

52nd Gregynog Statistical Conference 15th – 17th April 2016



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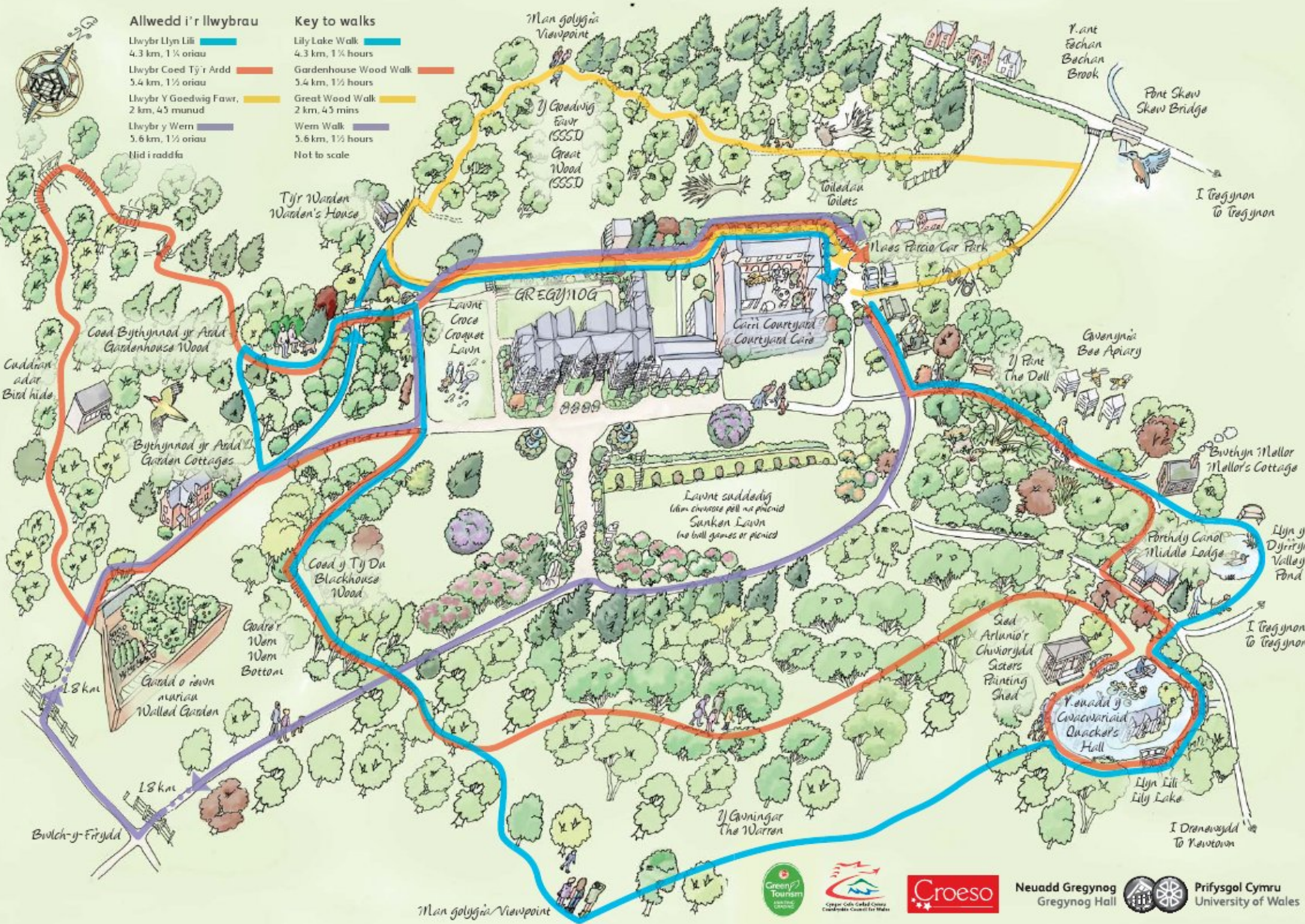
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Allwedd i'r llwybrau

- Llwybr Llyn Lili █
4.3 km, 1½ oriau
- Llwybr Coed Tŷ i'r Ardd █
5.4 km, 1½ oriau
- Llwybr Y Goedwig Fawr █
2 km, 45 munud
- Llwybr y Wern █
5.6 km, 1½ oriau
- Nid i raddfa

Key to walks

- Lily Lake Walk █
4.3 km, 1½ hours
- Gardenhouse Wood Walk █
5.4 km, 1½ hours
- Great Wood Walk █
2 km, 45 mins
- Wern Walk █
5.6 km, 1½ hours
- Not to scale



Neuadd Gregynog
Gregynog Hall



Prifysgol Cymru
University of Wales

Man golygfa Viewpoint



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1 Administrative Details

1.1 About

- The “52nd Gregynog Statistical Conference” will take place from Friday, 15th – Sunday, 17th April 2016 at Gregynog Hall, in the fantastic Welsh countryside. The conference will comprise 1 short course, 8 research talks a Gregynog talk and a poster session aimed at a general mathematical audience. There will be lots of opportunity (particularly for research students) to get to know one another, explore the numerous walks around the hall, take an excursion to Powis Castle and Garden and even attend the final of the Gregynog Young Musicians Competition.
- Organising Committee: Maggie Chen (Swansea), Jane Hutton (Warwick) and Kim Kenobi (Aberystwyth) and Murray Pollock (Warwick).

1.2 Webpages

- Conference: www.warwick.ac.uk/gregynog
- Past Conferences / History: www.warwick.ac.uk/gregynog/past
- Gregynog Young Musicians Conference: https://en.wikipedia.org/wiki/Gregynog_Young_Musicians_Competition

1.3 Key Dates & Times

- **Arrival & Check-In:** 2pm, Friday (Gregynog Hall Shop).
- **Welcome:** 2.55pm, Friday (Seminar Room, 2nd Floor)
- **First Talk:** 3pm, Friday.
- **Poster Session:** 8pm, Saturday.
- **Breakfast:** 8am (Saturday / Sunday – Dining Room).
- **Coffee Breaks / Afternoon Tea:** 11am / 4pm (Blayney Room).
- **Lunch:** 12.30pm (Saturday / Sunday – Dining Room).
- **Dinner:** 7pm on Friday; 6pm on Saturday (Dining Room).
- **Bar:** 9pm (Friday / Saturday – Basement).
- **Departure:** 1.30pm, Sunday.

1.4 Internet Access

- Wireless access is available in the lecture rooms and public areas. Note that from experience the wireless can be poor.

1.5 Gregynog Speaker

- This year we are reprising the “Gregynog Speaker”. Originally the Gregynog conference had in addition to traditional academic talks a “Gregynog Speaker” - who either talked about Gregynog Hall, or were artists who talked about their work.
- This year Mary Oldham, who is the librarian at Gregynog, will talk to us about the printing press and library at Gregynog .
- Library: <http://www.gregynog.org/visit/library>
- Press: https://en.wikipedia.org/wiki/Gregynog_Press

1.6 Gregynog Young Musicians Conference

- Gregynog Young Musicians Competition began in 2005, originally as part of the Gregynog Festival, and more recently as a free-standing event. It is held at Gregynog Hall and is open to instrumentalists under the age of 18.
- The competition will take place on Saturday evening, and those interested in attending (time has been made in the schedule) ought to refer to the following website to purchase a ticket:
- Webpage: <http://www.gregynogymc.co.uk>

1.7 Powis Castle Excursion

- An optional excursion to Powis Castle will take place on the Saturday after lunch. Please speak to Jane Hutton for further details and to register your interest.
- Powis Castle (Welsh: Castell Powis) is a medieval castle, fortress and grand country mansion located near the town of Welshpool, in Powys, Mid Wales. The residence of the Earl of Powis, the castle is known for its extensive, attractive formal gardens, terraces, parkland, deerpark and landscaped estate. The property is under the care of the National Trust, who operate it under the name “Powis Castle and Garden”. Princess Victoria (later Queen Victoria) visited the castle as a child when her mother took her to tour England and Wales in 1832.
- Webpage: www.nationaltrust.org.uk/powis-castle

2 Getting to Gregynog

2.1 Venue Details

- **Address:** Gregynog Hall, Tregynon, Nr. Newtown, Powys, SY16 3PW
- **Telephone:** 01686 650224
- **Webpage:** www.gregynog.org
- **Contact / Travel Information:** www.gregynog.org/contact/



2.2 Getting there by Minibus

- A minibus will leave from Warwick Statistics common room at 12pm *sharp* on the Friday going to Gregynog Hall, and leave from the Gregynog Hall dining room at 1.30pm *sharp* on the Sunday returning to Warwick. Individuals must request a place on the minibus. There will be limited space on the minibus, so please do not overpack.

2.3 Getting there by Car

- Gregynogs location near the quiet village of Tregynon, 6 miles north of Newtown in Powys, makes it reachable within 3 hours from all parts of Wales, within 2 hours from Birmingham, Manchester, Chester and Liverpool and just 50 minutes from Shrewsbury.
- **From Newtown**

- Entering Newtown from the South, keep on the A489 until you reach the traffic lights at McDonalds. Turn left at the traffic lights (keeping McDonalds on your left).

Go over the river bridge following signs for the hospital. Take the fifth turning on the right (opposite the Bell Hotel). Carry on up the hill out of Newtown for approx. 6 miles.

The entrance to Gregynog is sign-posted on the left just before the village of Tregynon.

- **From Welshpool**

- Head towards Newtown on the A483 for approx. 4 miles. Turn right towards Berriew (B4390).

In Berriew village take the second turning on the left, sign posted Bettws Cedewain 5 miles.

In Bettws follow the road round to the right (keeping the New Inn pub on your right) sign-posted Tregynon 2.5 miles.

At the next T junction the entrance to Gregynog is sign posted straight opposite.

- **For satellite navigation**

- Use the postcode SY16 3PL, which will bring you into the Hall grounds via the main Estate entrance. From the Berriew direction, it may also direct you to turn right towards Brooks, which is a steep single track road. Please ignore this and continue onto Bettws Cedewain.

2.4 Getting there by Train

- Rail links are via the Birmingham Aberystwyth line. The local train station is Newtown (Powys), approximately a 12 taxi journey from Gregynog Hall. There are direct trains to Newtown (Powys) from Birmingham Int'l and Birmingham New Street.

2.5 Local Taxi Companies

- **Station Taxis:** 01686 621818
- **Pauls Taxis:** 01686 624314
- **Ross Taxis:** 01686 627600

3 About Gregynog

3.1 History

Gregynog has existed for 800 years. By the 16th century it was the home of the Blayney family, local gentry who claimed descent from the early Welsh princes and whose courage and benevolence were praised by the court poets. Their coat of arms is the centrepiece of the fine oak carvings in what we now call the Blayney Room.

For hundreds of years Gregynog was one of Montgomeryshires leading landed estates, at the heart of the community and the local economy. The Blayney squires gave way to the Lords Sudeley, then Lord Joicey.

After several hundred years of private ownership, in 1913 a huge estate sale saw Gregynogs farms, cottages and woodlands sold off, many to their tenants. Gregynog Hall might have been demolished had not the wealthy Davies sisters acquired it in 1920 to become the headquarters of their enterprise to bring art, music and creative skills to the people of Wales in the aftermath of the First World War.

For twenty years the house was full of music, fine furniture and ceramics, hand-printed books from the Gregynog Press and, most extraordinary of all, the sisters collection of paintings by artists such as Monet, Cezanne and Van Gogh. Leading lights, such as George Bernard Shaw and Gustav Holst visited during these years for musical concerts or simply to enjoy the beautiful gardens and woodland walks.

At the end of the 1950s, after wartime use as a Red Cross convalescent home, Gregynog was bequeathed to the University of Wales as a conference centre. It welcomed its first students in 1963 and theyve been coming ever since! But the old Gregynog lives on the music, the art, the printing press and the gardens. It is still a magical, timeless place where you can walk in the grounds on a quiet evening and listen to the birdsong just as the Davies sisters did many decades ago.

3.2 Walks

The gardens at Gregynog are unrivaled, offering a mixture of formal and woodland walks.

To assist our visitors in fully appreciating the beauty and diversity of the estate, we have created a variety of colour-coded woodland walks. The walks are of varying length and difficulty, weaving their way through the estate to offer tantalising views of both the Hall and the stunning Montgomeryshire countryside.

The new Lily Lake Walk, Warren Walk, Great Wood Walk and Valley Walk have been created to offer something of interest to everyone.

Attractions on the walks include the secluded Mellors cottage, the Davies sisters painting shed and Quackers Hall, perched in the middle of the lily lake, and a birdwatching hide located deep in the Garden House Wood. Simultaneously striking and amusing is the stone statue of a giant hand protruding from the earth, a particular favourite of passers-by taking a woodland stroll. Against this backdrop, the meandering Bechan Brook flows through the estate attracting birds, including kingfishers.



The Bee Apiary, acknowledged to be the prettiest in Wales, is located in the Dell. Visitors can see the bees flying from their hives and coming back again after collecting pollen from the gardens. The attractive viewing shelter has been designed to allow close but safe access to the bees: there are over one million of them, and contains interpretation boards describing the importance of bees, their life cycle and the various types of hives within the apiary. Find out about when the beekeepers will be in the apiary, as they will bring frames of bees close enough for you to see and smell, by visiting the Monty Bees website.

With support from Natural Resources Wales, a number of wildlife interpretation boards are installed throughout the estate, enabling visitors to understand the importance of the natural environment within Gregynog, recently designated a National Nature Reserve.

Our walks are naturally maintained, mainly by people's feet and dogs' paws with minimal interference in this unspoilt environment. You may find yourself bashing through bracken and wading through muddy patches at times .. just a perfect escape in the wilds of Wales, but bring your boots!

3.3 Library

A unique collection of books

The fine arts, Gregynog Press books, Welsh history, literature, culture and language

The books on open access in the west corridor and in the Thomas Jones Library and Dora Herbert Jones Library are the most visible part of a substantial collection of books and



archive material held at Gregynog. Many of the books once belonged to the Davies sisters, although most of the general non-fiction collection has been acquired since the 1960s when the University of Wales took over the hall. The policy behind the development of the library over the years has been firstly, to complement the activities which take place at Gregynog; secondly, to offer insights into its history and its special significance to music, art and fine printing; and thirdly, to reflect its nature as an institution at the heart of Welsh cultural life.

In addition, a considerable number of documents and other items relating to the history of the house have been collected over the years and these are now listed and stored securely. This includes a full set of Gregynog Press and Gwasg Gregynog publications which can be consulted on application.

However it should be noted that most surviving archive material relating to Gregynog, including items such as the Visitors Book kept here in the 1920s and 1930s, is now in the National Library of Wales in Aberystwyth.

Gregynog Library books are not available for external loan, but we welcome Visiting Readers. By becoming a Gregynog Member you can apply for a Visiting Readers ticket which will entitle you to visit Gregynog on most occasions when the house is open, to research, study or just browse in the library.

Books on open access for browsing and private reading are arranged as follows:

1 The Library Corridor

The books on open access in the library corridor are general non-fiction books and literature. Subjects include philosophy, religion, history and literature. There is a large collection of books on the fine arts, including Impressionist and Post-Impressionist painters, also printing, binding and the book arts. Journals include *The Studio* magazine dating back to the early 20th century, also *The Burlington Magazine* and other art related journals.

Gregynogs collection of material relating to Irish language and literature is shelved here, and at the far end of the corridor is a separate collection of material relating to Arthurian myth and legend as it spread from its Celtic roots to German, France and beyond.

2 The Thomas Jones Library

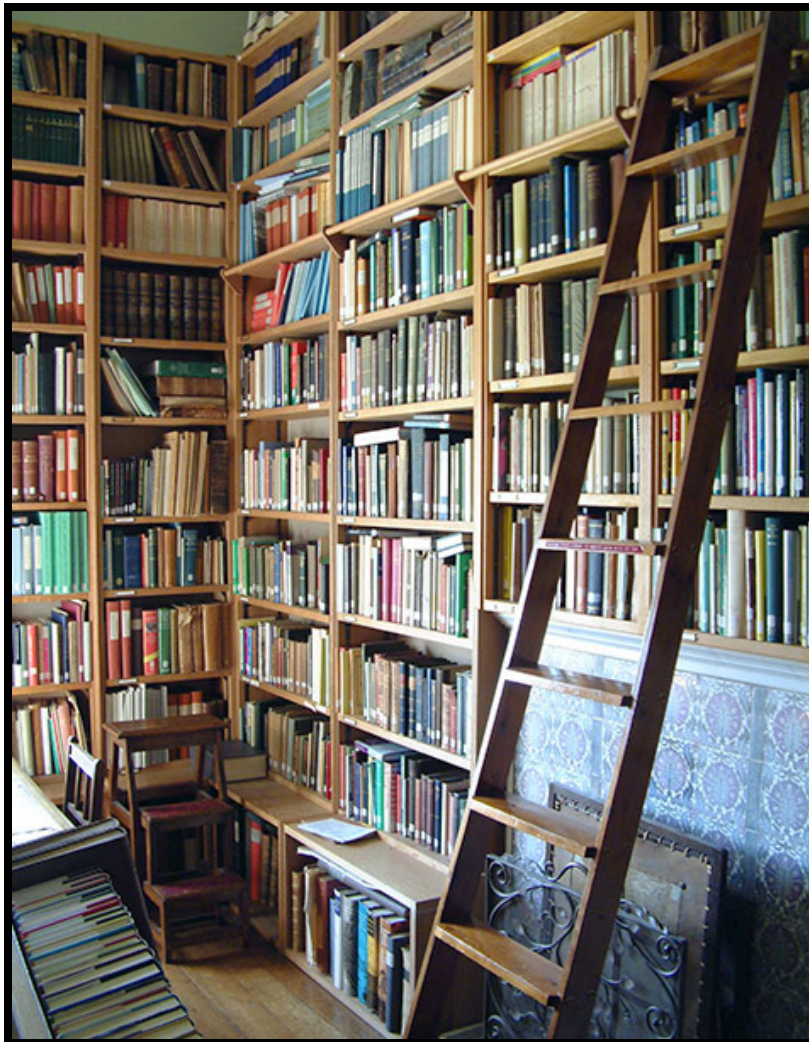
The Thomas Jones library houses a collection of reference books, encyclopaedias, dictionaries, atlases etc., including some useful horticultural reference books. A section of the Fine Art Collection is also housed in this room, which is in regular use for meetings and seminars.

3 **The Music Library**

This is a collection of books shelved in the corridor next to the Music Room. It includes an early edition of Groves Dictionary of Music, and a large collection of biographies of musicians and composers.

4 **The Dora Herbert-Jones Library**

This is what is known as the small library at the far end of the library corridor, where the Librarians desk and computer are also located. All the books and journals in this library relate to Wales and the Celtic countries, either in Welsh or other Celtic languages, or about Wales and the Celtic countries, their history, literature and culture.



4 Timetable

4.1 Friday 15th April

All talks will take place in the Seminar Room, 2nd Floor.

Time	Presenter	Title	Pg
12:00	Warwick Minibus	Departure from Statistics Common Room 12:00 sharp	-
14:30	Arrival & Check-In	Gregynog Hall Shop	-
14:55	Murray Pollock	Welcome and Information	-
15:00	Theo Kypriaos	Recent Developments in Bayesian Non-Parametric Inference for Epidemic Models	19
16:00	Afternoon Tea	Blayney Room	-
17:00	Deirdre Hollingsworth	Providing useful insights when working on a neglected tropical disease	17
18:00	Mary Oldham	The Gregynog library and printing press	-
19:00	Dinner	Dining Room	-
20:15	David Colquhoun	The misinterpretation of p values and the reproducibility of science: why haven't statisticians told us?	16
21:15	Bar	Basement	-

4.2 Saturday 16th April

All talks will take place in the Seminar Room, 2nd Floor.

Time	Speaker	Title	Pg
08:00	Breakfast	Dining Room	-
09:00	Simon Spencer	Bayesian inference and model selection for stochastic epidemics (with special attention to <i>Escherichia coli</i> O157:H7 in cattle)	19
10:00	Andy Golightly	Building bridges: Improved bridge constructs for stochastic differential equations	17
11:00	Coffee Break	Blayney Room	-
11:30	Tom Nichols	Meta-Analysis: Review and new developments in neuroimaging	15
12:30	Lunch	Dining Room	-
13:00	<i>Free Afternoon</i>	<i>Optional Powis Castle trip 13:00-16:45</i>	-
16:00	Afternoon Tea	Blayney Room	-
17:00	Andreas Artemiou	Sufficient Dimension Reduction in Regression	16
18:00	Dinner	Dining Room	-
19:00	<i>Free Time</i>	<i>Optional Gregynog Young Musicians Conference</i>	-
20:00	Poster Session	-	-
	Muteb Alharthi	Bayesian model choice for epidemic models with missing data	-
	Francois-Xavier Briol	Probabilistic Integration with Theoretical Guarantees	20
	Jake Carson	Unbiased Solutions of PDE Models via the Feynman-Kac Formulae	-
	Cyril Chimisov	Adaptive Gibbs Sampling	-
	Jon Cockayne	Probabilistic Numerical Methods for the Solution of Partial Differential Equations	20
	Ruth Harbord	Inferring Brain Connectivity with the Multiregression Dynamic Model	-
	Jere Koskela	Efficient sequential Monte Carlo sampling of rare trajectories in reverse time	21
	Boryana Lopez Kolkovska	Survival Analysis Models on MESS epilepsy data	21
	Audrey Kueh	Modelling Penumbra in Computed Tomography	21
	Matt Moores	Lorentzian mixture model for Raman spectroscopy	-
	Murray Pollock	Exact Simulation in a Nutshell	-
	Ewart Shaw	Statistical Inference, Orthogonal Polynomials and Electrostatics	-
	Simone Tiberi	Bayesian hierarchical stochastic analysis of multiple single cell Nrf2 protein levels	22
	Panayiota Touloupou	Scalable inference for Markovian and non-Markovian Epidemic Models	-
21:15	Bar	Basement	-

4.3 Sunday 17th April

All talks will take place in the Seminar Room, 2nd Floor.

Time	Speaker	Title	Pg
08:00	Breakfast	Dining Room	-
09:00	Ruth King	Incorporating memory into capture-recapture models using a first-order hidden Markov model(!)	18
10:00	Chris Jewell	Forecasting for outbreaks of vector-borne diseases: a data assimilation approach	18
11:00	Coffee Break	Blayney Room	-
11:20	Group Photo	Location weather dependent	-
11:30	Tom Nichols	High- and low-tech solutions for multiple testing in large scale inference	15
12:30	Lunch	Dining Room	-
13:30	Departure	-	-
13:30	<i>Warwick Minibus</i>	<i>Departure from dining room immediately after lunch</i>	-

5 Abstracts

5.1 Short Course Abstracts

Meta-Analysis: Review and new developments in neuroimaging

Tom Nichols
University of Warwick

Meta-analysis is the combination of independent statistical results, with the goal of obtaining greater sensitivity and understanding whether some positive findings in the literature are evidence of a true effect or just idiosyncratic. I will review the standard tools of meta-analysis, and show how they have been adopted (or not) into my area, brain imaging. Brain imaging presents several special challenges, in particular because the full statistical results are usually not shared, but instead only a sparse summary is reported. I will describe work from my group using spatial Bayesian point process methods to conduct neuroimaging meta-analyses on these type of summary data.

High- and low-tech solutions for multiple testing in large scale inference

Tom Nichols
University of Warwick

Modern scientific methods typically rely on massive data where thousands to millions of variables are measured (e.g. gene expression, single nucleotide polymorphisms, brain images, etc), and often on just 10's of subjects or units. This massive multiplicity must be accounted for in the inference procedures, and with such small samples asymptotic methods cannot be necessarily depended on. I will review the multiple testing problem in general (for any type of data) and the approaches that are used to address it. I will then describe my own work on multiple testing for brain imaging, showing how both 'high-tech' methods using the geometry of random fields as well as 'low-tech' resampling-based methods are needed to make inferences on brain images while controlling for the multiple testing problem.

5.2 Talk Abstracts

Sufficient Dimension Reduction in Regression

Andreas Artemiou
Cardiff University

In this talk I will give an overview of Sufficient Dimension Reduction (SDR) and how it can be used in regression and classification problems. I will start with a historical overview, to emphasize the fact that Principal Component Analysis (PCA) - an unsupervised dimension reduction method - may fail in regression. SDR as a class of supervised dimension reduction methods is being developed the last 25 years and I will present some of the key developments. Lastly I will discuss about the development of a new class of SDR methodology which incorporates the use of Support Vector Machines (SVM) and its variants for more accurate and robust estimation of the reduced subspace in these methodology. I will try to present key ideas with main references and stay away from complicated formulas.

The misinterpretation of p values and the reproducibility of science: why haven't statisticians told us?

David Colquhoun
University College London

There's nothing wrong with P values. They do what it says on the tin. The problem lies in the fact that what they do is not what experimenters want. What they want to know is the probability that, if they claim an effect is real, they'll be wrong. Many experimenters believe that this is what the P value tells you, but of course it isn't. It is easy to show that, if you observe $P = 0.047$ in a single test of significance, and claim on that basis that the effect is real, you'll be wrong at least 26% of the time (and a great deal more often if the hypothesis is implausible) - eg see <http://rsos.royalsocietypublishing.org/content/1/3/140216> - This alone is sufficient to account for much of the reproducibility crisis that has engulfed some areas of science, e.g. experimental psychology. Although the argument behind this conclusion is Bayesian (which is probably why I took so long to notice it) I believe that it is free of any subjective elements. By failing to emphasize this in elementary courses, and by being complicit in allowing the tyranny of $P = 0.05$ in papers, I fear that statisticians may have contributed to the irreproducibility crisis that it is their job to prevent.

Building bridges: Improved bridge constructs for stochastic differential equations

Andy Golightly
Newcastle University

We consider the task of generating discrete-time realisations of a nonlinear multivariate diffusion process satisfying an Ito stochastic differential equation conditional on an observation taken at a fixed future time-point. Such realisations are typically termed diffusion bridges. Since, in general, no closed form expression exists for the transition densities of the process of interest, a widely adopted solution works with the Euler-Maruyama approximation, by replacing the intractable transition densities with Gaussian approximations. However, the density of the conditioned discrete-time process remains intractable, necessitating the use of computationally intensive methods such as Markov chain Monte Carlo. Designing an efficient proposal mechanism which can be applied to a noisy and partially observed system that exhibits nonlinear dynamics is a particularly challenging problem, and is the focus of this talk. By partitioning the process into two parts, one that accounts for nonlinear dynamics in a deterministic way, and another as a residual stochastic process, we develop a class of novel constructs that bridge the residual process via a linear approximation. As well as compare the performance of each new construct with a number of existing approaches, we illustrate the methodology in a real data application.

Providing useful insights when working on a neglected tropical disease

Deirdre Hollingsworth
University of Warwick

Neglected tropical diseases (NTDs) are a group of infections which predominantly affect the bottom billion, or the poorest people in the world. They are responsible for chronic suffering as well as mortality in these hard to reach populations. In recent years there has been a drive to reduce the burden of these diseases through an international effort to roll out interventions at a global scale. There is a need for epidemiological modelling to assess the required duration and coverage of these interventions, as well as to evaluate whether additional interventions will be required to reach the 2020 goals, and perhaps even permanently interrupt transmission. NTDs are neglected not only in terms of their public health burden, but also in our limited understanding of their biology and life cycles, with remarkably few epidemiological studies from which to parameterise or, in some cases, even hypothesise structures for transmission models. However, this need not limit the public health policy aspirations for control - Guinea worm is close to global eradication despite remarkably limited knowledge about its biology within the host. Many other NTDs have had their prevalence and incidence reduced substantially through application of relatively straightforward interventions, but elimination may prove more challenging. Mathematical models are being used to inform policy and guide the development of new strategies to reduce transmission. Even simple mathematical models can capture much of the qualitative behaviour of these systems, but developing, validating and testing models which can be used to give detailed policy guidance is more challenging.

Forecasting for outbreaks of vector-borne diseases: a data assimilation approach

Chris Jewell

Lancaster University

In August 2012, the first case of a novel strain of *Theileria orientalis* (Ikeda) was discovered in a dairy herd near Auckland, New Zealand. The strain was unusually pathogenic, causing haemolytic anaemia in up to 35% of animals within an infected herd. In the ensuing months, more cases were discovered in a pattern that suggested wave-like spread down New Zealand's North Island. *Theileria orientalis* is a blood-borne parasite of cattle, which is transmitted by the tick vector *Haemaphysalis longicornis*. This tick was known to exist in New Zealand, but although its behaviour and life cycle were known from laboratory experiments surprisingly little was known about its country-wide distribution. Predicting the spread of *T. orientalis* (Ikeda) for management and economic purposes was therefore complicated by not knowing which areas of the country would be conducive to transmission, if an infected cow happened to be imported via transportation. The approach to prediction presented here uses a Bayesian probability model of dynamical disease spread, in combination with a separable discrete-space, continuous-time spatial model of tick abundance. This joint model allows inference on tick abundance by combining information from independent disease screening, expert opinion, and the occurrence of theileriosis cases. A fast GPU-based implementation was used to provide timely predictions for the outbreak, with the predictive distribution used to provide evidence for policy decisions.

Incorporating memory into capture-recapture models using a first-order hidden Markov model(!)

Ruth King

University of Edinburgh

In this talk we focus on incorporating memory into ecological models. In particular we consider capture-recapture studies, where observers going into the field at a series of capture events. At the initial capture event all observed individuals are uniquely marked, recorded and released back into the population. At each subsequent capture event previously unmarked individuals are marked and all observed individuals are recorded before being released. This leads to data of the form of the capture history of each individual observed, recording whether or not they are observed at each capture event.

We will initially describe how standard capture-recapture models can be expressed as a hidden Markov-type model. We describe the advantages of specifying the models in this framework, including efficient model-fitting techniques and incorporating additional processes. In particular, we focus on open multi-state capture-recapture data, where individuals are recorded in a given discrete time-varying state when they are observed. For example, state may refer to breeding/not breeding or hungry/not hungry. For mathematical convenience it is often assumed that transitions between states can be modelled as first-order Markovian (and hence memoryless). However, this is often biologically unrealistic. We will consider the incorporation of memory in a parsimonious manner via the specification of a semi-Markovian transition model and describe how the models can be efficiently fitted using a first-order Markov approximation. We apply the approach to house finch data where state corresponds to infected or not infected with conjunctivitis.

Recent Developments in Bayesian Non-Parametric Inference for Epidemic Models

Theo Kypriaos
University of Nottingham

Despite the enormous attention given to the development of methods for efficient parameter estimation, there has been relatively little activity in the area of non-parametric inference. That is, drawing inference for the quantities which govern transmission, i) the force of infection and ii) the period during which an individual remains infectious, without making certain modelling assumptions about its (parametric) functional form or that it belongs to a certain family of parametric distributions. In this talk we will describe three approaches which allow Bayesian non-parametric inference for the force of infection; namely via Gaussian Processes, Step Functions, and B-splines. We will also illustrate the proposed methodology via both simulated and real datasets.

Bayesian inference and model selection for stochastic epidemics (with special attention to *Escherichia coli* O157:H7 in cattle)

Simon Spencer
University of Warwick

Model fitting for epidemics is challenging because not all of the information needed to write down the likelihood function is observable, for example the times of infection and recovery are not usually observed. Furthermore, the data that are available from diagnostic tests may not be perfectly accurate. These considerations are typically overcome by applying computationally intensive data augmentation techniques such as Markov chain Monte Carlo. To make things even more difficult, most of the interesting epidemiological questions are best expressed as model selection problems and so fitting just one model is not sufficient to answer them. Instead we must fit a range of different models, each representing an important epidemiological hypothesis, and then make meaningful comparisons between them. I will describe how to overcome (most of) these difficulties to learn about the epidemiology of *Escherichia coli* O157:H7 in cattle. Joint work with Panayiota Touloupou, Bärbel Finkenstädt Rand, Pete Neal and TJ McKinley.

5.3 Poster Abstracts

Probabilistic Integration with Theoretical Guarantees

Francois-Xavier Briol

University of Warwick

The field of probabilistic numerics focuses on the study of numerical problems from the point of view of statistical inference, often from a Bayesian perspective. In the specific case of integration, Bayesian Quadrature (BQ) provides estimators for the value of integrals together with a measure of our uncertainty over the result, which takes the form of a posterior variance. These estimators have been shown empirically to converge quickly to solution of the integral, however, no explicit rates of convergence were known until very recently. This poster will present a recent paper which provides the very first rates of convergence and posterior contraction of BQ. Those are obtained by combining BQ with a convex optimisation algorithm called the Frank-Wolfe algorithm. This allows for a very efficient quadrature method which can have up to exponential convergence in the number of samples, and hence compares favourably to most Monte Carlo methods. Our approach is applied to successfully quantify numerical error in the solution to a challenging Bayesian model choice problem in cellular biology.

Probabilistic Numerical Methods for the Solution of Partial Differential Equations

Jon Cockayne

University of Warwick

Recent work establishes probabilistic foundations for models of the numerical error arising in the numerical solution by finite element approximation of ordinary and partial differential equations (PDEs). Such methods are of particular interest for PDEs since explicit solutions are rarely available, and obtaining numerical estimates at arbitrary precision is often computationally infeasible. Thus, a rigorous quantification of uncertainty in the approximate solution is important. We seek to develop methods for obtaining probabilistic measures of uncertainty for linear and nonlinear PDEs when solved numerically.

Efficient sequential Monte Carlo sampling of rare trajectories in reverse time

Jere Koskela

University of Warwick

Rare event simulation seeks estimate probabilities of unlikely but significant events, such as extreme weather, market crashes, or failure rates in communications networks. In complex models the probabilities of such events are often intractable, and naive simulation fails because of the low probability of the event of interest. Sequential Monte Carlo provides a practical method for sampling rare events by biasing probability mass toward the event of interest, though as always the design of good proposal distributions is difficult but crucial. The typical approach for sampling rare trajectories of a stochastic process is an exponential twisting of the forward dynamics, motivated by approximating a large deviation principle. I present an alternative, based on the observation that a forwards-in-time trajectory conditioned to end in a rare state coincides with an unconditioned reverse-time trajectory started from the rare state. This observation has led to very efficient simulation methods in coalescent-based population genetics. I will introduce reverse-time SMC as a generic algorithm, discuss settings in which it is advantageous, and present some novel applications both for coalescents and other stochastic processes.

Survival Analysis Models on MESS epilepsy data

Boryana Lopez Kolkovska

University of Warwick

In the Multicentre study of early Epilepsy and Single Seizures (MESS) study, patients diagnosed with epilepsy were subjected to a randomized controlled trial policies of immediate versus deferred treatment. We are interested in providing a prognosis for the patients and clinicians from the study, and propose to apply Survival Analysis methods. A first approach proposed by J. Rogers is presented, where the times to a first seizure are modeled by a negative binomial mixture model, with a gamma distributed random effect. The model considers the existence of a proportion of patients who attain remission post-randomization, and terms such proportion of patients as a cure fraction of the population. For this model each patient is considered to have an individual seizure rate, which is assumed to change when randomized to an anti-epileptic drug. The underlying seizure rate, post-randomization rate change for each patient and the population's heterogeneity coefficient are estimated from Rogers model. For this type of live recurrent events, Cox proportional hazards models are commonly used. We perform a residual analysis on Cox and Rogers models, in order to compare and study their goodness of fit. From such results and the inherent nature of patients diagnosed with epilepsy, we present a truncated negative binomial mixture model.

Modelling Penumbra in Computed Tomography

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The spot geometry in Computed Tomography (CT) may fluctuate from scan to scan. A model is thus proposed to measure the spot geometry by analysing the image itself.

Bayesian hierarchical stochastic analysis of multiple single cell Nrf2 protein levels

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We will present a Bayesian hierarchical analysis of multiple single cell fluorescent Nrf2 reporter levels in nucleus and cytoplasm. Nrf2 is a transcription factor regulating the expression of several defensive genes protecting against various cellular stresses. We propose a reaction network based on five reactions, including a distributed delay and a Michaelis-Menten non-linear term, for the amount of Nrf2 protein moving between nucleus and cytoplasm. The diffusion approximation is used to approximate the original Markov jump process. To explain the between-cell variability for multiple single cell data, we embed the model in a Bayesian hierarchical framework. Furthermore, we introduce a measurement equation, which involves a proportionality constant and a bivariate error, for the nuclear and cytoplasmic measurements, in order to relate the unobservable stochastic population process to the observed data. Bayesian inference is performed via a data augmentation procedure by alternatively sampling from the conditional distributions of the model parameters and the latent process. We show inferential results obtained on simulation studies and on experimental data from single cells under the basal condition and under the induction by a stimulant, sulforaphane.
