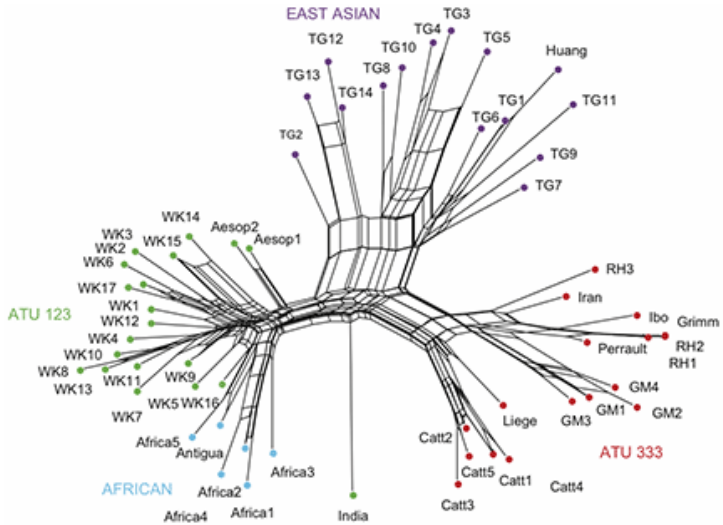
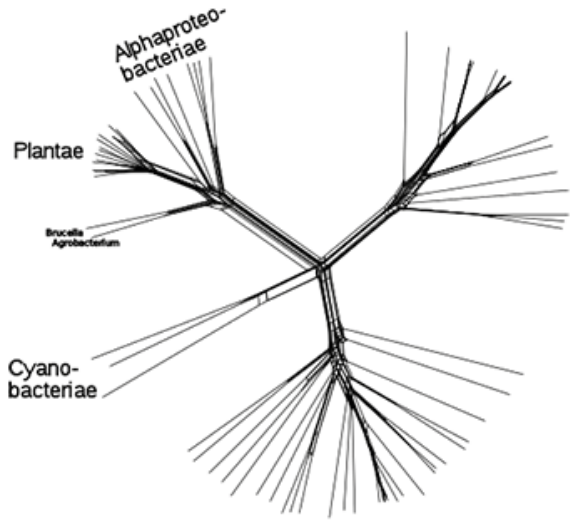


LANGUAGE, GENES AND PREHISTORY: A ONE-DAY INTERDISCIPLINARY WORKSHOP



THE UNIVERSITY OF
SYDNEY

School of
Literature, Art,
and Media





View of the Great Hall, c1859, photo by Professor John Smith, University of Sydney Archives

LANGUAGE, GENES AND PREHISTORY

A ONE-DAY INTERDISCIPLINARY WORKSHOP

Friday, 14 June 2019
F23 Level 1 Seminar Rooms, University of Sydney

Hosted by the University of Sydney Department of Linguistics,
Molecular Ecology, Evolution, and Phylogenetics Lab, China Studies Centre

Linguistics and genetics have traditionally pursued different approaches to the reconstruction of human prehistories, applying different methods and often working at different time-scales (Blench, Ross and Sanchez-Mazas 2008). In recent years, however, research has emerged which attempts a direct correlation of linguistic and genetic indicators of population migrations (Poloni, Sanchez-Mazas et al 2008; van Driem 2014), and a rapidly-growing field of inquiry applies methods developed in the context of computational phylogenetics and cladistics to various types of language data to derive probabilistic models of language evolution and, therefore, language relationships (Gray and Atkinson 2003; Dunn, Burenhult et al 2011; Zhang, Shi et al 2019, among many others). These methods build on centuries-old insights into similarities among language and biological evolution (Bromham 2017). Yet some fundamental questions continue to be asked: how comparable are words and genes as replicators? Can phylogenetic methods adequately capture the interplay of vertical and horizontal transfer in the history of languages? - for example, in cases of language convergence due to multilingualism? And how readily can assumptions regarding timescales, or pace of change, be applied to languages, which can be differentially subjected to more or less rapid and repeated transformations over the course of millennia?

The goal of this interdisciplinary workshop is to bring together linguists and molecular geneticists from the University of Sydney and the Australian National University, both those who are currently working independently on these or related issues, and those whose recent research explicitly addresses the methodological intersection of genetics and linguistics in the reconstruction of prehistory, for a single day of focused exchange. A particular emphasis of the workshop will be on students (both undergraduate and HDR) and early-and-mid-career researchers from both linguistics and genetics who are not currently engaged in interdisciplinary discussion around these issues, with the aim of creating opportunities and exploring potential for collaboration.

SCHEDULE

From 8.30 Coffee served/meet and greet

9:30-10:00 **Welcome and introduction**
Mark W. Post (University of Sydney)

10:00-11:00 “In praise of horizontal transfer between linguistics
and evolutionary biology”
Lindell Bromham (Australian National University)

11:00-12:00 “Languages and Genes in Eastern Eurasia”
George van Driem (Universität Bern)

12:00-12:45 **Lunch**

12:45-2:30 “Phylogenetic analysis of genes and languages”
Simon Ho and colleagues (University of Sydney)

2:30-3:30 “New methods for measuring coherence:
A case study from northern Australia”
Xia Hua (Australian National University)

3:30-4:30 Summary and group discussion, with a focus on the
Asia-Pacific region
Paul Sidwell (University of Sydney)

4:30-5:00 **Coffee/wind-down**

Languages and genes in eastern Eurasia: Method vs. madness
George van Driem (University of Berne)

Languages and genes tell us much about our collective past, but linguistic phylogeny can only be based on historical comparative linguistic evidence, and biological ancestry only on molecular genetic evidence. In 1872, at the time when the Aryan myth first gained hold in certain circles in the West, Max Müller travelled back from Oxford to Germany to lecture to his countrymen against confounding language and biological ancestry. Sadly, this essential distinction was to be lost on many people, and not just in Germany.

In 1997, a Swiss-Italian team of population geneticists discovered the father tongue correlation as a principle in the founding dispersals of linguistic phyla based on the global ubiquity, albeit not the universality, of the correlation of Y chromosomal markers with language families. The relative chronology of branching and geographical distribution of Trans-Himalayan, Hmong-Mien, Austroasiatic and Austro-Tai are observed to correlate with four distinct paternal subclades of Y chromosomal haplogroup O.

Even when languages and genes happen to exhibit a correlation, such a relationship is not to be confused with identity. The correlation of a particular chromosomal marker with the distribution of a certain language family may not be simplistically equated with populations speaking languages of a particular linguistic phylum. Rather, molecular markers may serve as proxies or tracers for the movements of a particular subset of ancestors.

Just as the Y chromosomal tree is defined by mutations, the branches of language family trees are defined by shared and nested innovations and sound laws. Old inherited morphology is to be distinguished from innovated accretions to morphological systems. Subclades in phylogeny are not defined by extended phenotypical coincidence. Therefore, lexicostatistics, even when rebranding itself as “phylolinguistics” or disguising itself behind sophisticated mathematics, remains an invalid method for determining language family trees.

In praise of horizontal transfer between linguists and biologists

Lindell Bromham (Macroevolution & Macroecology, Research School of Biology, Australian National University)

Linguists and biologists, recognizing the similarities between language change and biological evolution, have a long history of borrowing concepts from each other's fields. This cross-disciplinary exchange is flourishing, particularly with the development of phylogenetic methods that can be applied to both linguistic and genetic data. To illustrate this two-way exchange of ideas, I will consider some of the things that evolutionary biologists can learn from language evolution, for example through contemplation of alternative evolutionary systems that may not share some of the fundamental traits of genetic evolution (such as randomness of mutation). I will also look at some of the things that linguistics can gain from talking to evolutionary biologists, such as practical ways of analysing data that overcome the covariation due to shared history and common environments.

Phylogenetic analysis of genes and languages

Simon Ho and colleagues (University of Sydney)

Evolutionary relationships can be reconstructed using statistical phylogenetic methods. These methods can be applied to any data that have been produced through a gradual process of descent with modification, including genome sequences and cognate words. In this hands-on exercise you will use phylogenetic software to analyse genetic and linguistic data sets.

New methods for measuring coherence: A case study from northern Australia
Xia Hua (Australian National University)

Sociolinguists have long demonstrated how variation in a speech community indexes social categories such as age, gender, social class and ethnicity. Most analyses have been based on the indexical nature of individual variants, however some studies have also examined whether clusters of variants co-occur in speech of individuals of particular social categories, i.e. linguistic coherence. Few studies show strong support for linguistic coherence, which we suggest may be the result of the limited size of data sets and the methods used. Our Gurindji Kriol dataset from northern Australia consists of 78 speakers from three generations coded for their use of Gurindji, Kriol and Innovative variants across 120 variables (with 292 variants) and a range of social factors. We demonstrate how a large data set and three different modes of statistical analysis can reveal important patterns in language change within speaker communities. In particular, we develop an innovative modification of classic population genetics methods to investigating temporal change in linguistic data. We track changes in variant use over three generations of Gurindji people by adapting the Wright-Fisher population model. We show that the adoption of variants into Gurindji Kriol was not random, but biased towards Kriol variants and Innovations. However, this bias is not explained by simplification. Instead, peer pressure, education only in English, and the amount of exposure to Gurindji have strong influence on the retention of Gurindji variants in Gurindji Kriol.

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FACULTY OF ARTS AND SOCIAL SCIENCES

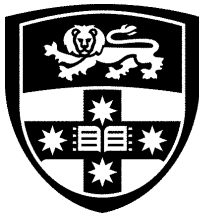
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