Lattice of Topologies

Jorge Bruno

School of Mathematics, Statistics, and Applied Mathematics. NUI, Galway.

Supervised by Dr. Aisling McCluskey

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Motivation

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Given a set X and two arbitrary topologies, τ and σ (on the given set), can we trace a continuous path, $\gamma : [0, 1] \to \mathsf{Top}(X)$, so that $\gamma(0) = \tau$ and $\gamma(1) = \sigma$?

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Maybe... However, such a path will not be canonical; for reasons that we will shortly discover.

$2^{\mathcal{P}(X)}$ and Top(X)

First, the ambient set: $2^{\mathcal{P}(X)}$

Let $2 = \{0, 1\}$ be given the discrete topology and take $|\mathcal{P}(X)|$ copies of it. Next, define $2^{\mathcal{P}(X)} = \Pi_{\beta \in |\mathcal{P}(X)|} 2_\beta$ - the topological product of all such copies.

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There are two, equivalent, ways of looking at this space:

- as a space where points are strings of 0s and 1s of length $|\mathcal{P}(X)|$, or
- simply as $\mathcal{P}(\mathcal{P}(X))$ - in which case, a topology on X is a point in $\mathcal{P}(\mathcal{P}(X))$.

We can biject the above by sending a string of 0s and 1s to $A \subseteq \mathcal{P}(X)$ for which $A \in \mathcal{A}$ *iff* the A^{th} entry is a 1.

$2^{\mathcal{P}(X)}$ and Top(X)

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As a topological space, $2^{\mathcal{P}(X)}$ is totally-disconnected, Hausdorff and compact. Sub-basic open sets are defined via projections. Equivalently, in $\mathcal{P}(\mathcal{P}(X))$ a basic open set is of the form

$$A^{+} = \{\mathcal{A} \subseteq \mathcal{P}(X) \mid A \in \mathcal{A}\},$$

or

$$A^{-} = \{\mathcal{A} \subseteq \mathcal{P}(X) \mid A \notin \mathcal{A}\}.$$

$2^{\mathcal{P}(X)}$ and Top(X)

Top(X) as a subspace of $2^{\mathcal{P}(X)}$

Since $2^{\mathcal{P}(X)}$ is a compact T_2 space, closed subsets are then compact. For instance:

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- the set of all ultra-filters and filters on X,
- the set of all ideals on X,
- the set of all sub-lattices of $\mathcal{P}(X)$, and
- the set of all sub-lattices of $\mathcal{P}(X)$ with X and $\emptyset$ in them (LatB(X)).

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Let us look at a more concrete example of X, for instance $X = Y \cup \mathcal{P}(Y)$ for Y a set, then

Theorem

For X *as above and* $A, B \subseteq X$ *we have* A^B *and* $\mathrm{Inj}(A^B) = \{f \in A^B \mid f \text{ is injective}\}$ *as compact subsets of* $2^{\mathcal{P}(X)}$.

$2^{\mathcal{P}(X)}$ and Top(X)

Top(X) as a subspace of $2^{\mathcal{P}(X)}$

In view of the above we have a nice model-theoretic result.

Theorem

Let $\mathcal{L}$ be a first order language sufficiently strong to describe the lattice-theoretic properties of $\mathcal{P}(X)$. Then a subset of $2^{\mathcal{P}(X)}$ is compact if it can be defined in terms of a universal sentence of $\mathcal{L}$.

The converse is false whenever X is infinite.

$2^{\mathcal{P}(X)}$ and Top(X)

Top(X) as a subspace of $2^{\mathcal{P}(X)}$

What about Top(X)? Well... let's see

Theorem

LatB(X) *is closed and contains Top*(X) *as a proper dense subset.*

Thus, Top(X) is not compact. For compact sets and closed sets are indistinguishable under a T_2 compact topology.

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Consequently, Top(X) is not locally compact! However,

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Theorem

Any sub-lattice of $2^{\mathcal{P}(X)}$ *is join and meet continuous.*

Since Top(X) is a meet sub-lattice of $2^{\mathcal{P}(X)}$, then it is meet continuous.

$2^{\mathcal{P}(X)}$ and $\mathrm{Top}(X)$

$\mathrm{Top}(X)$ as a subspace of $2^{\mathcal{P}(X)}$

Lastly, since total-disconnectedness is a hereditary property, a continuous path from $[0,1]$ into $\mathrm{Top}(X)$ is only possible with constant maps (unless we topologise $[0,1]$ with the Sorgenfrey topology!).

Analysis of an Observational Study in Colorectal Cancer Patients

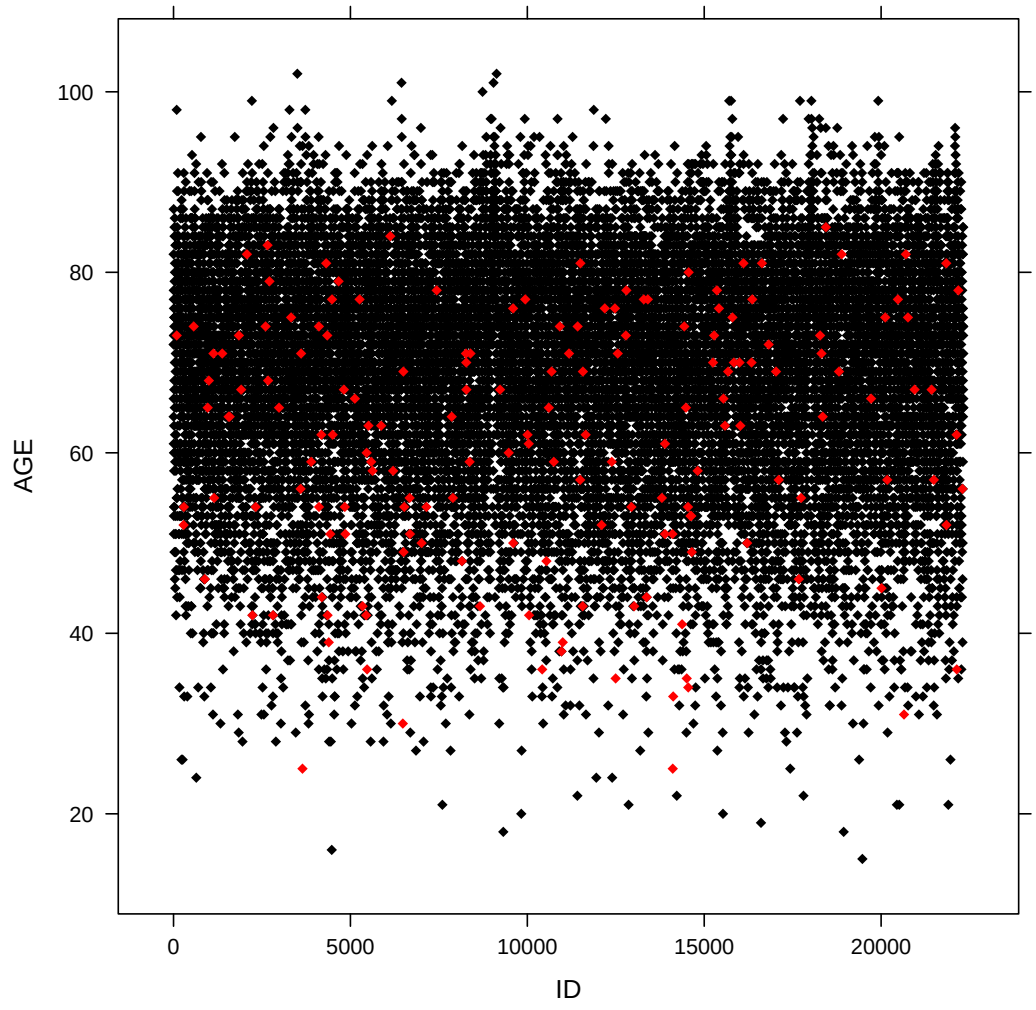
Cara Dooley

4 November 2010

Introduction

- An observational study using data from the National Cancer Registry of Ireland (NCRI)
- All individuals with colorectal cancer from January 1994 to December 2005 (n=22323)
- Subgroup of interest those with a secondary disease inflammatory bowel disease (IBD) (n=170)

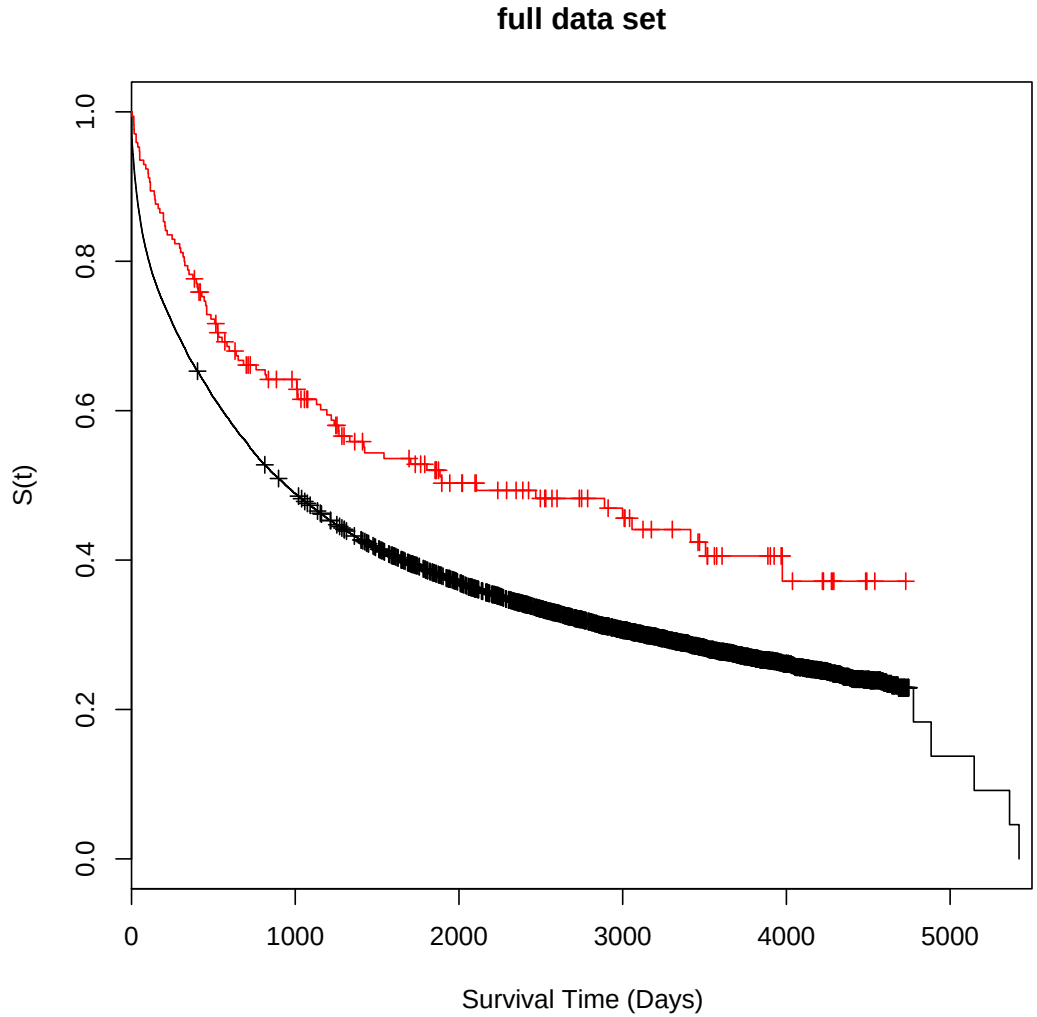
Age



Inital Analysis

- Initial analyis was to determine any differences between the two groups
- Using logistic regression
- Age, Gender, ICD10 Smoking Status and Grade were all found to be significantly different between the two groups

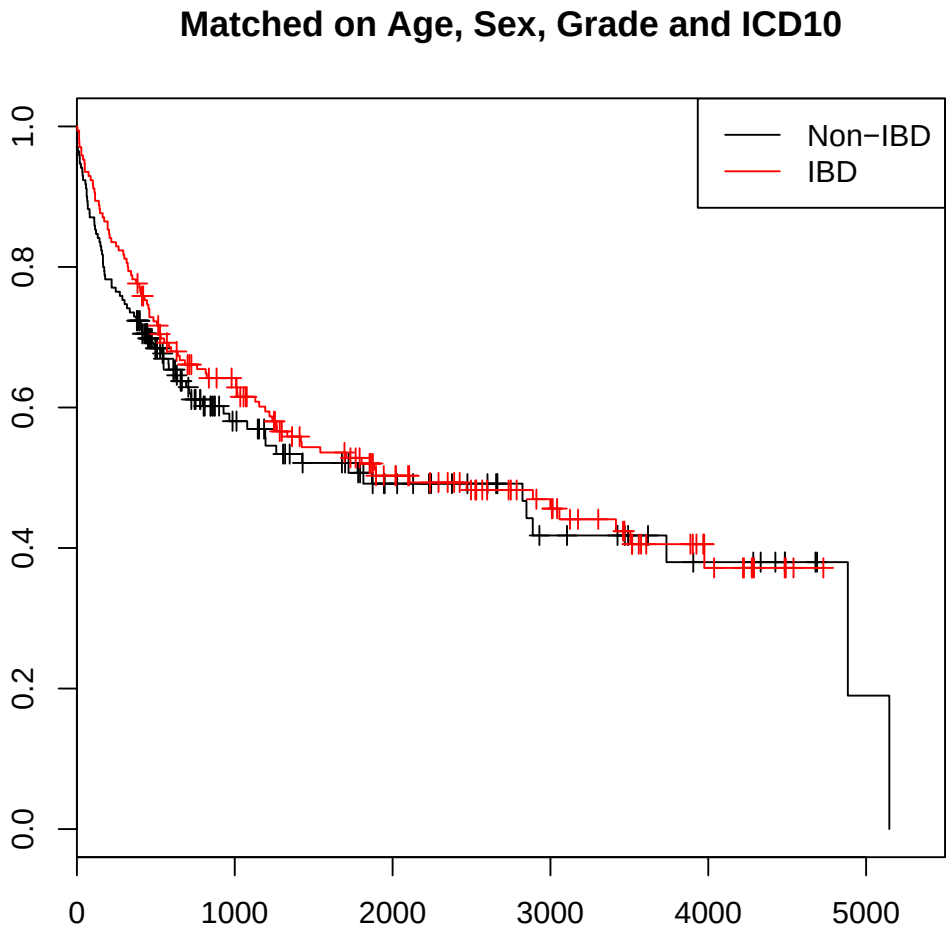
Whole Data Set : Kaplan-Meier



Why Match?

- Ideally, we would start with a designed experiment, this is not always possible. For example, Observational Studies
- We try to add in a design to the observational study, by matching controls and cases based on the information recorded
- So then, we have two groups of similar patients at time of diagnosis

After Matching:Kaplan-Meier



Weighted Kaplan-Meier

- Winnett and Sassieni (JASA 2002) suggest full matching and weighting the Kaplan- Meier estimates by the number of controls matched to each case.

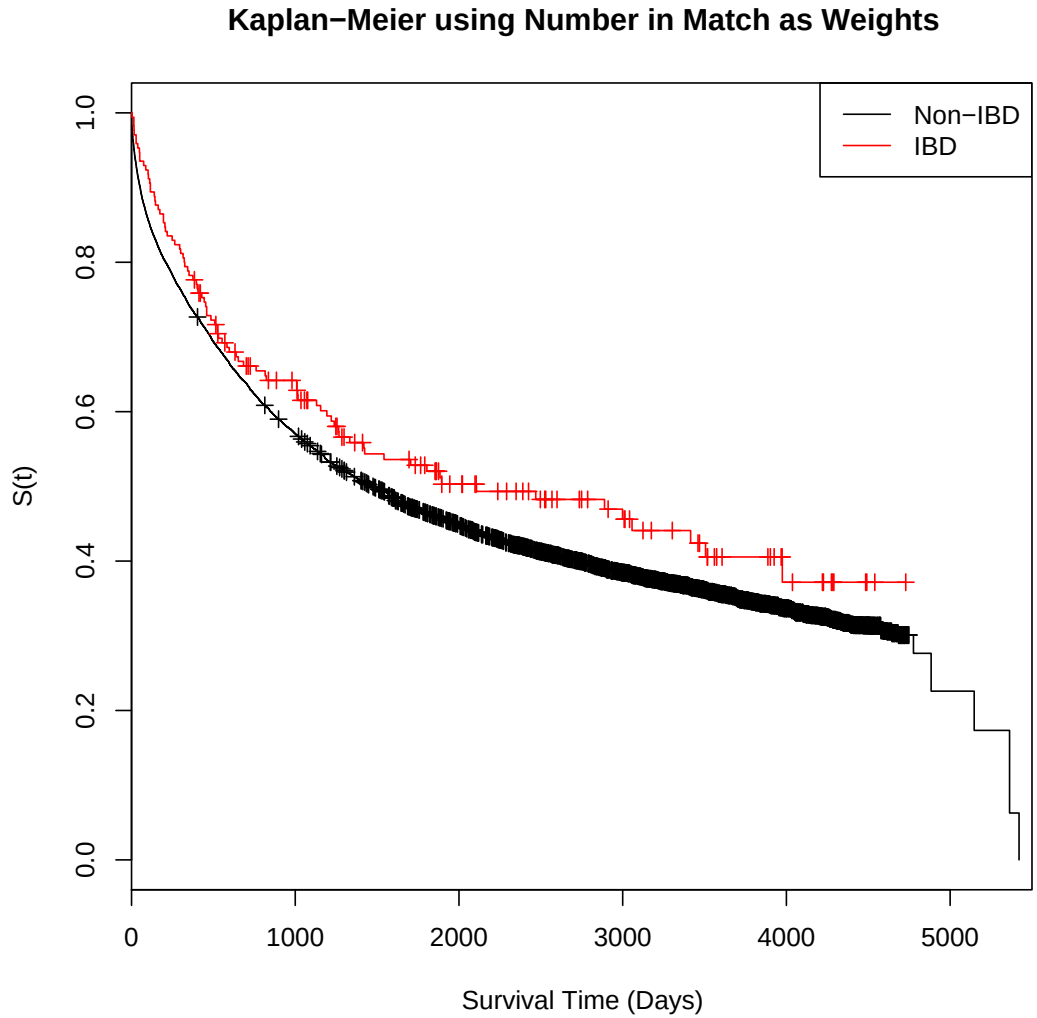
$$\hat{S}^w(t) = \prod_{u:u\leq t} [1 - \frac{\sum_{j=1}^{k} w_j d_j(u)}{\sum_{j=1}^{k} w_j r_j(u)}$$

where

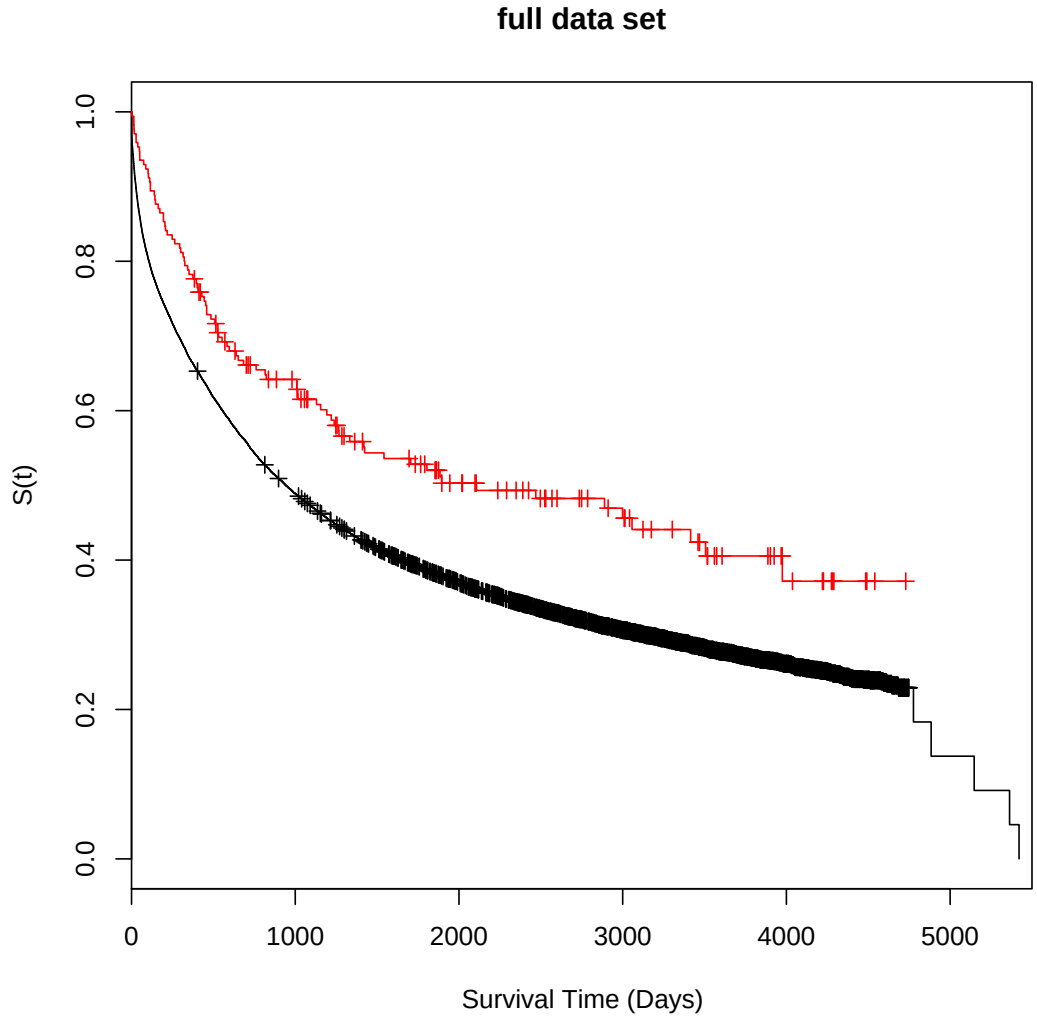
$d_j(u)$ = number of events at u in stratum j
$r_j(u)$= number at risk at u in stratum j
$w_j = \frac{1}{mj}$ reciprocal of the stratum size

- If the same number of controls are matched to each case this reduces to the usual KM estimates.

Weighted Kaplan-Meier



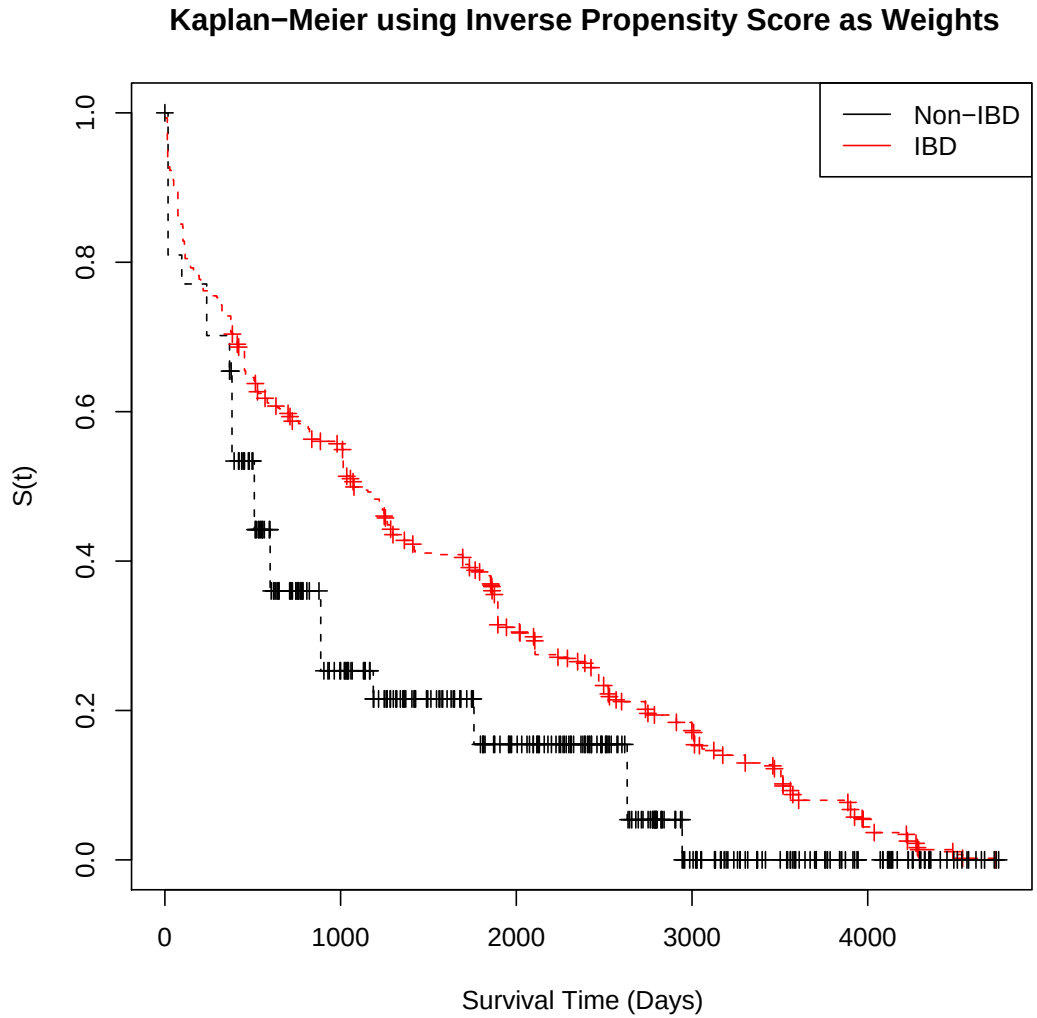
Whole Data Set: Kaplan-Meier



Adjusted Kaplan-Meier Estimator - AKME

- Xie and Liu (Stats in Med, 2005) suggest using the inverse of the propensity score to weight the Kaplan Meier. (AKME)
- Assign a weight $w_{ik} = 1/p_{ik}$ to each individual, where p_{ik} is the propensity score for individual i in group k
- Weighted number of events
  $d_{jk}^w = \sum_{i:T_i=t_j} w_{ik}\delta_i I(X_i = k) = \sum_{i:T_i=t_j} \frac{\delta_i I(X_i=k)}{p_{ik}}$
- Weighted number at risk
  $Y_{jk}^w = \sum_{i:T_i\geq t_j} w_{ik} I(X_i = k) = \sum_{i:T_i\geq t_j} \frac{I(X_i=k)}{p_{ik}}$
- So the AKME for the kth group is
  $$\hat{S}^k(t) = \begin{cases} 1 & \text{if } t < t_i \\ \prod_{t_j \leq t}[1 - d_{jk}^w / Y_{jk}^w] & \text{if } t_i \leq t \end{cases}$$

AKME


Kaplan−Meier using Inverse Propensity Score as Weights
Non−IBD
IBD
S(t)
0.0
0.2
0.4
0.6
0.8
1.0
0
1000
2000
3000
4000
Survival Time (Days)

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Gastroenterology, Submitted.


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Angela Winnett and Peter Sasieni.
Adjusted Nelson-Aalen estimates with retrospective matching.
Journal of the American Statistical Association,
97(457):245–256, 2002.


Jun Xie and Chaofeng Liu.
Adjusted Kaplan-Meier estimator and log-rank test with inverse probability of treatment weighting for survival data.
Statistics in Medicine, 24(20):3089–3110, 2005.

The Discontinuity Geometry Framework

N.Humphries and P.T.Piiroinen

n.humphries1@nuigalway.ie petri.piiroinen@nuigalway.ie

School of Mathematics, Statistics and Applied Mathematics,
National University of Ireland, Galway

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Impacting Systems

Real-world examples of hybrid dynamical systems include electrical (e.g. relay systems), mechanical (e.g. gearing systems), biological (e.g. cell differentiation) and economic (e.g. interest rate change effects) systems or even their control. They can be modelled with a smooth free-flight inbetween 'impacts' - e.g. a combination of an ODE with a discrete map (that introduces a discontinuities).

Often they exhibit periodic steady-state solutions (orbits) with very regular behaviour over a wide range of parameter variation, but then suddenly lose stability at critical parameter values without going through any of the standard (i.e. smooth) bifurcations.

While many techniques already exist for the local analysis of such systems, there is little or no understanding of them globally, and so this study is trying to build such a global picture by using a geometric/topological approach - **Discontinuity Geometry**.

The Discontinuity Surface V_c

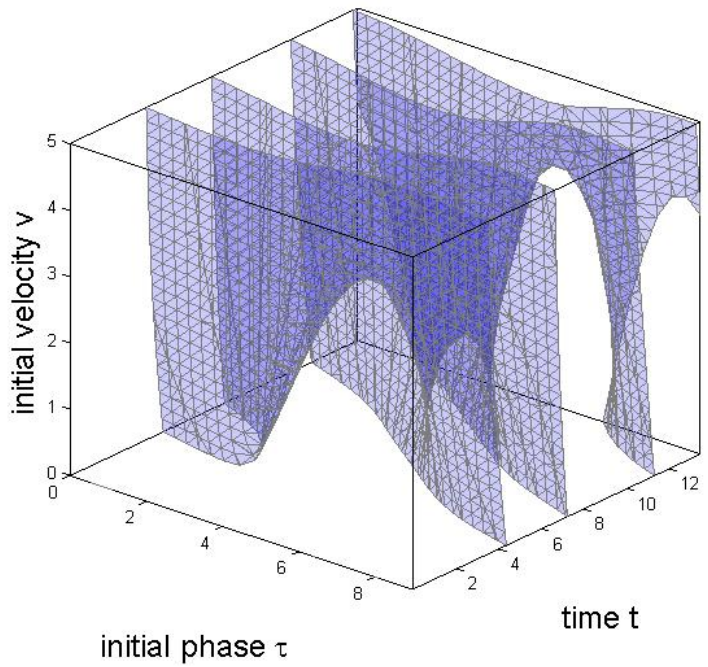
Let $x_c(\tau, v; t)$ represent the solution of

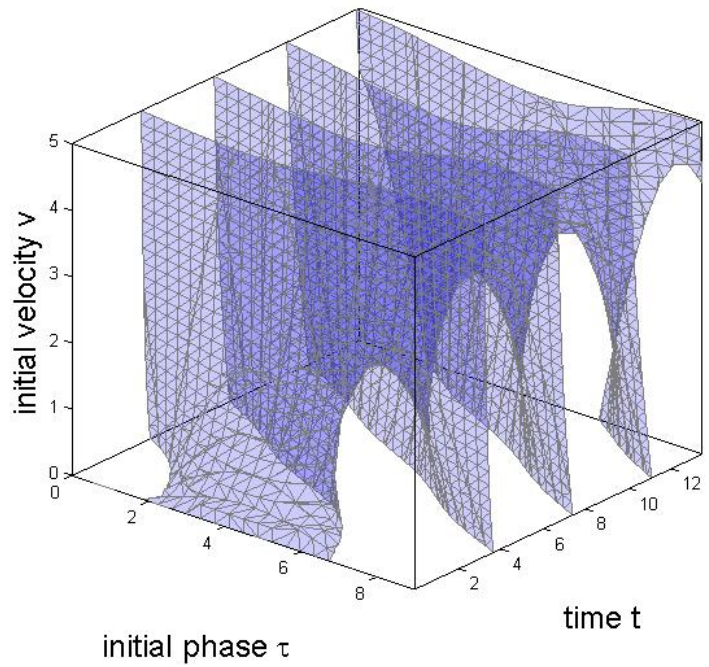
$$\ddot{x} + 2\mu\dot{x} + kx = h\cos\omega(t+\tau),\ x(0) = c,\ \dot{x}(0) = v \geq 0,$$

with $\dot{x}(t_i^+) = -r\dot{x}(t_i^-)$ at $x = c$ where t_i is the time to impact. The forcing is periodic with period $T = \frac{2\pi}{\omega}$ and an orbit with m impacts in n forcing periods will be denoted as a (m, n)-orbit.

The Discontinuity Surface $V_c = \{(\tau, t, v) \in \mathbb{R}^3 \mid x_c(\tau, v; t) = c\}$

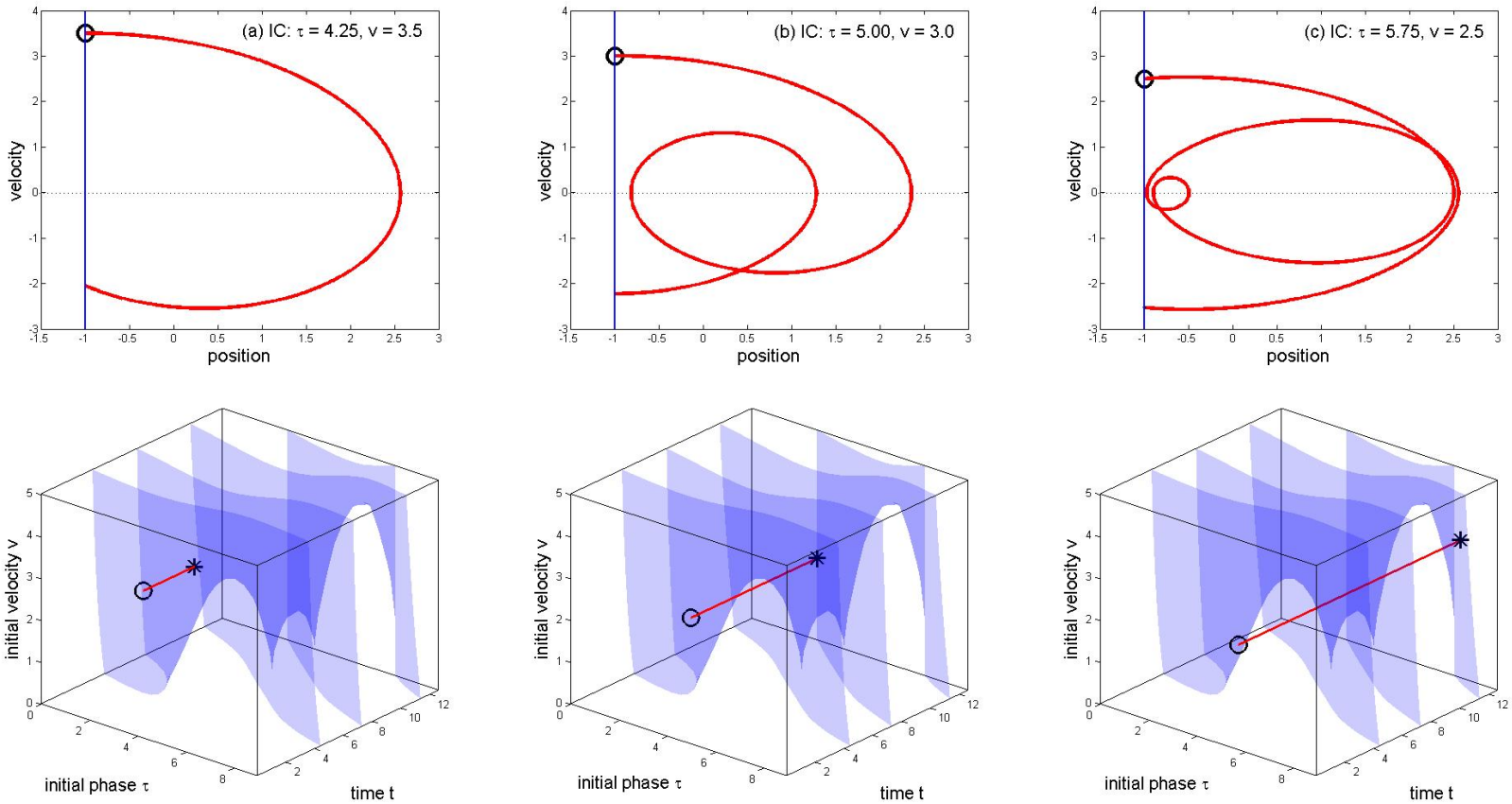
V_c is a contour set of the 3-variable function $x_c(\tau, v; t)$





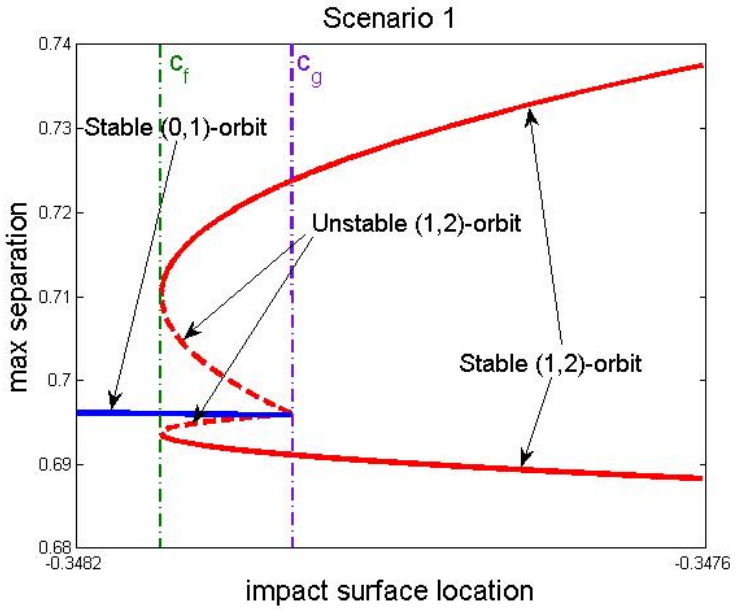
Trajectories

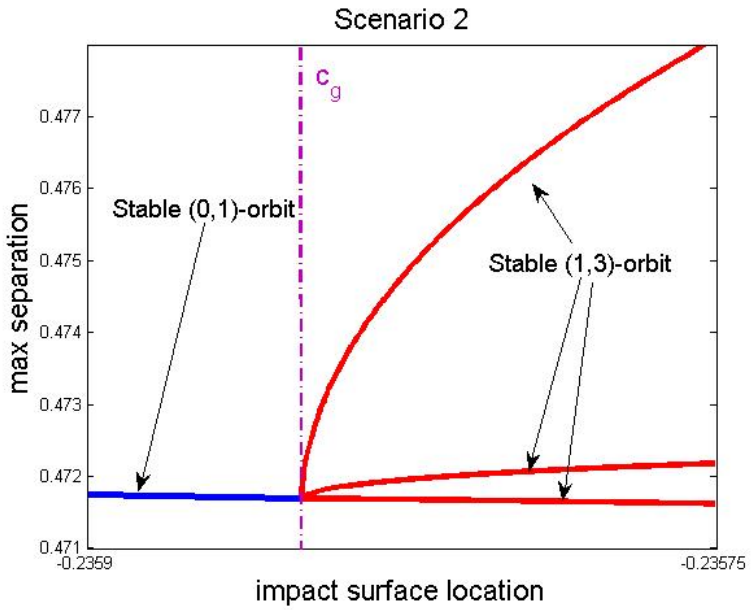
An individual free-flight (trajectory) is traditionally represented with a phase-plot diagram, plotting position against velocity.
In discontinuity geometry it is represented by the straight line from $(\tau, 0, v) \in \Pi_0$ to $(\tau, t_i, v) \in V_c$.



Bifurcation Diagrams

Changes in the periodic orbits of the system under parameter variation are traditionally represented by bifurcation diagrams, with some aspect of the orbit plotted against the value of the varying parameter. For this system, if $c = -\infty$ the only orbit is a non-impacting $(0, 1)$-orbit. As c is increased, this orbit is destroyed at a grazing bifurcation when $c = c_g = -\frac{h}{\sqrt{(\omega^2 - k)^2 + (2\mu\omega)^2}}$.



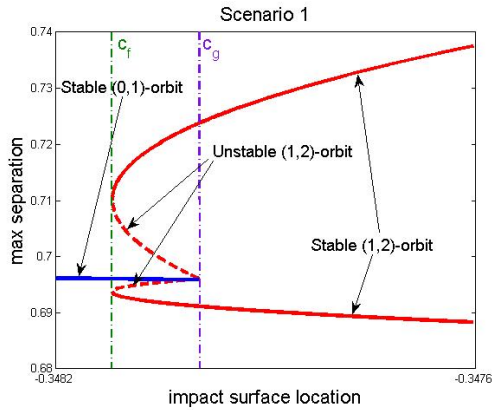


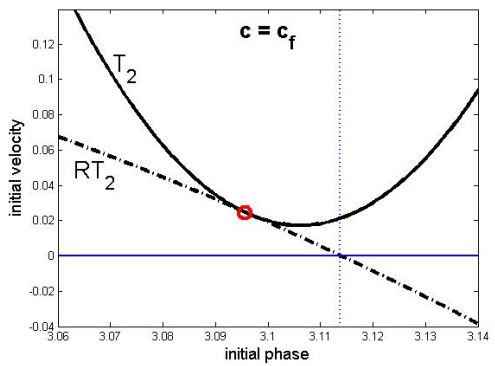
T_n/RT_n Diagrams

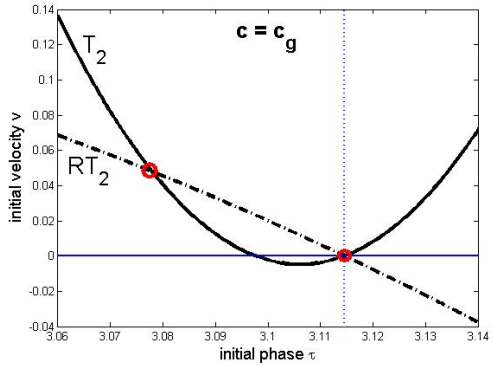
If a $(1,n)$-orbit exists, impact occurs at $t = nT$ and the initial velocity $v = -r\dot{x}_c(\tau, v; nT)$ the post-impact velocity, so define

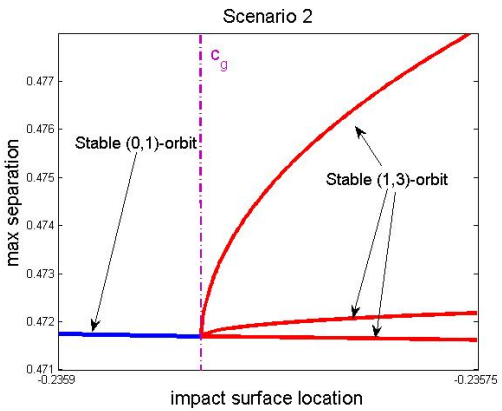
$$T_n = V_c \cap \Pi_n = \{(\tau, nT, v) \in \mathbb{R}^3 \mid x_c(\tau, v; nT) = c\},$$
$$RT_n = \{(\tau, nT, -r\dot{x}_c(\tau, v; nT)) \in \mathbb{R}^3 \mid x_c(\tau, v; nT) = c\},$$

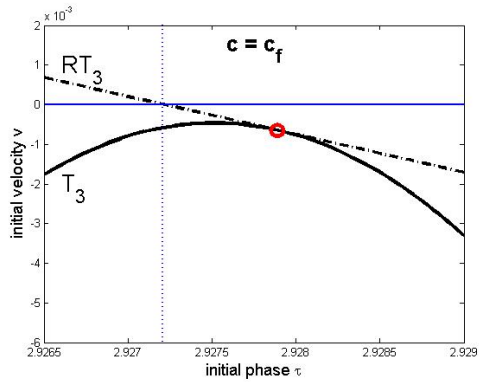
and now any point $\in T_n \cap RT_n$ is a potential $(1,n)$-orbit

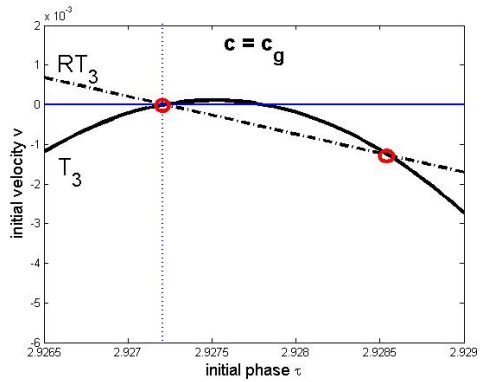












This work has grown out of the basic methodology proposed in

- D.R.J.Chillingworth, 2002, 'Discontinuity geometry for an impact oscillator', *Dynamical Systems*, Vol. 4, pp. 389-420.

A more complete description of both the framework in general and the results of using the framework to explore the dynamics of a PFIO in the vicinity of a grazing bifurcation are given in

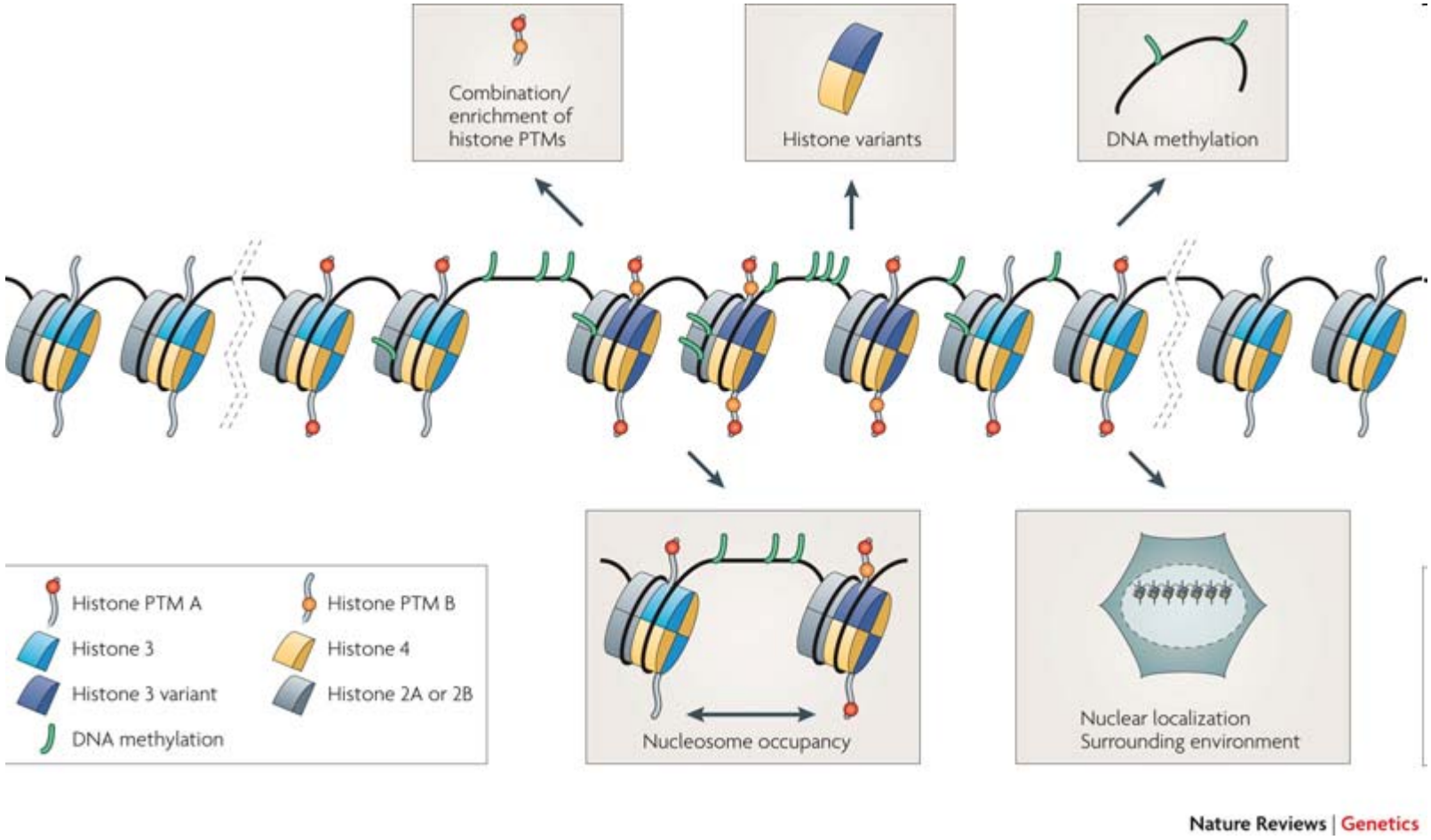
- N.Humphries, P.T.Piiroinen, 'A discontinuity geometry view of the relationship between saddle-node and grazing bifurcations', *in submission* to *Physica D* for a special issue on non-smooth systems.

THANK YOU FOR YOUR ATTENTION

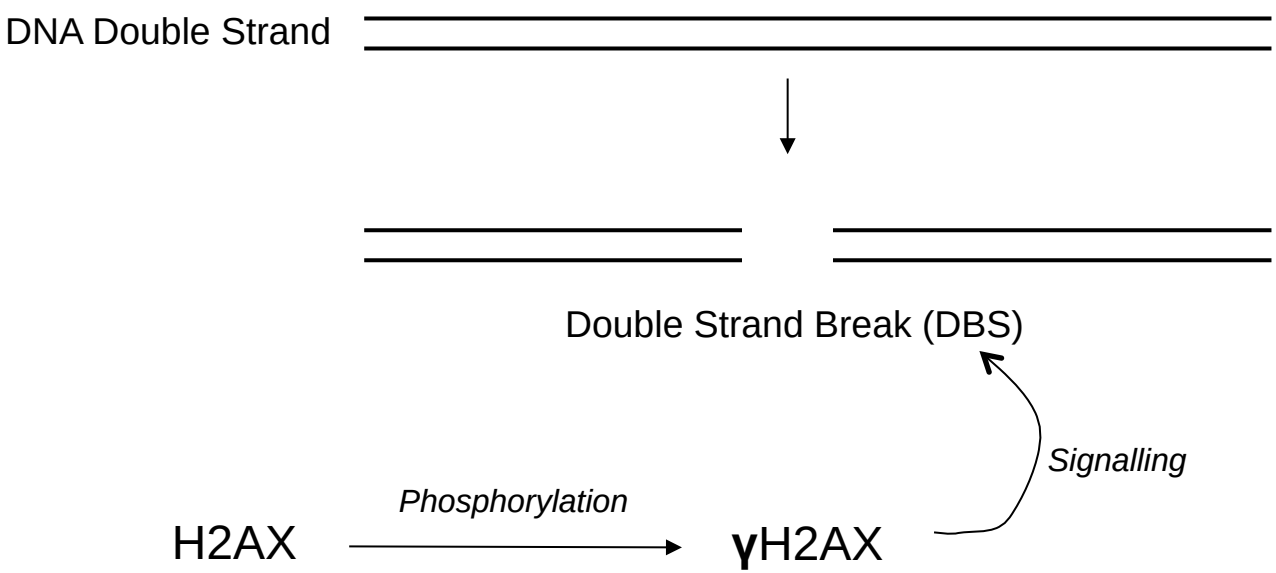
Genome-wide Distribution of DNA Damage Dependent Histone H2AX

Presenter: NGUYEN Trung Thong

Characteristics of a chromatin domain

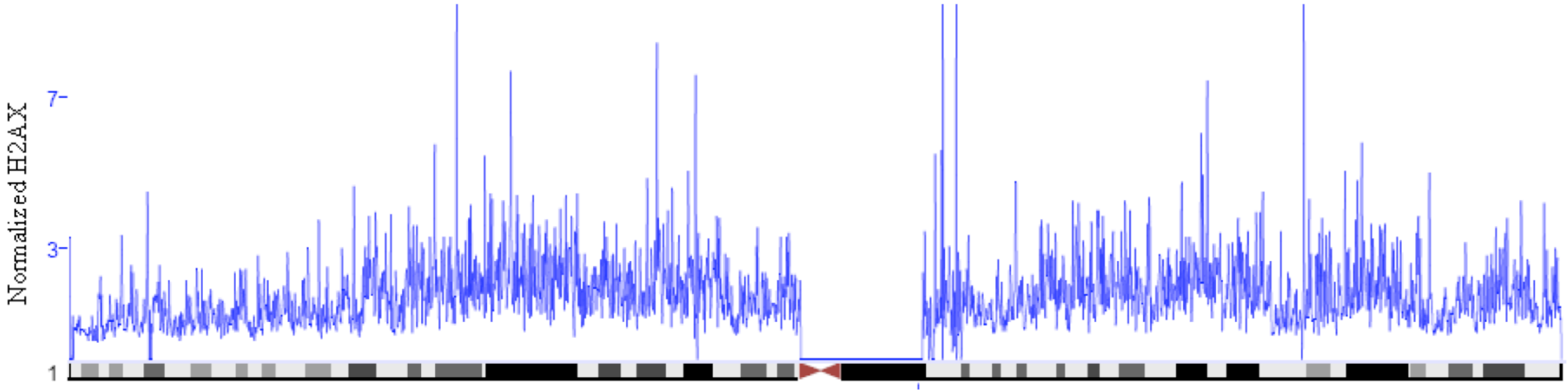


H2AX and DNA repair



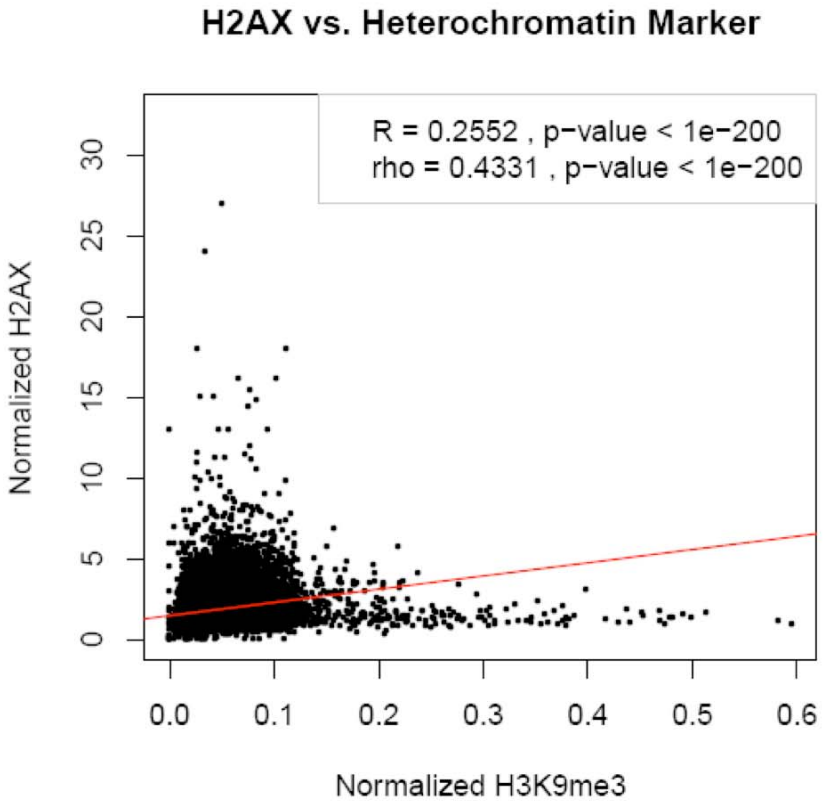
Aims: Finding the genome-wide localization of H2AX and its association with the genomic features.

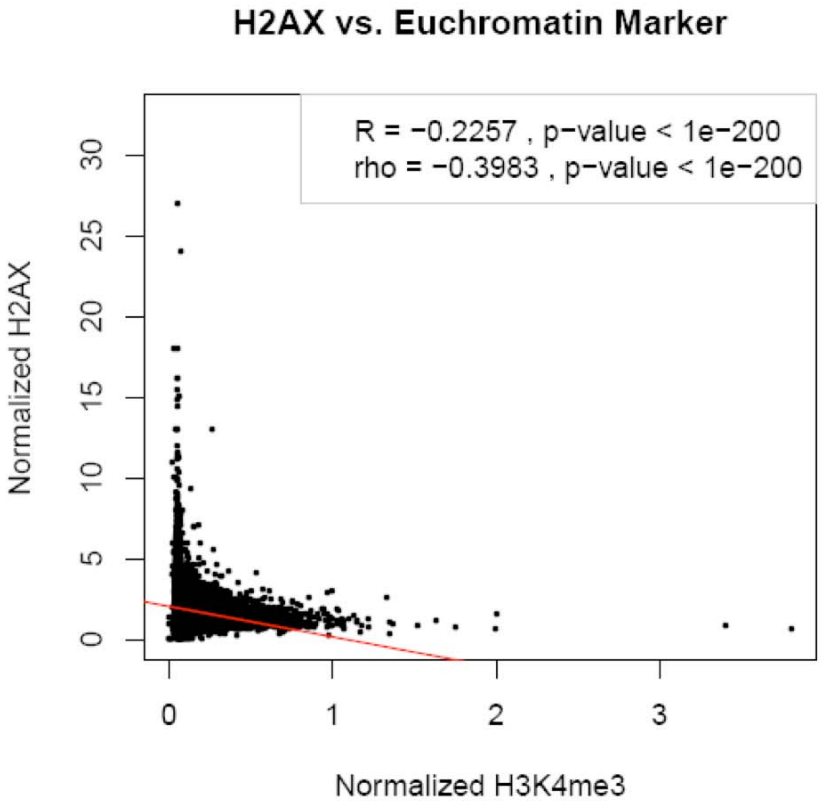
Genome-wide distribution of H2AX



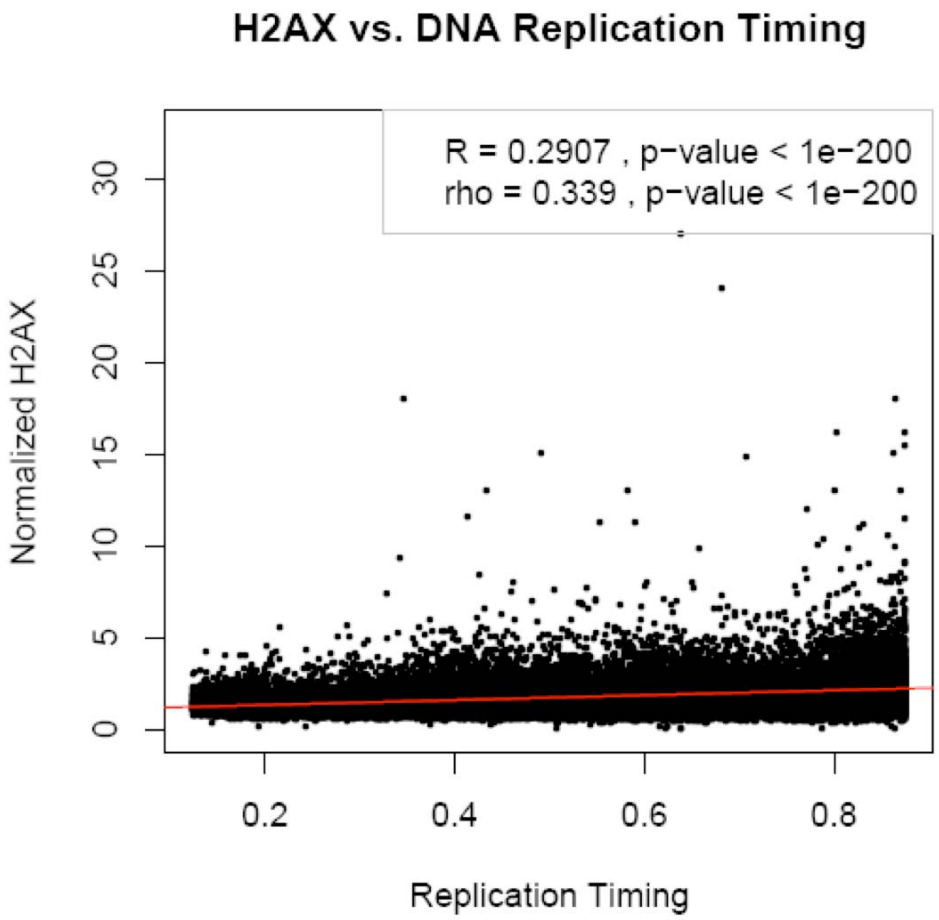
Human chromosome 1

H2AX correlates with heterochromatin, anti-correlates with euchromatin markers





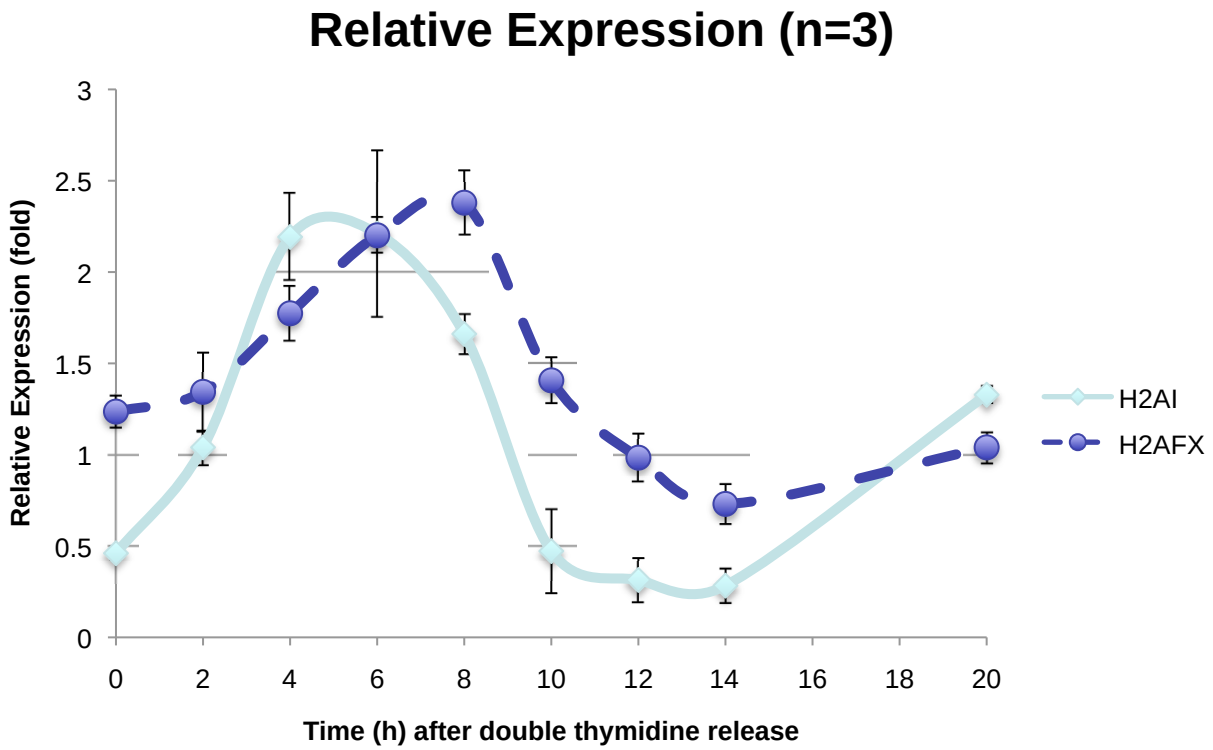
H2AX is abundant in late replicated chromatin



ChIP-seq DNA replication timing profiles were obtained from:

Chen et al. Impact of replication timing on non-CpG and CpG substitution rates in mammalian genomes. Genome Res. (2010)

H2AX is abundant in late replicated chromatin: experimental validation (by Helen)



- Experiments based on 3 biological replicates (in plate triplicates)
- Endogenous control used is GAPDH
- Error bars are standard error of the mean

Survival Trees

Alberto Alvarez Iglesias[1] John Newell[1,2]
John Hinde[1]

[1]School of Mathematics, Statistics and Applied Mathematics, NUI, Galway, Ireland.

[2]HRB Clinical Research Facility, NUI, Galway, Ireland.

Galway, November 4, 2010.

Survival Analysis

Outcome of interest: **Time until an event occurs**

A typical data set

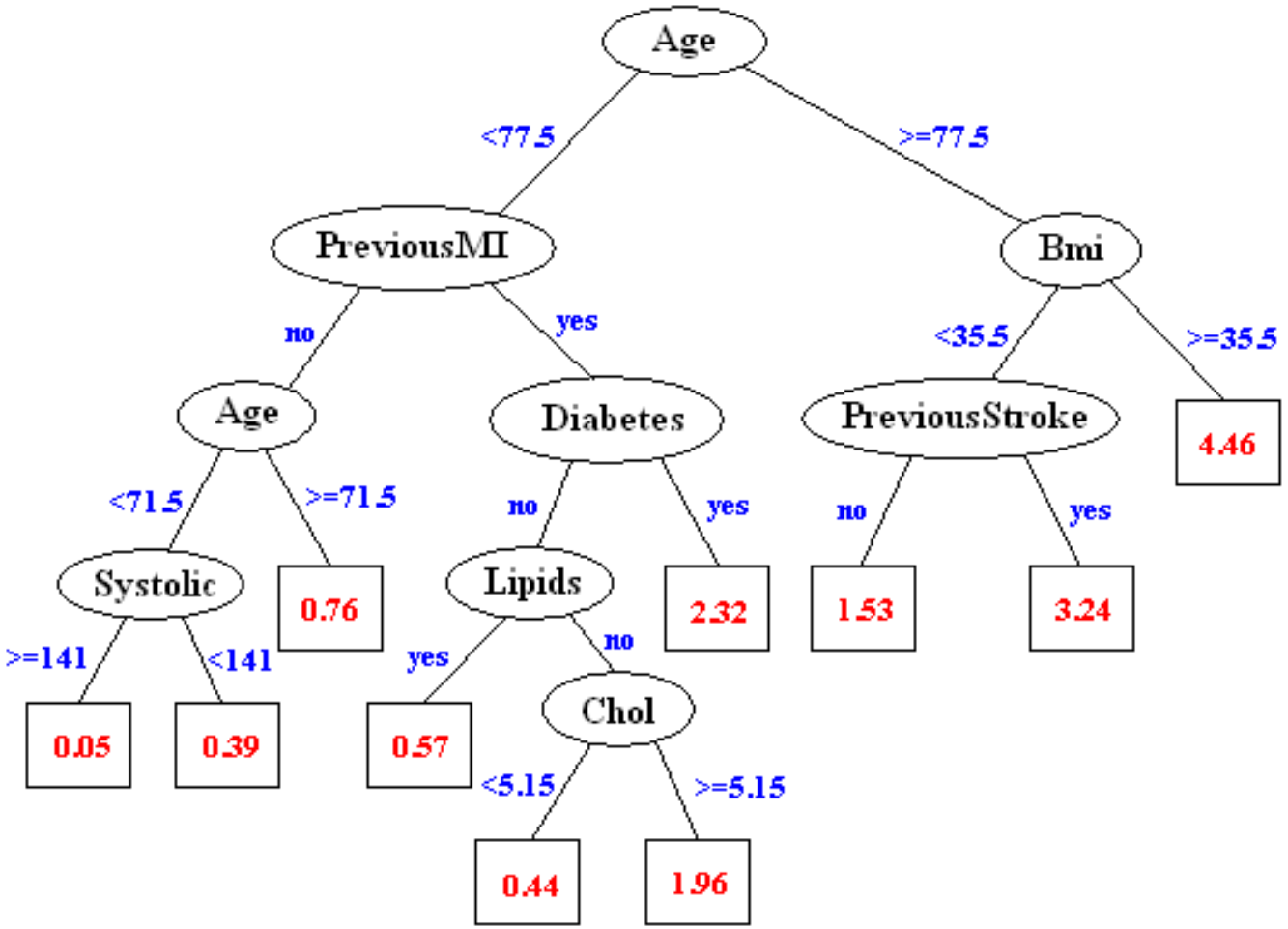
times	status	age	gender	previousMI	$\cdots$
311	1	76	F	no	
231	1	80	F	yes	$\cdots$
939	0	79	M	no	
$\vdots$		$\vdots$		$\vdots$	

The Cox Proportional Hazards Model

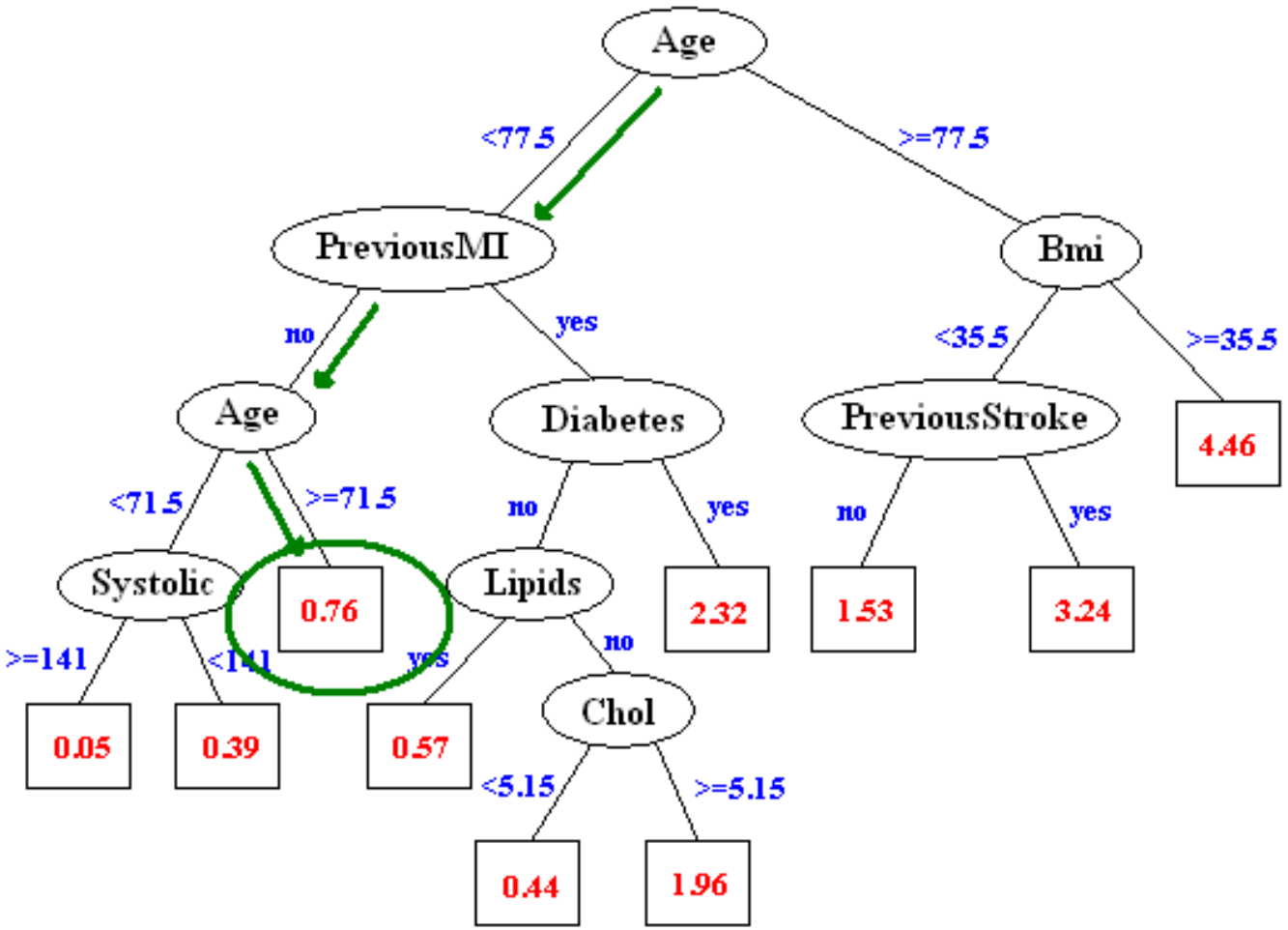
$$\lambda(t|X_1,,X_p) = \lambda_0(t)e^{\sum_{i=1}^{p}\beta_i X_i}$$

$\lambda_0(t)$: Baseline hazard.

Survival Trees

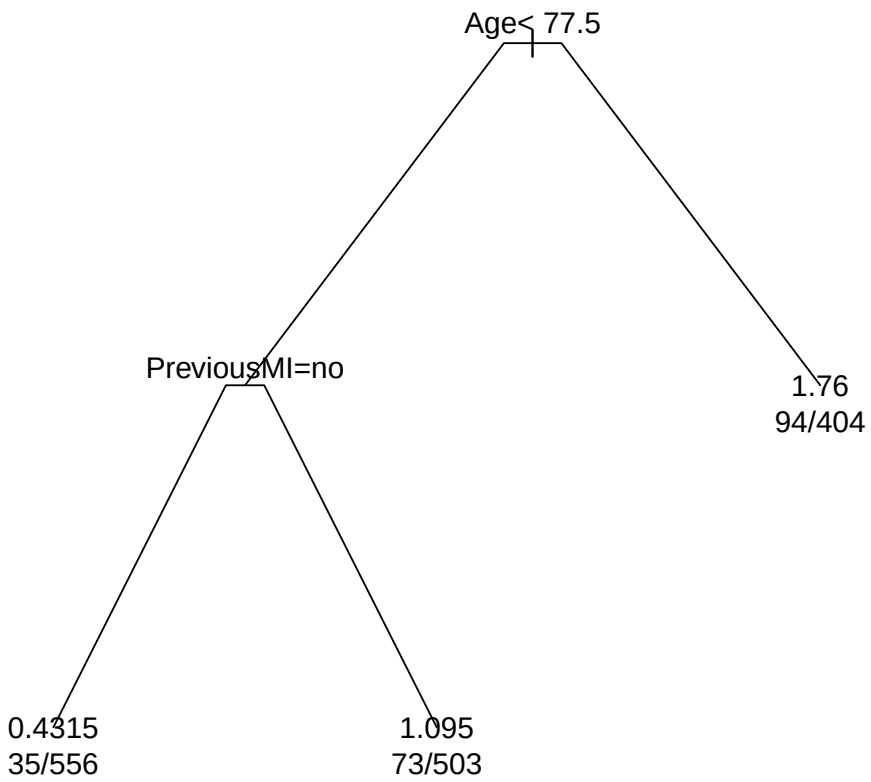


Survival Trees



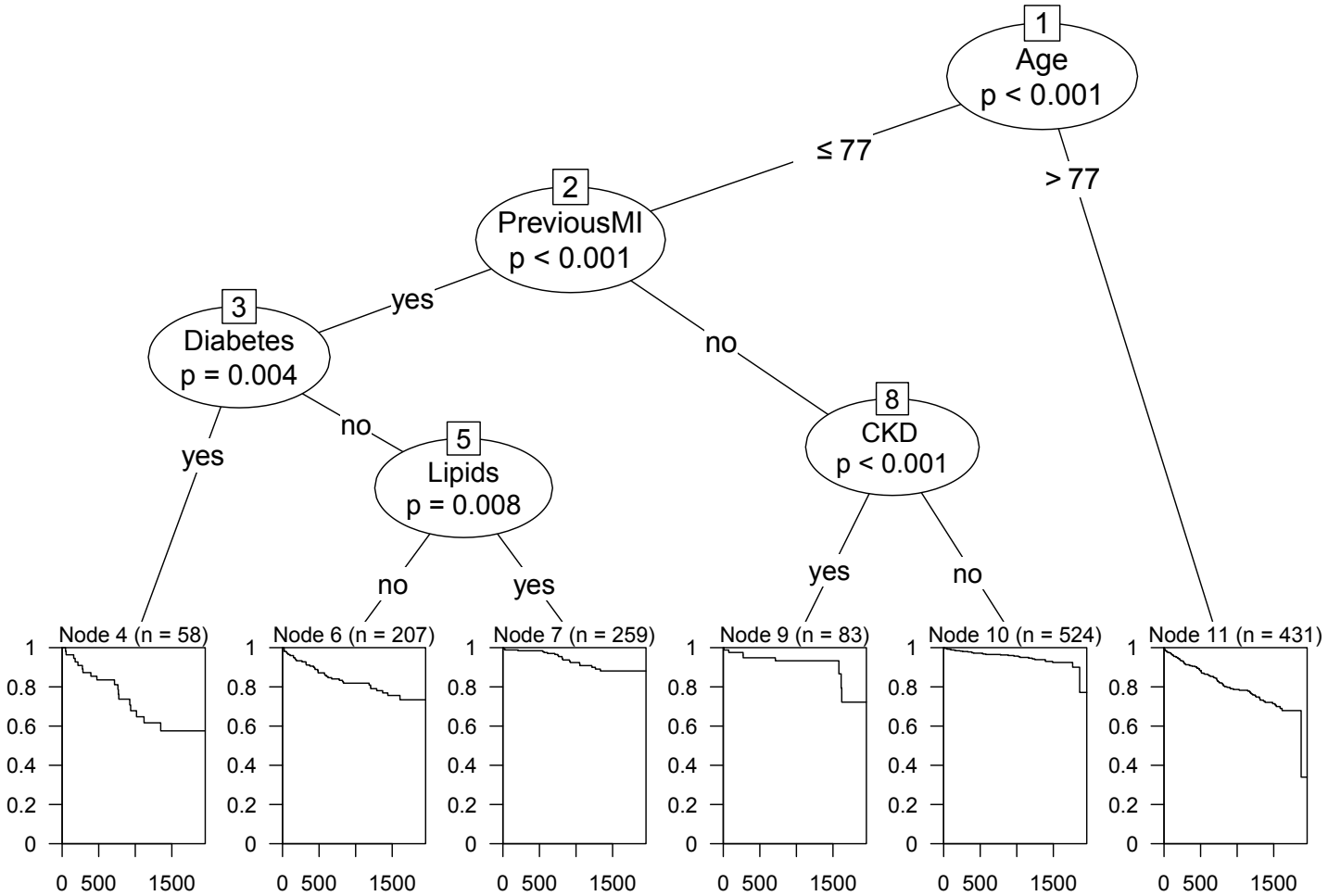
Examples

- Leblanc and Crowley (1992). *rpart*



Examples

- Hothorn et al (2006). *party*



Random survival forest

- Breiman (2002).
- Hothorn (2006).

Ishwaran (2008). *randomSurvivalForest*

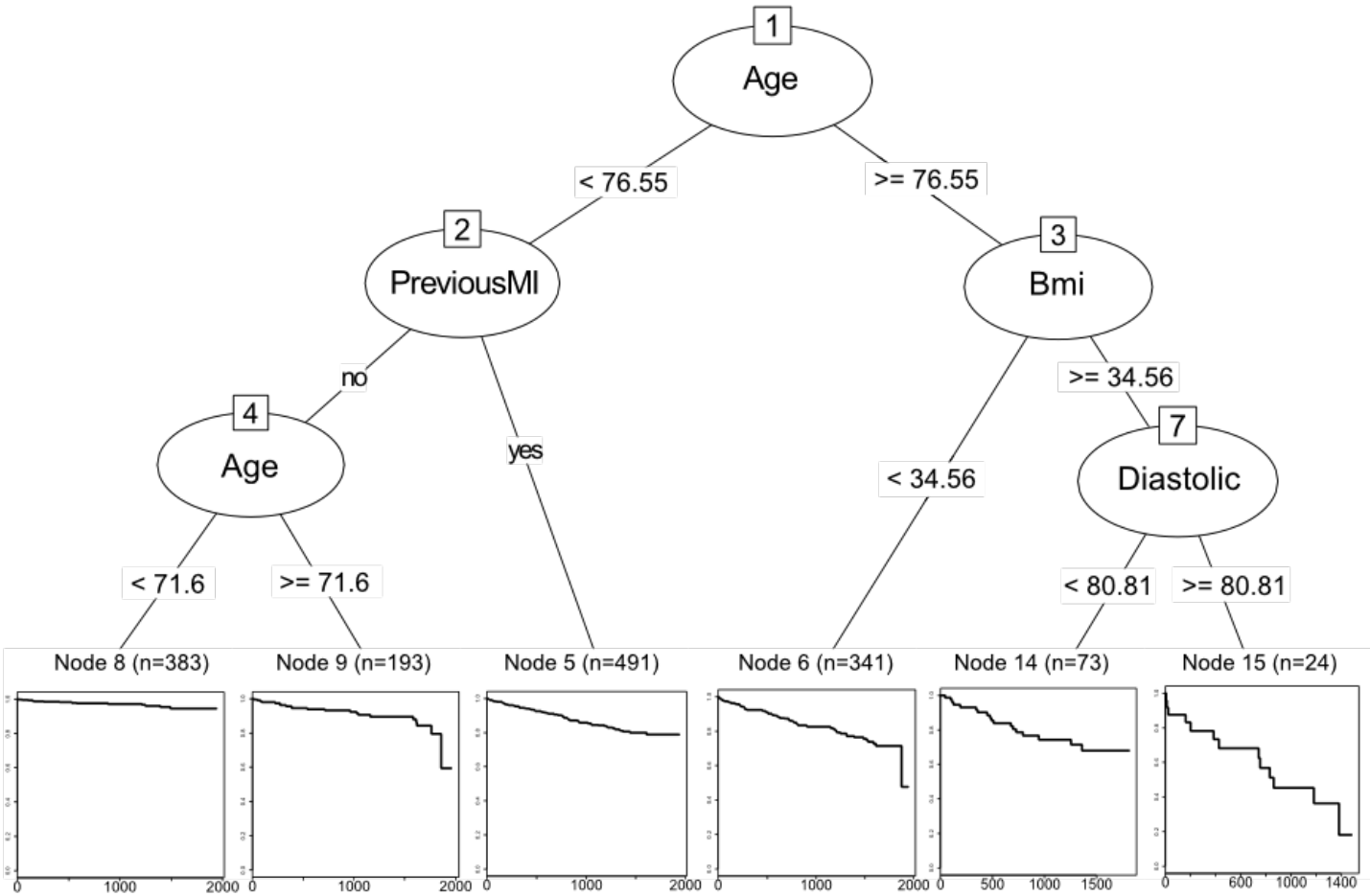
1. Draw bootstrap samples from the original data.
2. Grow a saturated tree for each bootstrapped data set. At each node of the tree only a random selection of predictors is considered.
3. Calculate a cumulative hazard function (CHF) for each tree. Average to obtain the ensemble CHF (different ensemble CHF for each individual).
4. Sum over the unique event times to get the ensemble mortality (predicted outcome).

Resampling at node level

IWSM 2010 Glasgow, 5th - 9th July.

1. For each node, generate bootstrap replicates of the original data.
2. Choose the predictor that more often appears as the best predictor.
3. Use the bootstrap distribution of the cutpoints to choose the splitting point.
4. Stop if the differences between the two daughter nodes are non significant for the predictor and cutpoint selected in steps 2 and 3.
5. Repeat steps 1-4.

Tree grown using resampling at node level



A Study of Structural Equation Modeling in Students' Academic Achievement

Nur Fatihah Mat Yusoff

School of Mathematics, Statistics and Applied Mathematics,
National University of Ireland, Galway

4 November 2010

NUI Galway
OÉ Gaillimh

1.0 Background of Study

- This study is concerned with; (i) reducing the dimension in an instrument, and (ii) Develop and propose a new model of students' academic achievement.
- Investigate the dimension-reduction techniques in psychometric testing by using Principal Component Analysis (PCA) and Correspondence Analysis (CA).
- Psychometric research- interested in the theory and techniques of education and psychological measurement- concerned with the construction and validation of measurement instruments.
- Develop a model using Structural Equation Modeling (SEM).

2.0 Introduction to Data

2.1 Population and Sampling

- Population: Second year and above of undergraduate students in University Malaysia Sarawak, Malaysia (4237 students).
- 2 stages of data collection process; Pilot survey and Final survey.
- Sampling Technique: Multistage Sampling (combination of cluster and random sampling).
- Pilot survey: 100 students were randomly selected, only 80 students had returned back the questionnaire.
- Final survey: Over 1200 questionnaires were distributed; 955 or almost 80% had been returned; only 899 were complete.

Introduction to Data (cont.)

2.2 Instruments

- This survey was based on two original instruments; "The Big Five Inventory (BFI)" developed by Oliver P. John and Sanjay Srivastava from University of California, Barkeley in 1999 and "Motivated Strategies for Learning Questionnaire (MSLQ)" developed by Paul R. Pintrich, David A.F. Smith, Teresa Garsia and Wilbert J. McKeachie in 1991.
- BFI - assess 5 personality traits
- MSLQ - assess students' motivation (6 factors) and learning strategies (9 factors).
- There were 4 section in questionnaire : Section A (student ID, gender, year of study, faculty, ethnicity, previous academic level, previous academic achievement, and current academic achievement), Section B (Personality traits - 44 items), section C (Motivation - 31 items), and Section D (Learning strategies - 50 items).

3.0 Statistical Methods

(i) Dimension reduction techniques (PCA and CA)

- We believe that some of the items, or even dimensions are not relevant in the Malaysian context- our aim is to produce the best instrument that can represent all of the variables that we are interested.
- PCA goal is to extract the important information from the table - represent it as principal components.
- Mathematically, PCA creates uncorrelated components, where each component is a linear weighted combination of the initial variables.For example:

$$PC_1 = a_{11}X_1 + a_{12}X_2 + ... + a_{1n}X_n$$

$$\vdots$$

$$PC_m = a_{m1}X_1 + a_{m2}X_2 + ... + a_{mn}X_n \quad (1)$$

where a_{mn} represent the weight for the mth principal component and the nth variables.

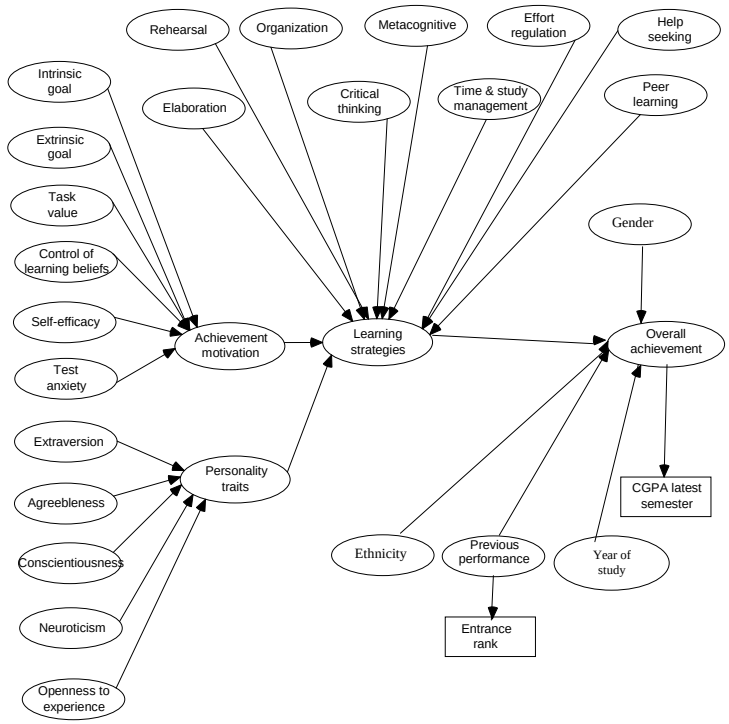
3.0 Statistical Methods (cont.)

- CA is a well known technique for identifying, and visualizing the association between two or more categorical variables.
- CA can be considered as a factor method for the categorical variables and is often linked with producing a low-dimensional graphical display of variables and units.
- CA includes four basic concepts; a profile point in multidimensional space, a mass (r), a distance function between the points (d), and inertia which is defined as the sum of the quantities rd^2.

3.0 Statistical Methods (cont.)

(ii) Structural Equation Modeling

- Is a statistical technique for testing construct validity and is used to describe the association between variables.
- Standard SEM models include regression analysis, path analysis, and confirmatory factor analysis.
- This figure shows the proposed overall model:



4.0 Analysis

As one application of how PCA operates, this plot illustrates the biplot of Neuroticism and Openness:

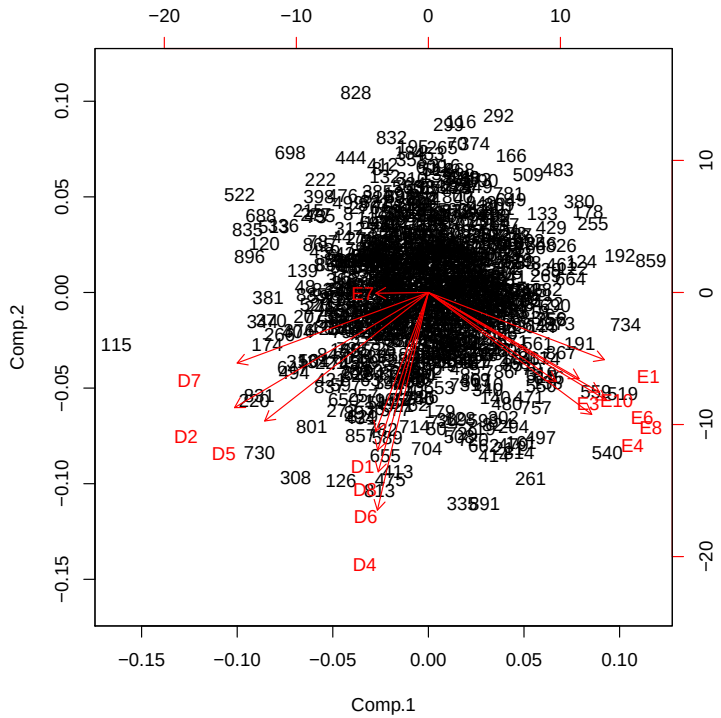


Figure: Biplot of Neuroticism and Openness

Component	Eigenvalue	Proportion of variance	Cumulative
1	2.7214	0.1943	0.9143
2	2.1489	0.1536	0.3479

Algorithms for Nilpotent Matrix Groups

Tobias Rossmann

4 November 2010

Supervisors: Dane Flannery, Alla Detinko

This work is supported by the Research Frontiers Programme of Science Foundation Ireland

Introduction

Project

Develop algorithms for problems involving nilpotent matrix groups over fields of characteristic zero (mostly: number fields).

- Matrix groups: one of the fundamental ways of representing groups on a computer.
- Nilpotent matrix groups: well-understood structure theory; well-suited for computations.
- Number fields: rich theory; allow exact computations.

Problems

Irreducibility and primitivity testing.

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Irreducibility testing

Definition

A group $G \leqslant \mathrm{GL}_d(K)$ is **reducible** if there exists a proper G-invariant subspace of K^d, otherwise G is **irreducible**.

Irreducibility testing

Given G, decide if G is irreducible. If G is reducible, construct an invariant subspace.

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Given G, decide if G is irreducible. If G is reducible, construct an invariant subspace.

Results

- We obtained an algorithm for constructive irreducibility testing of finite nilpotent matrix groups over number fields (and some other classes of fields of characteristic zero).
- The algorithm is quite practical. Exceptions occur when equations $x^2 + y^2 = -1$ (arising from quaternion groups) have to be solved.
- An implementation in MAGMA is publicly available.
- For an infinite nilpotent matrix group over a number field, we can decide irreducibility; finding submodules seems to be difficult for certain classes of groups.

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Nilpotent matrix groups and crossed products

Proposition

Let $G \leqslant \mathrm{GL}_d(K)$ be a completely reducible nilpotent group and let $A \triangleleft G$ be maximal abelian and homogeneous. Let $Z = \mathrm{Z}(K[G])$. Then $K[G]$ is a crossed product of $L = K[A]$ by $\Gamma = \mathrm{Gal}(L/Z) \cong G/A$.

- This proposition relates reducibility of G to problems in algebraic number theory ("Galois cohomology").
- The index of $K[G]$ is the order of an element of $H^2(\Gamma, L^\times)$ (Brauer-Hasse-Noether). This allows us to decide irreducibility of G.
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4 years in 5 slides

Padraig Ó Catháin

National University of Ireland, Galway

November 2010

How short can a presentation be?

"For sale: baby shoes, never worn."

Symmetric 2-designs

- Let $\mathcal{V}$ a set of cardinality v whose elements are called points.
- Let $\mathcal{B}$ be a set of distinct k-subsets of $\mathcal{V}$, of cardinality v whose elements are called blocks.
- Suppose that $\left|b_i \cap b_j\right| = \lambda$ for all $i \neq j$.
- Then $\mathcal{D} = (\mathcal{V}, \mathcal{B})$ is a symmetric 2-(v, k, λ) design.
- An automorphism of $\mathcal{D}$ is a permutation of $\mathcal{V}$ which preserves $\mathcal{B}$.

Difference sets

- Let G be a group of order v, and D a k-subset of G.
- Suppose that every non-identity element of G has λ representations of the form $d_i d_j^{-1}$ where $d_i, d_j \in D$.
- Then D is a (v, k, λ) difference set in G.

Theorem

Suppose G contains a (v, k, λ)-difference set. Then there exists a 2-(v, k, λ) design on which G acts regularly. Conversely, a 2-(v, k, λ) design on which G acts regularly corresponds to a (v, k, λ) difference set in G.

Proof - the first half

Proof.

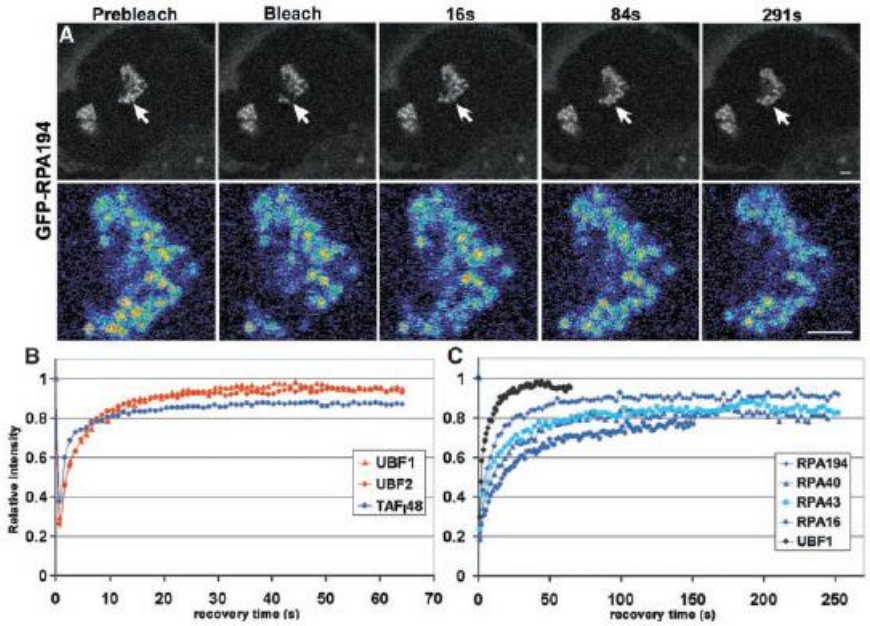
- Denote by D the difference set in G (written multiplicatively).
- Define an incidence structure, $\mathcal{D}$, by $\mathcal{V} = \{g \mid g \in G\}$ and $\mathcal{B} = \{Dg \mid g \in G\}$.
- Let $g \in \mathcal{V}$ be incident with $Dh \in \mathcal{B}$ if $g \in Dh$.
- Every block has size k: $|Dg| = |Dh|$.
- Furthermore $|Dg \cap Dh| = \lambda$: consider the equation $d_i g = d_j h$ with $d_i, d_j \in D$, $g \neq h$. Rewrite as $d_i d_j^{-1} = hg^{-1}$.
- There are precisely λ solutions, since D is a difference set.
- Thus $\mathcal{D}$ is a $2-(v,k,\lambda)$ design as required.

Modelling the Centromeric Chromatin Network

Kevin Doherty, Martin Meere, Petri Piiroinen

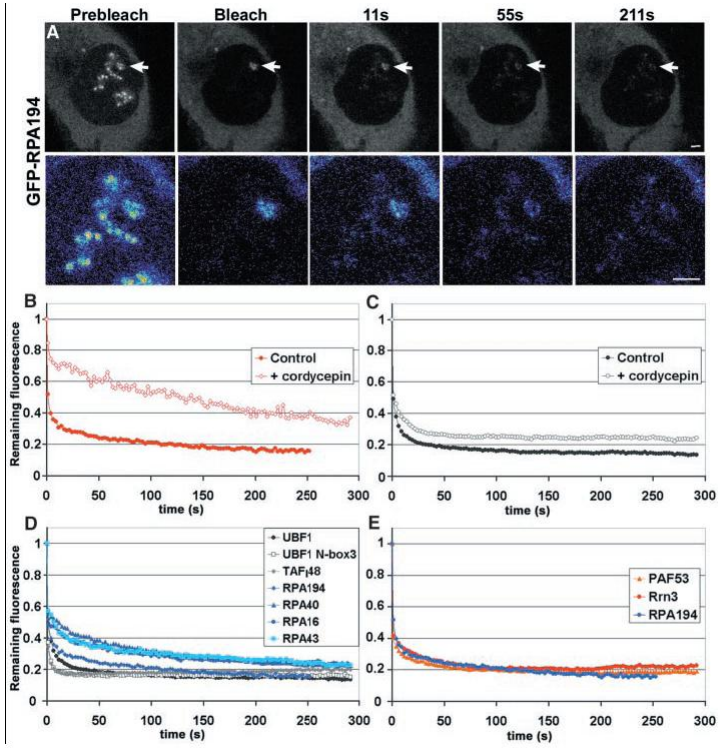
4/11/10

FRAP - Fluorescence Recovery After Photobleaching



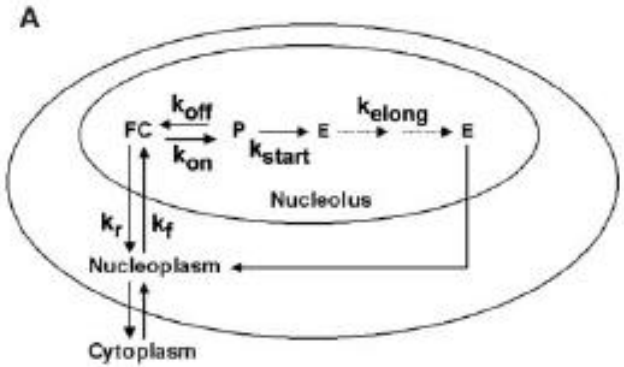
Dundr et. al. 2002

Modelling RNA Polymerase in vivo
iFRAP - Inverse FRAP



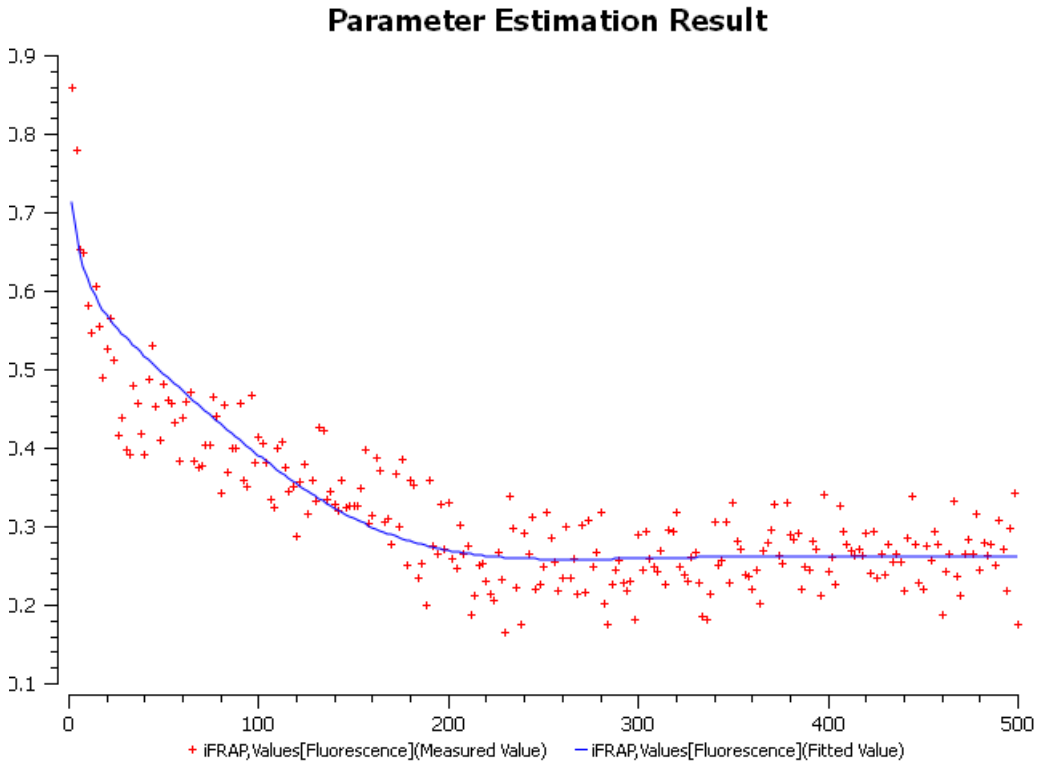
Dundr et. al. 2002

Dundr et. al. (2002) developed a model for attachment of RNA polymerase components at fibrillar centres and their subsequent elongation of chromatin in the nucleoplasm.

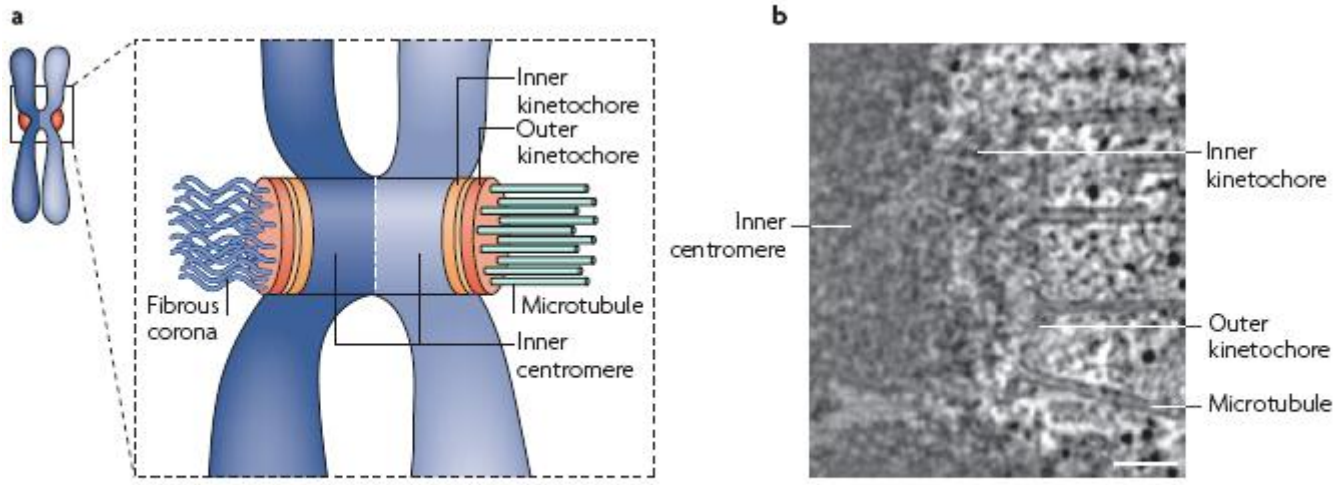


Dundr et. al. 2002

Their model output was fitted to experimental data using a least squares best fit to estimate parameter values.



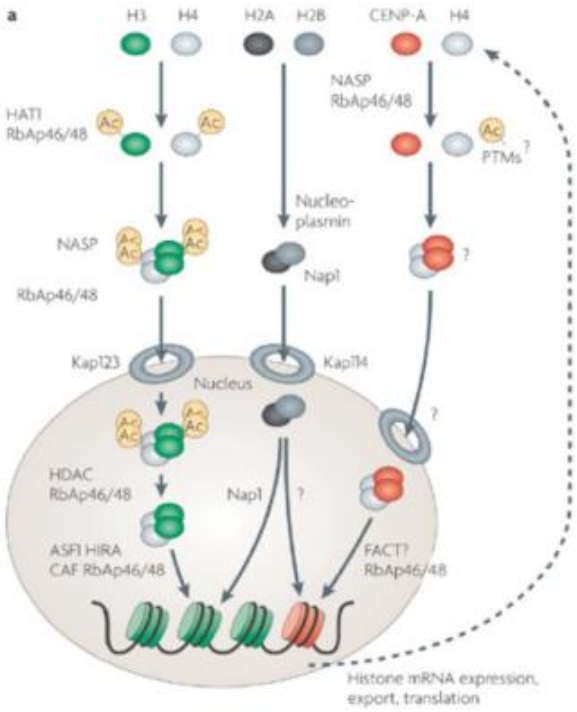
Modelling the centromeric chromatin network



Cheeseman, Desai 2008

So far there have been at least 80 kinetochore proteins identified in eukaryotes (Cheeseman, Desai. 2008).

So far there have been at least 19 centromeric network proteins identified in humans (Przewloka, Glover. 2009).



Karpen, Allshire 2008

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