
- The Comprehensive R Archive Network (CRAN) (2017) Cran. <https://cran.r-project.org/>. Accessed: 24/03/2017.
- The ENCODE Project Consortium (ENCODE) (2004) The ENCODE (ENCyclopedia Of DNA Elements) Project. *Science*, **306**(5696): 636–640.
- The International Cancer Genome Consortium (ICGC) (2017) ICGC Data Portal. <https://dcc.icgc.org/>. Accessed: 06/02/2017.
- The National Cancer Institute (NCI) (2015) The genetics of cancer. <https://www.cancer.gov/about-cancer/causes-prevention/genetics>. Published: 22/04/2015, Accessed: 22/03/2017.
- The New Zealand eScience Infrastructure (NeSI) (2017) NeSI. <https://www.nesi.org.nz/>. Accessed: 25/03/2017.
- The Pharmaceutical Management Agency (PHARMAC) (2016) Approval of multi-product funding proposal with roche.
- Tierney, L., Rossini, A.J., Li, N., and Sevcikova, H. (2015) *snow: Simple Network of Workstations*. R package version 0.4-2.

- Tiong, K.L., Chang, K.C., Yeh, K.T., Liu, T.Y., Wu, J.H., Hsieh, P.H., Lin, S.H., Lai, W.Y., Hsu, Y.C., Chen, J.Y., *et al.* (2014) Csnk1e/ctnnb1 are synthetic lethal to tp53 in colorectal cancer and are markers for prognosis. *Neoplasia*, **16**(5): 441–50.
- Tischler, J., Lehner, B., and Fraser, A.G. (2008) Evolutionary plasticity of genetic interaction networks. *Nat Genet*, **40**(4): 390–391.
- Tomasetti, C. and Vogelstein, B. (2015) Cancer etiology. Variation in cancer risk among tissues can be explained by the number of stem cell divisions. *Science*, **347**(6217): 78–81.
- Tong, A.H., Evangelista, M., Parsons, A.B., Xu, H., Bader, G.D., Page, N., Robinson, M., Raghibizadeh, S., Hogue, C.W., Bussey, H., *et al.* (2001) Systematic genetic analysis with ordered arrays of yeast deletion mutants. *Science*, **294**(5550): 2364–8.
- Tong, A.H., Lesage, G., Bader, G.D., Ding, H., Xu, H., Xin, X., Young, J., Berriz, G.F., Brost, R.L., Chang, M., *et al.* (2004) Global mapping of the yeast genetic interaction network. *Science*, **303**(5659): 808–13.
- Travers, J. and Milgram, S. (1969) An experimental study of the small world problem. *Sociometry*, **32**(4): 425–443.
- Tsai, H.C., Li, H., Van Neste, L., Cai, Y., Robert, C., Rassool, F.V., Shin, J.J., Harbom, K.M., Beaty, R., Pappou, E., *et al.* (2012) Transient low doses of dna-demethylating agents exert durable antitumor effects on hematological and epithelial tumor cells. *Cancer Cell*, **21**(3): 430–46.
- Tutt, A., Robson, M., Garber, J.E., Domchek, S.M., Audeh, M.W., Weitzel, J.N., Friedlander, M., Arun, B., Loman, N., Schmutzler, R.K., *et al.* (2010) Oral poly(adp-ribose) polymerase inhibitor olaparib in patients with *BRCA1* or *BRCA2* mutations and advanced breast cancer: a proof-of-concept trial. *Lancet*, **376**(9737): 235–44.
- van der Meer, R., Song, H.Y., Park, S.H., Abdulkadir, S.A., and Roh, M. (2014) RNAi screen identifies a synthetic lethal interaction between PIM1 overexpression and PLK1 inhibition. *Clinical Cancer Research*, **20**(12): 3211–3221.
- van Steen, K. (2012) Travelling the world of genegene interactions. *Briefings in Bioinformatics*, **13**(1): 1–19.
- van Steen, M. (2010) *Graph Theory and Complex Networks: An Introduction*. Maarten van Steen, VU Amsterdam.

- Vapnik, V.N. (1995) *The nature of statistical learning theory*. Springer-Verlag New York, Inc.
- Vargas, J.J., Gusella, G., Najfeld, V., Klotman, M., and Cara, A. (2004) Novel integrase-defective lentiviral episomal vectors for gene transfer. *Hum Gene Ther*, **15**: 361–372.
- Vizeacoumar, F.J., Arnold, R., Vizeacoumar, F.S., Chandrashekhar, M., Buzina, A., Young, J.T., Kwan, J.H., Sayad, A., Mero, P., Lawo, S., *et al.* (2013) A negative genetic interaction map in isogenic cancer cell lines reveals cancer cell vulnerabilities. *Mol Syst Biol*, **9**: 696.
- Vogelstein, B., Papadopoulos, N., Velculescu, V.E., Zhou, S., Diaz, L.A., and Kinzler, K.W. (2013) Cancer genome landscapes. *Science*, **339**(6127): 1546–1558.
- Vos, C.B., Cleton-Jansen, A.M., Berx, G., de Leeuw, W.J., ter Haar, N.T., van Roy, F., Cornelisse, C.J., Peterse, J.L., and van de Vijver, M.J. (1997) E-cadherin inactivation in lobular carcinoma in situ of the breast: an early event in tumorigenesis. *Br J Cancer*, **76**(9): 1131–3.
- Wang, K., Singh, D., Zeng, Z., Coleman, S.J., Huang, Y., Savich, G.L., He, X., Mieczkowski, P., Grimm, S.A., Perou, C.M., *et al.* (2010) MapSplice: accurate mapping of RNA-seq reads for splice junction discovery. *Nucleic Acids Res*, **38**(18): e178.
- Wang, K., Yuen, S.T., Xu, J., Lee, S.P., Yan, H.H., Shi, S.T., Siu, H.C., Deng, S., Chu, K.M., Law, S., *et al.* (2014) Whole-genome sequencing and comprehensive molecular profiling identify new driver mutations in gastric cancer. *Nat Genet*, **46**(6): 573–582.
- Wang, X. and Simon, R. (2013) Identification of potential synthetic lethal genes to p53 using a computational biology approach. *BMC Medical Genomics*, **6**(1): 30.
- Wappett, M. (2014) Bisep: Toolkit to identify candidate synthetic lethality. r package version 2.0.
- Wappett, M., Dulak, A., Yang, Z.R., Al-Watban, A., Bradford, J.R., and Dry, J.R. (2016) Multi-omic measurement of mutually exclusive loss-of-function enriches for candidate synthetic lethal gene pairs. *BMC Genomics*, **17**: 65.

- Warnes, G.R., Bolker, B., Bonebakker, L., Gentleman, R., Liaw, W.H.A., Lumley, T., Maechler, M., Magnusson, A., Moeller, S., Schwartz, M., *et al.* (2015) *gplots: Various R Programming Tools for Plotting Data*. R package version 2.17.0.
- Watts, D.J. and Strogatz, S.H. (1998) Collective dynamics of 'small-world' networks. *Nature*, **393**(6684): 440–2.
- Weinstein, I.B. (2000) Disorders in cell circuitry during multistage carcinogenesis: the role of homeostasis. *Carcinogenesis*, **21**(5): 857–864.
- Weinstein, J.N., Akbani, R., Broom, B.M., Wang, W., Verhaak, R.G., McConkey, D., Lerner, S., Morgan, M., Creighton, C.J., Smith, C., *et al.* (2014) Comprehensive molecular characterization of urothelial bladder carcinoma. *Nature*, **507**(7492): 315–322.
- Weinstein, J.N., Collisson, E.A., Mills, G.B., Shaw, K.R., Ozenberger, B.A., Ellrott, K., Shmulevich, I., Sander, C., Stuart, J.M., Chang, K., *et al.* (2013) The Cancer Genome Atlas Pan-Cancer analysis project. *Nat Genet*, **45**(10): 1113–1120.
- Wickham, H. and Chang, W. (2016) *devtools: Tools to Make Developing R Packages Easier*. R package version 1.12.0.
- Wickham, H., Danenberg, P., and Eugster, M. (2017) *roxygen2: In-Line Documentation for R*. R package version 6.0.1.
- Wong, S.L., Zhang, L.V., Tong, A.H.Y., Li, Z., Goldberg, D.S., King, O.D., Lesage, G., Vidal, M., Andrews, B., Bussey, H., *et al.* (2004) Combining biological networks to predict genetic interactions. *Proceedings of the National Academy of Sciences of the United States of America*, **101**(44): 15682–15687.
- World Health Organization (WHO) (2017) Fact sheet: Cancer. <http://www.who.int/mediacentre/factsheets/fs297/en/>. Updated February 2017, Accessed: 22/03/2017.
- Wu, M., Li, X., Zhang, F., Li, X., Kwoh, C.K., and Zheng, J. (2014) In silico prediction of synthetic lethality by meta-analysis of genetic interactions, functions, and pathways in yeast and human cancer. *Cancer Inform*, **13**(Suppl 3): 71–80.
- Yu, H. (2002) Rmpi: Parallel statistical computing in r. *R News*, **2**(2): 10–14.

- Zhang, F., Wu, M., Li, X.J., Li, X.L., Kwoh, C.K., and Zheng, J. (2015) Predicting essential genes and synthetic lethality via influence propagation in signaling pathways of cancer cell fates. *J Bioinform Comput Biol*, **13**(3): 1541002.
- Zhang, J., Baran, J., Cros, A., Guberman, J.M., Haider, S., Hsu, J., Liang, Y., Rivkin, E., Wang, J., Whitty, B., *et al.* (2011) International cancer genome consortium data portala one-stop shop for cancer genomics data. *Database: The Journal of Biological Databases and Curation*, **2011**: bar026.
- Zhong, W. and Sternberg, P.W. (2006) Genome-wide prediction of c. elegans genetic interactions. *Science*, **311**(5766): 1481–1484.
- Zweig, M.H. and Campbell, G. (1993) Receiver-operating characteristic (roc) plots: a fundamental evaluation tool in clinical medicine. *Clinical Chemistry*, **39**(4): 561–577.