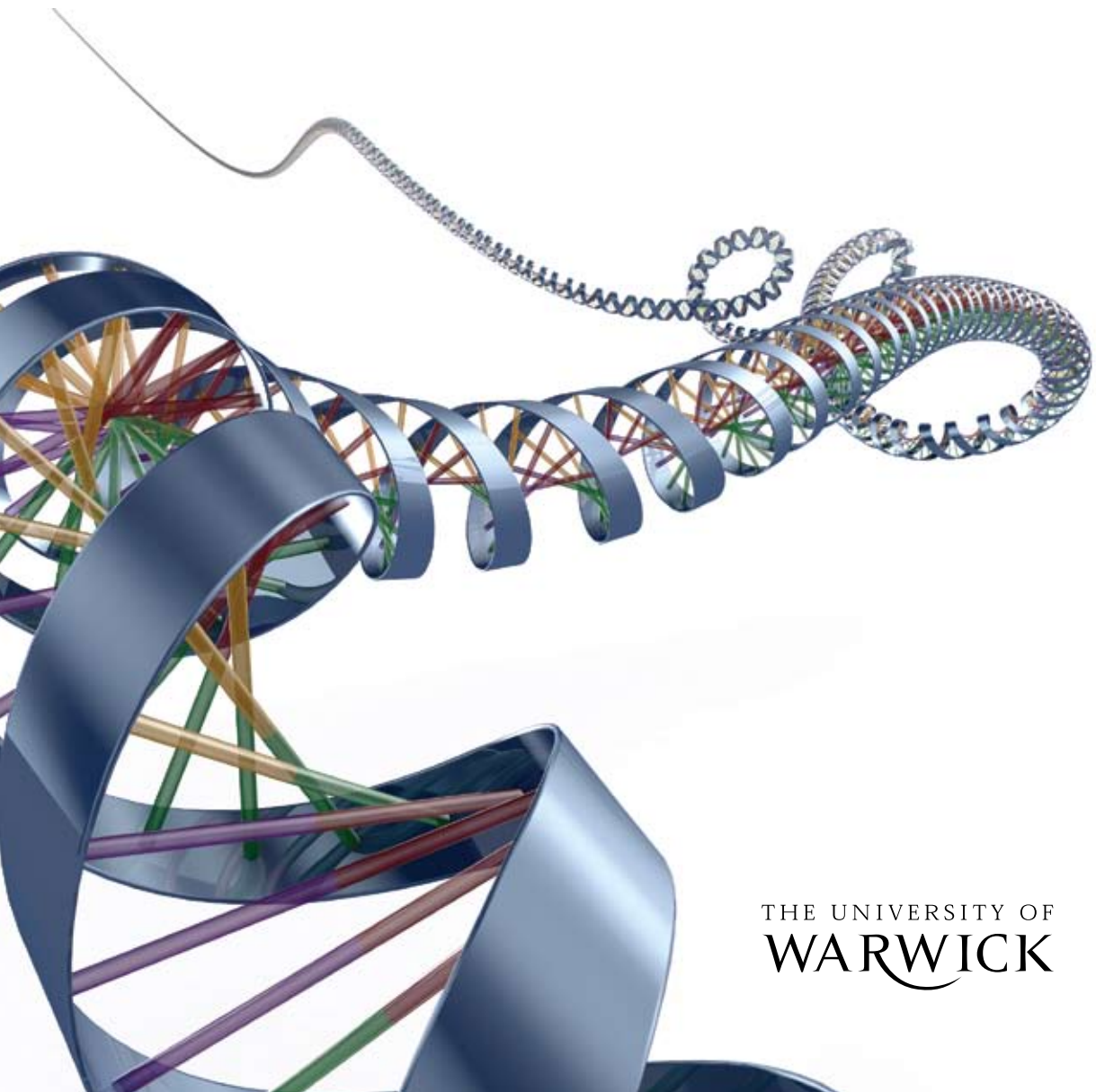
Warwick
Systems Biology Centre



THE UNIVERSITY OF
WARWICK

Core Staff

Director
Professor David Rand

Professor Jim Beynon
(joint with W-HRI, plant sciences, plant resistance to diseases)

Dr Hugo van den Berg
(mathematical biologist, energy allocation, neurobiology, theoretical immunology)

Dr Till Bretschneider
(modelling, quantitative image analysis, cell motility and cytoskeleton, excitation waves)

Professor Nigel Burroughs
(mathematician, modelling, phylogenetics, theoretical immunology, gene network inference, image analysis)

Dr Katherine Denby
(joint with W-HRI, plant sciences, plant pathogens)

Professor Martin Feelisch
(WMS, NO-related metabolites in disease and signaling)

Dr Sascha Ott
(bioinformatics, network inference, transcription factor prediction)

Dr Naila Rabbani
(joint with Medical School, proteomics, protein damage, diabetes, lipoproteins)

Professor David Rand
(mathematician, regulatory and signaling networks)

Dr Magnus Richardson
(theoretical neurobiology)

Professor Paul Thornalley
(joint with Medical School, proteomics, protein damage, diabetes, renal failure, anti-stress gene response)

Dr Matthew Turner
(joint with Physics, cellular mechanics & disease, genetic networks)

Dr Keith Vance
(epigenetic regulation, transcriptional regulation, single cell imaging)

Professor David Wild
(bioinformatics, network inference, proteomics)

Bioinformatics and scientific computing team:
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Paul Brown
Roxane Legaie

Warwick Associates
Warwick Medical School:
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Dr T Shmygol
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Warwick-HRI
Dr V Buchanan-Wollaston
(Director of Doctoral Training Centre)

Biological Sciences:
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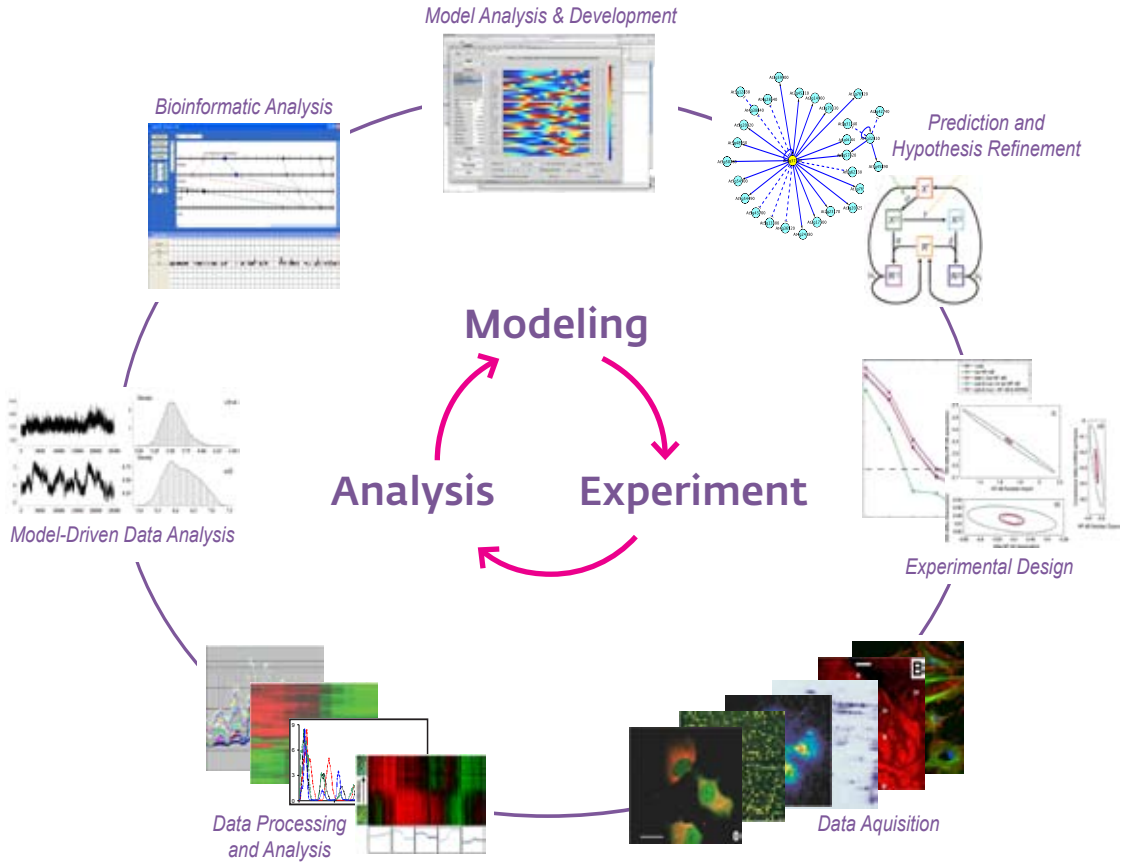
Professor D Hodgson
Professor Liz Wellington
Professor Georgy Koentges

Computer Science:
Professor Jianfeng Feng

Statistics:
Dr. B. Finkenstadt,
Dr Sach Mukherjee,
Professor J Smith

Modelling, Analysis, Experiment

Warwick Systems Biology Centre (WSB) represents an £11m investment by the University of Warwick to create an autonomous centre to capitalise on strengths in multidisciplinary research, funding 12 new staff, purpose-designed accommodation, and experimental and computing equipment.



WSB wishes the thank the variety of sources that currently fund our work

BBSRC bioscience for the future
EPSRC Engineering and Physical Sciences Research Council
The Leverhulme Trust
MRC Medical Research Council
wellcome trust

WSB and its many collaborators use an iterative cycle of theory and experimental research. In practice the interactions are network-like with extensive cross links.

WSB has a huge range of projects which enables unique interactions between researchers of different disciplines both at the University of Warwick and internationally. This brochure provides a detailed overview of the research carried out at the WSB and contact names for those individuals leading these cutting-edge projects.

Modelling, data analysis and software development

A key interest within WSB is the development of tailor made solutions to data interpretation and data analysis, often bringing together mathematical modelling and high level statistical computation. Thus, many of the projects detailed in this brochure will have an element of model development within the context of the specific biological problem. Specific areas where WSB is developing tools include:

- deducing transcription profiles and degradation, translation and folding rates from gene reporter and related data, using this to link to models, to compare multiple reporters in the same cell, to understand cellular stochasticity and to uncover the roles of gene regulatory modules;
- deducing network parameters structure and dynamics from time-series imaging data;
- transcription factor binding prediction;
- tools for the analysis of circadian rhythms;
- imputing network structure and clustering genes from microarray data;
- analytical tools for sensitivity analysis, parameter reduction and experimental optimisation.
- developing models that infer network structure by integration across experimental data types (transcriptomics, proteomics, metabolomics), and with bioinformatics data, eg transcription factor motifs.
- Analysis of model performance and comparison, thereby determining which model best fits the experimental data. Model variants include Gaussian and heavy tail noise models, linear and nonlinear models, hidden variable and augmentation models.
- Novel Bayesian hierarchical clustering methods for correlated data, eg time series.

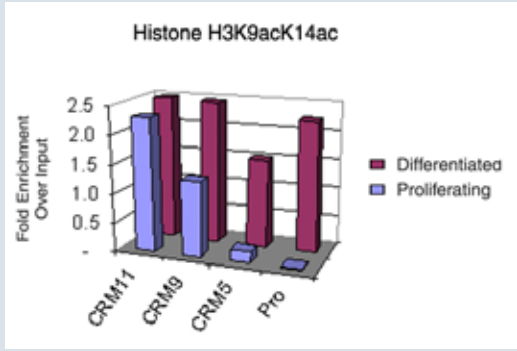
Software can be downloaded from our website:
http://go.warwick.ac.uk/systemsbiology

Transcription

Understanding cis-regulatory information processing in mesenchymal stem cells

This project involves:

- computational identification of cis-regulatory modules (CRMs) involved in transcriptional control using comparative genomics
- identification of transcription factor binding sites and CRM organization using computational predictions coupled with ChIP, bandshift and footprinting assays
- measurement and manipulation of CRM activity in live stem cells using FACS and live cell imaging
- mathematical modeling of transcription rates and cis-regulatory logic
- generation of chromatin state maps and integration of epigenetic status with ReMo function
- correlation of chromatin structure and CRM activity changes with cell fate decisions using a defined cell culture system



Chromatin Structure Changes During Myogenesis Control CRM Usage

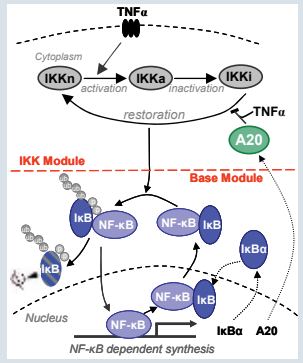
WSB staff: Ott, Bretshneider, Rand, Vance.
Collaborators: Koentges (Warwick)

Cell Signalling

Dynamics and function of the NF-κB signalling system

(Funding includes approx. £5million SABR grant, led by M White (Liverpool), Rand directs the theory.)

- Develop and apply a set of quantitative experimental tools coupled to an intensive theoretical analysis to properly analyse the dynamic function of the NF-κB signalling system
- How do the complex feedback loops control NF-κB dynamics and downstream gene expression? How do cells achieve appropriate cell fate decisions in response to time-varying signals?
- Experimental work will integrate dynamic cell and single molecule imaging, quantitative proteomics, chromatin immunoprecipitation analysis (for the dynamics of NF-κB binding to target promoters) and RT-PCR and DNA microarray analysis (for measurement of endogenous gene expression).
- Theoretical work will develop: (a) new data analysis tools to interpret and direct experimental strategy, (b) deterministic and (c) stochastic mathematical models of the system.



WSB staff: Finkenstadt, Rand, Ott.
Collaborators: White, Sée, Paszek, Bearon, Sanderson, Beynon, Harper, Spiller, Lévy (Liverpool) Jackson, Kell, Broomhead, Paton, Gaskell, Fernandes, Taylor, Reid (Manchester)

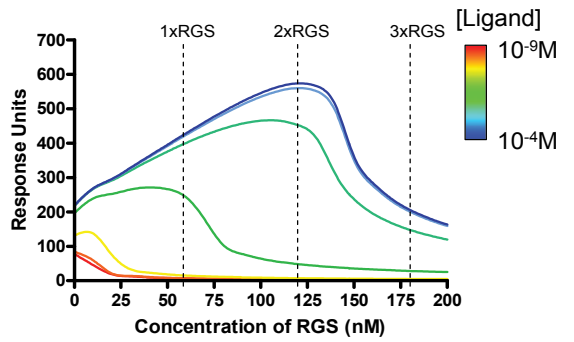
Eukaryotic G protein-mediated signalling

Recent work in G Ladd's laboratory, MOAC (Ben Smith) and WSB has:

- indicated that GTP hydrolysis arising from ligand activation of a GPCR, far from being solely responsible for desensitisation, is essential if cells are to achieve their maximal signalling output
- developed a qualitative computational model that informs our *in vivo* experimentation and predicts the existence of a novel Ga subunit intermediate that is bound to GTP, but is inactive
- identified a new generic dynamic motif that we wish to test against G protein-mediated signalling networks in all eukaryotes.

This project aims

- to verify the existence of this state; and
- continue a systems biology approach to utilise state-of-the-art *in vivo* experimental techniques to generate kinetic data so producing a quantitative model, thereby increasing its accuracy for informing experimental design.



WSB staff: Ladds, Rand, van den Berg, Davey
Collaborators: Ben Smith (Warwick, MOAC student)

Medical Systems Biology

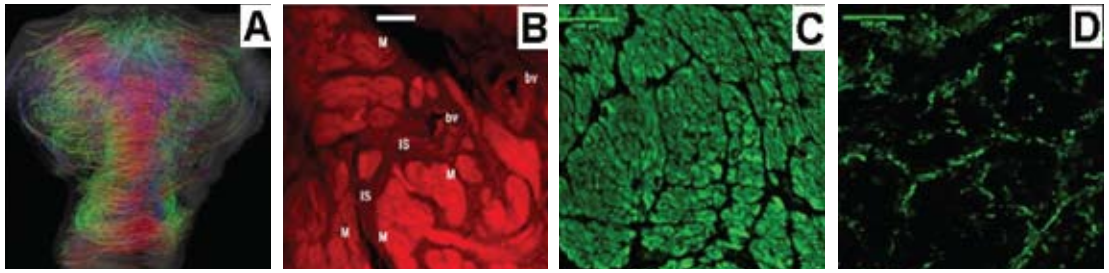
Reproductive medicine. Emergent dynamics in coupled heterogeneous networks in uterine systems

- Reconstruction of tissue-level electrogenesis in smooth muscle from morphological, biophysical and genomic data. The main purpose is to combine both experimental and mathematical approaches to identify the functions of genes resulting from the expression of various ionic channel proteins in the initiation and conduction of electrical excitations in uterine systems, This will take account of tissue spatial structure and histo-chemistry and chart, in both space and time, proteomic micro-heterogeneity and connectivity patterns.

Aims:

- to assess quantitatively how these patterns determine the origin and propagation of the myometrial action potential (MAP)
- to integrate detailed experimental data into a coherent mathematical and computational platform to develop a predictive tool that enables evaluation of the functional roles of proteins (principally ion channels) of smooth muscle cells and interstitial cells of Cajál (ICC)
- to understand how gestational changes in the expression of ion channels and electrogenic pumps change the myometrium from quiescence to auto-rhythmic excitation; and
- to pioneer a novel genomics-driven mathematical modelling strategy in physiology, which will connect tissue-level physiology with high-throughput molecular data.

Fig 1. Tissue architecture and cell types of human myometrium



A: Diffusion tensor magnetic resonance imaging of human uterus.

B: Confocal microscopic scan of picrosirius red stained term pregnant human uterus in the fundal region. Myometrial smooth muscle cells (M) occur in bundles, isolated from each other by interstitial spaces (IS) consisting of dense collagen matrix and blood vessels (BV). Scale bar 50µm.

C: Confocal microscopic scan of 10µm section of lower segment myometrium taken at term. Smooth muscle bundle (green) architecture is depicted by fluorescent stain of F-actin by the actin-binding toxin Phalloidin conjugated to Alexa-488.

D: Serial section of C depicted ICC-like network (green) surrounding smooth muscle bundles.

WSB staff: van den Berg, Blanks, Rand, Richardson.
Collaborators: Shmygol (WMS), Thornton. Zhang (Manchester), A Holden (Leeds)

Network inference of energy balance regulation and whole-body metabolic control

Research objectives are:

- to study how control of food intake in mammals adapts to various energy regimes, focussing on the control of gene expression by signal transduction pathways and the resulting change in the electrophysiology of individual neurons and networks
- to develop a whole organism model for neuroendocrine control of nutrient intake, energy balance & growth
- to develop a macrochemical model of dynamics of body composition & its regulation. Manipulating the sugar rearrangement system to manage glucose load in diabetes; and
- to control continuous infusion of insulin in diabetic patients through continuous-time glucose monitoring.

WSB staff: van den Berg, Feng, Kumar, Ott, Rabbani, Rand, Richardson, Spanswick, Thornalley.

Preganglionic motor neurones are responsible for a number of crucial autonomic responses, in particular the preparation of the body for "fight-or-flight". They form an extensive, gap-junction network of electrically active cells.

- Computational and mathematical models of the properties of sympathetic-neuronal networks have been built using the extensive intracellular patch-clamp-recording data generated in the Spanswick lab.
- These demonstrate that these networks have unique properties that are not seen in the more commonly studied chemical-synapse networks; in particular, they move into a critical "avalanche" state which has unusual and potentially useful computational properties, such as being highly responsive to input signals.

WSB staff: Richardson,
Collaborators: Spanswick (WMS), Beauvais (WMS)

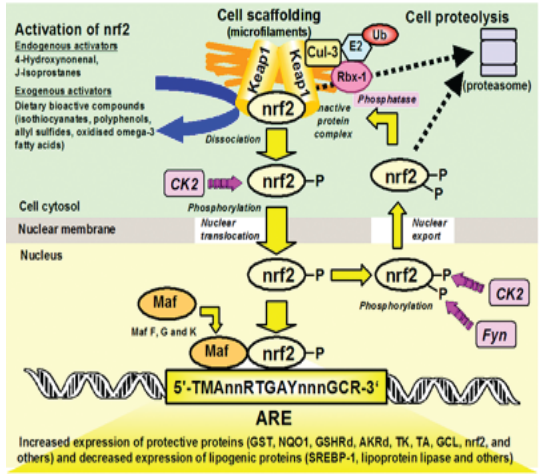
Analytical platform-technology for the assessment of nitric oxide (NO)/oxidative stress-related metabolites

- This enables trace-level quantification of all major NO metabolites in complex biological matrices spanning from yeast to blood and mammalian cells/tissues, allowing an unparalleled insight into systems-wide signalling processes.
- Additional utilisation of tracer technology will allow us to distinguish between endogenous and exogenous (e.g. nutritional) sources and will put us in a position to become a world-leader in assessing regional and global NO/ Reactive Oxygen Species status of complex organisms in basic and translational studies. In conjunction with collaborators.

WSB staff: Feelisch (WMS & WSB)

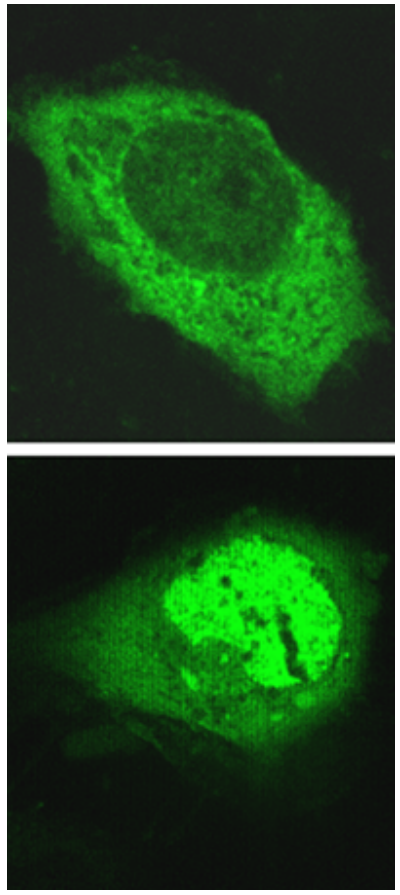
NF-E2-related factor-2 (nrf2) and the anti-stress gene response for good vascular health and healthy ageing. (BBSRC grants and other support, PI Thornalley)

- Use of a fluorescent nrf2 reporter *in vitro* to identify dietary bioactive compounds that provide potent and enduring activation of nrf2 thus activating antioxidant protective genes.
- Custom quantitative gene expression array for screening of health beneficial compounds.
- Mathematical models refined to predict dietary exposure-vascular health benefits.
- Mathematical models refined to healthy ageing benefits.
- Nrf2 activator contents of a some plant lines (rapeseed, tomatoes, broccoli and Rocket salad) foodstuffs rich in bioactives.



Nrf2 activation and ARE-linked gene expression for increased protective and decreased lipogenic response.

Key: CK2, casein kinase 2; E2, ubiquitin activating protein; Fyn, 59-kDa src family-related protein tyrosine kinase; –P, phosphorylation; Ub, ubiquitin.



Nuclear translocation of nrf2 in human HMEC-1 endothelial cells in vitro activated by sulforaphane.

Confocal images of HMEC-1 endothelial cells transfected to express nrf2-GFP fusion protein. Incubation conditions were: left, 5 mM glucose; right - 5 mM glucose + 4 μM SFN. Incubation time: 6 h.

WSB staff: Buchanan-Wollaston, Rabbani, Rand, Thornalley, van den Berg.

Dysfunctional thiamine metabolism and therapy in diabetes

- Increased clearance and tissue-specific deficiency of thiamine in diabetes, link to vascular complications and high dose thiamine therapy.
- Mathematical modelling (physiologically-based pharmacokinetic models) of thiamine metabolism in diabetes to predict tissue-specific deficiency and correction by high dose therapy.

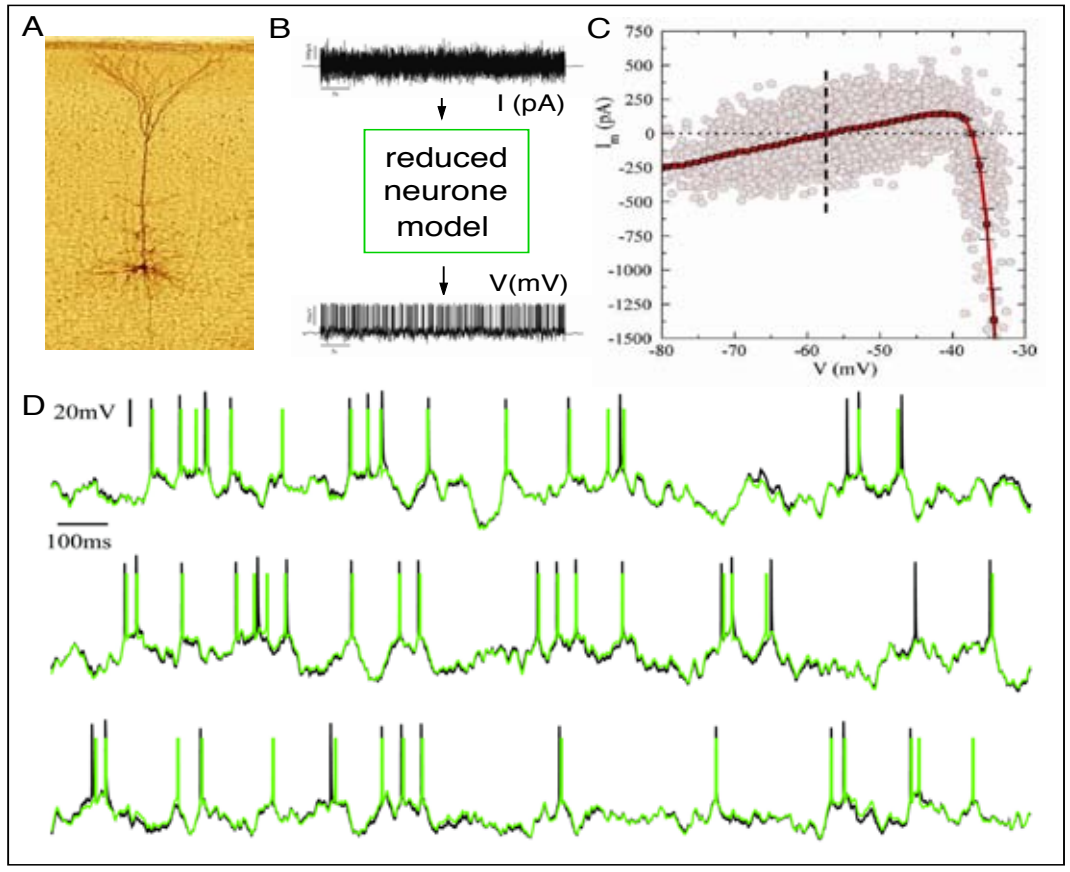
WSB staff': Thornalley, Rabbani,

Computational Neuroscience

Computational neuroscience bridges the gap between cellular and systems level neuroscience.

Recent work has involved:

- the development of a framework to predict the emergent states and information processing capabilities of nervous systems from experimentally measured stochastic properties of the component neurons.
- experimental derivation and testing of reduced neuron models.
- methods for solving the network dynamics of reduced neuron models and for extracting synaptic amplitudes from experiment.
- models of shot-noise synaptic drive and conductance increase, short-term synaptic dynamics, and the shaping of spiking dynamics by sub-threshold resonance in neurons.
- exploration of several important issues related to heath care and diseases such as memory formation, hormone homeostasis, Parkinson's disease, and aging.



Fitting tractable, reduced neurone models to voltage traces of layer-5 cortical pyramidal cells (panel A). The model is derived by matching current and voltage traces (panel B) to yield the I-V curve (panel C) measured under stochastic current injection. The agreement between model (green) and experiment (black) shown in panel D is the current state-of-the-art for reduced model fitting (for more details see: Badel et al, J. Neurophysiol, 2008).

WSB staff: Richardson, Feng
Collaborators: Frengnelli (Warwick)

Plant Systems Biology

PRESTA-Plant responses to environmental stress in Arabidopsis

(Funding includes approx. £5m SABR grant, led by Beynon)

This research aims to combine functional genomics and computational modelling into a novel integrative systems approach, based on a probabilistic modelling technique (Bayesian state-space models), to elucidate key transcriptional networks and underlying regulatory mechanisms controlling plant responses to pathogens, high light and drought. We aim to learn networks integrating transcriptional data with the production of hormones and specific metabolites with well-defined biological activity. One attraction of a Bayesian approach to network structure learning is that it should be possible to incorporate prior information, in the form of known gene-gene regulatory influences that are supported by sources such as the literature, or bioinformatics databases, into the model learning and inference process.

Thus the Bayesian model at each stage can be seen as a distillation of the experimental data obtained up to that point, and since it is a probabilistic model it can be used as an expert prior for the model trained on the next data set. A Bayesian sequential learning strategy can therefore be employed, instead of waiting for all the data to be collected before training the first model. Another key theoretical aim of this project will be the extension of these methods to nonlinear and time-dependent dynamical systems models.

Example gene regulatory network inferred from expression data from *B. cinerea* infected *Arabidopsis* leaves.

Aims:

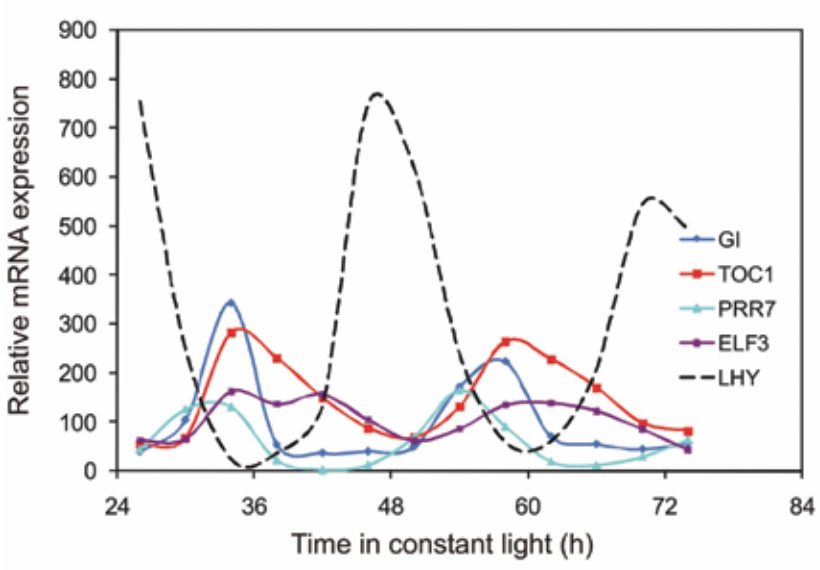
- to build a mathematical model of how the plant leaf switches between alternative responses during environmental challenges
- elucidate the network of transcriptional pathways and underlying regulatory mechanisms controlling plant stress responses; and
- develop and apply novel mathematical/ statistical tools aimed at inferring global networks, modelling, parameterising local networks and predicting the optimal subsequent experiments.
- To identify regulatory regions containing transcription factor binding sites (TFBS) responsible for controlling gene expression in plants.
- To use this information will be used to provide hypotheses to experimental biologists, and to feed into gene regulatory network models.
- TFBS are known to be short degenerate sequences therefore determining them precisely is non-trivial. Our approach utilises information derived from the comparison of homologous sequences that reduces the search space to informative regions of conserved sequence alignment that we term regulatory modules (ReMos).
- We are developing new software platform, "Analysis of Plant Promoter-Linked Elements" (APPLES), which aims to enable sophisticated and biologically meaningful queries surrounding the understanding of transcriptional regulation.

WSB staff: Beynon, Buchanan-Wollaston, Denby, Ott, Rand, Wild.
Collaborators: Finkenstadt (Warwick Statistics), Grant, Smirnoff (Exeter), Mullineaux, Baker (Essex)

Regulation of rhythmic gene expression by the circadian clock.

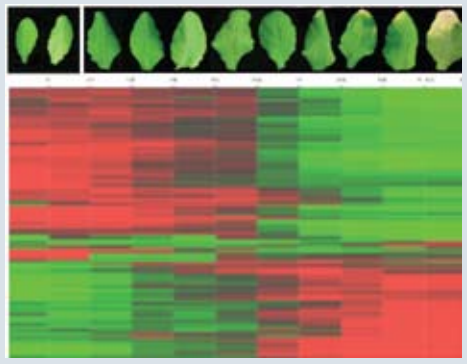
This BBSRC-funded project aims to investigate how the clock can generate a wide range of rhythmic gene expression patterns using a relatively small number of oscillator components. We are focusing our efforts on a transcription factor called LHY, which is one of the central components of the clock. The rhythmic pattern of expression of LHY is known to underlie oscillatory expression of a large number of target genes, which are expressed with a variety of phases.

- We will test whether different on- and off-rates of binding of LHY to different target promoters can account for their different temporal pattern of activation.
- We will identify co-factors that modulate the effect of LHY on its target promoters.
- We will test the contribution of mRNA degradation rates to the timing of mRNA accumulation.
- Novel analysis tools and mathematical models will be produced to understand the regulatory logic underlying different gene expression patterns.



LHY target genes exhibit a wide range of circadian expression patterns

WSB staff: Carre, Rand, Finkenstadt, Ott, Picot, Veflingstad.
Collaborators: Stockley (Leeds)



AGRON-OMICS

€12m Framework VI SB project
(Warwick PI Vicky Buchanan-Wollaston)

Aims:

- study the growth of the leaf following initiation to the end of cell expansion
- analyse leaf development at the phenotypic, transcriptomic, proteomic and metabolomic level; and
- assess the role of different genetic components in altering leaf growth characteristics.

WSB staff: Beynon, Buchanan-Wollaston, Rand.
Collaborators: Hilson (Ghent)

Regulation of biological signalling by temperature (ROBuST)

(Funding includes approx. £5m SABR grant, led by Karen Halliday (Edin.))

- for Arabidopsis, understand the biological basis of network robustness, sensitivity and plasticity of molecular network comprising the phytochrome photoreceptor, circadian clock and cold acclimation pathways with respect to temperature changes in the range from 4 to 27 degrees C
- provide the first detailed understanding of temperature responses across any complex biological signalling network.

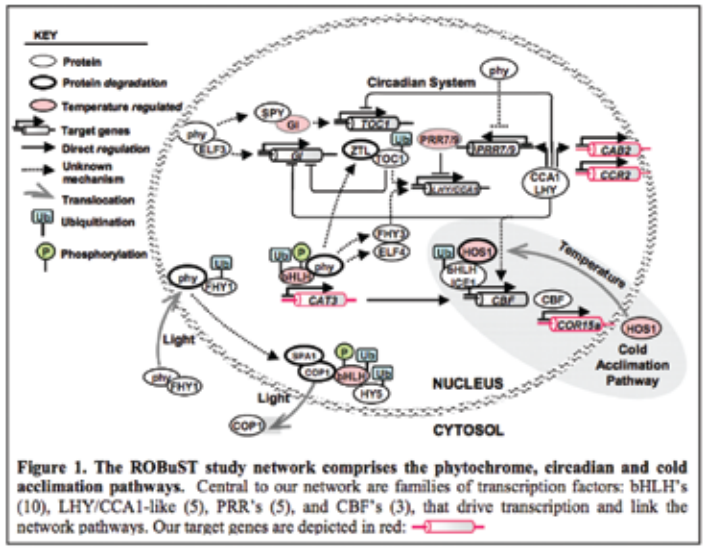


Figure 1. The ROBuST study network comprises the phytochrome, circadian and cold acclimation pathways. Central to our network are families of transcription factors: bHLH's (10), LHY/CCA1-like (5), PRR's (5), and CBF's (3), that drive transcription and link the network pathways. Our target genes are depicted in red:

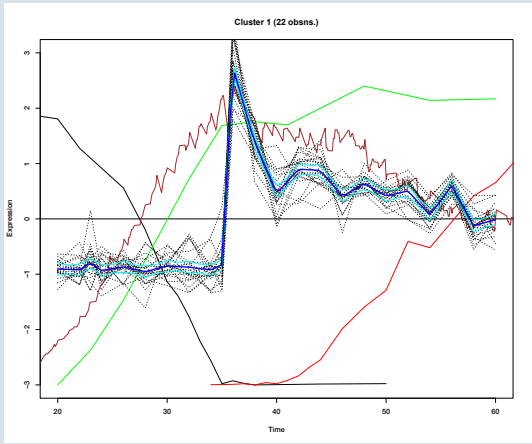
WSB staff: Rand, Finkenstädt.
Collaborators: Halliday, Millar, Goryanin, M Williams (Edinburgh) Graham, Penfield (York) Hall, White (Liverpool)

Microbiology

Global metabolic switching in Streptomyces coelicolor

Funded by a €4.5m SysMO grant (Warwick share approx £1.5m, PI: Liz Wellington) to:

- understand pathway networking in a complex oligotroph where there are clear links between primary and secondary metabolism (antibiotic and other bioactive metabolite production)
- determine the utilisation networks of phosphate, carbon and nitrogen, from environment monitoring (eg PhoP/PhoR for phosphate), through to their impact on the secondary metabolism profiles, incorporating restructuring of primary metabolism (e.g. catabolism network regulation); and
- determine the integration and convergence of regulatory pathways.



Cluster of phosphate related genes showing massive up-regulation as phosphate is depleted.

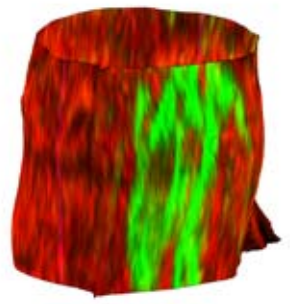
WSB staff: Burroughs, Hodgson, Rand, Wellington and Wild
Collaborators: Smith (Aberdeen), Wohlleben, Nieselt (Tubingen), Dijkhuizen, Breitling, Takano (Groningen), Martin (INBIOTEC), Ellingsen (NTNU)

Spatial Systems Biology

Cellular spatial processes and their dynamics are a particularly challenging field in Systems Biology, incorporating both the challenges of dealing with high dimensional data and the challenge of information processing implicit in image data. Key interests in WSB are in (statistical) information extraction, mechanistic modelling and model fitting; verification of particular mechanisms (or models) being a significant ongoing problem. We specialise in developing system specific quantitative image analysis and statistical methods to analyse complex spatio-temporal dynamics in a (semi)-automated fashion.

The Natural Killer cell synapse and signalling

- Develop tools for analysis of membrane patternation from 2-colour 3D scanning confocal images
- Develop and fit models for receptor relocation and exclusion dynamics to image data
- Generate chimeric HLA-cw6 length mutants and determine dependence of patternation on the length of the MHC-KIR bond
- Test the hypothesis that extracellular domain size is the major factor in patternation
- Determine NK cell function dependence on patternation.

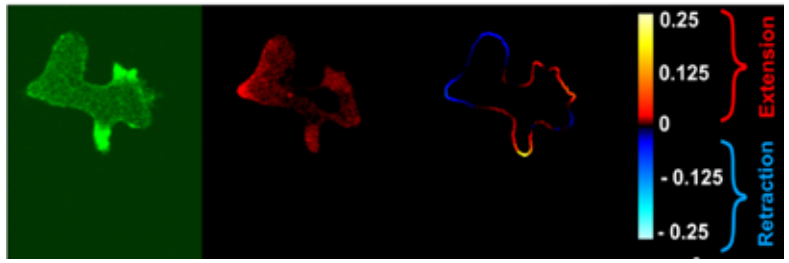


A reconstructed 3D view of HLA-cw6 enrichment (green) and ICAM exclusion (red) from a z-stack of NK cell:target cell conjugate. The limit of the contact interface is indicated in black.

WSB staff: Burroughs.
Collaborators: van der Merwe (Oxford), Davis (Imperial), Gould (Imperial).

Single cell tracking and gene expression in high throughput experiments

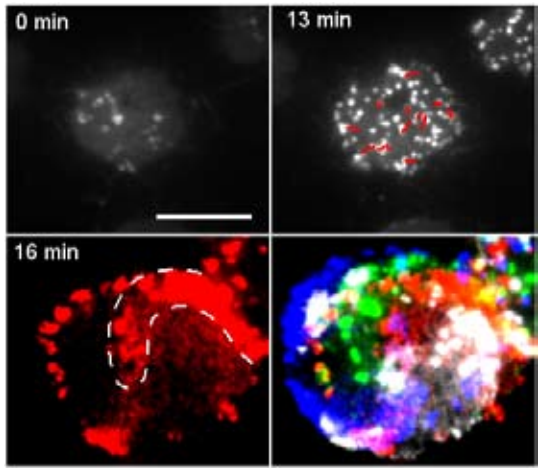
We are developing image segmentation and tracking routines to study the regulation of gene expression and protein dynamics in single cells (see projects NFkappaB signalling, transcriptional control by cis-regulatory modules, spatio-temporal dynamics of the actin cytoskeleton). Through such techniques we are able to determine levels of protein reorganisation, its correlation with signalling and possible causal event sequence.



Automatic quantification of cortical F-actin and Myosin-II dynamics in Dictyostelium cells treated with the chemoattractant cAMP. Active contour methods are used to automatically sample fluorescence intensities within the reference frame of the moving cell, and correlate them with motility parameters like the "Area change" which discriminates between extending (red) and retracting regions (blue).

WSB staff: Bretschneider, Vance, Ott.
Collaborators: Bosgraaf, P. van Haastert (Groningen), Konetges (Warwick), White (Liverpool)

Actin cytoskeleton dynamics and regulation



Actin is highly showing complex patterns both spatially and temporally. Recent evidence suggests it is an excitable system; however achieving an understanding of macroscopic dynamics from the individual components is proving a major challenge. In WSB we use a variety of modelling and image analysis techniques to achieve a multi-scale modelling framework capable of explaining experimental observations.

Time course of reorganisation of the actin structures in Dictyostelium cells after complete depolymerisation with the drug Latrunculin A.

First stationary actin patches appear (0 min) which later become motile (13 min). In this example a propagating spiral waves appears at 16 min.

Bottom right: Superposition of subsequent frames in different colours show rotation around the centre of the cell.

WSB staff: Bretschneider, Burroughs, Turner.
Collaborators: Insall, Anderson (Glasgow), Whitelam (Berkeley)

Key Collaborators include:

K Anderson (Glasgow)
David Broomhead(Liverpool)
R Breitling (Groningen)
Rachel Bearon (Liverpool)
Robin W. Briehl (Albert Einstein Medical School)
D Dan Davis (Imperial)
L Dijkhuizen (Groningen)
T E. Ellingsen (NTNU)
Frank Ferrone, (Drexel)
Ian Graham (York)
Igor Goryanin (Edinburgh)
M Grant (Exeter)
A Holden (Leeds)
Anthony Hall (Liverpool)
Karen Halliday (Edinburgh)
Pierre Hilson (Ghent)
Robert Insall (Glasgow)
Dean Jackson (Manchester)
Robert Josephs, (Chicago)
Douglas Kell (Manchester)
P Krabben (UCL)
F Martin (INBIOTEC)
A Millar (Edinburgh)
Davide Marenduzzo (Edinburgh)
T Miyata (Tohoku, Japan)
P Mullineaux (Essex)
K Nieselt (Tubingen)
Norman Paton (Manchester)
Pawel Paszek (Liverpool)
Steve Penfield (York)
M C M Smith (Aberdeen)
Nick Socci (Memorial Sloan Kettering Cancer Center)
Pierre Sens (ESPCI, Paris)
Violaine Sée (Liverpool)
E Takano (Groningen)
A Van der Merwe (Oxford)
M White (Liverpool)
Matthew Williams (York)
W Wohlleben (Tubingen)
M Yamamoto (Tohoku, Japan)
H, Zhang (Manchester)

Doctoral Training Centre

Director: Vicky Buchanan-Wollaston

Successful research in Systems Biology demands a new breed of cross-disciplinary scientist who is not constrained by traditional categorisations and who can communicate with experts in both biological and physical sciences. Crucially, these scientists must work naturally in multidisciplinary teams, sharing their own skills as well as taking advantage of those of others.

At the Warwick Systems Biology Doctoral Training Centre (WSB-DTC) we have established a training program to meet this demand: to enable a new generation of scientists who can combine knowledge of the biological system under study with an understanding and ability to exploit statistical, computational and mathematical methods. Funding from the EPSRC and BBSRC supports around 10 students per year in a 1+3 year programme The one-year MSc in Systems Biology involves 8 taught modules and two mini-projects in two distinct research environments: 'wet' biology and computation/mathematics. Two intake streams (biological or theoretical) allow advanced training in a student's own discipline as well as underpinning training in the other.

This is followed by a 3 year PhD project where each student is made a key member of a multidisciplinary Systems Biology team, the core of which consists of two co-supervisors drawn from a life science and a physical science. Every student thus receives on-the-job training at the interface between the life sciences and mathematics, statistics, informatics etc. A distinctive feature of the WSB-DTC is the broad range of available life science research areas from biomedical to bacteria and plants as described above in this brochure.

The WSB-DTC provides a supportive environment within a dedicated home base, in close proximity to staff members and benefiting from the expertise of a cohesive cohort of fellow students with a range of biological and physical science backgrounds. The DTC is directed by Vicky Buchanan-Wollaston and is closely associated with another Warwick Doctoral Training Centre, MOAC (Molecular Organisation & Assembly in Cells) (Director: Alison Rodger, funded by the Life Sciences Programme of the EPSRC) with a shared administration team and common room facilities.

www2.warwick.ac.uk/fac/sci/sbdtc/

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