

SPWM 2010 Reunion Abstracts
January 14, 2010
San Francisco

The Off-Diagonal Fibonacci Operator
Janine Dahl

We will consider the off-diagonal Fibonacci operator, which has zero Lebesgue measure spectrum and purely singular continuous spectral measures, and show upper and lower bounds on the fractal dimension of the spectrum for large coupling.

A Knotty Group
Kate Kearney

Abstract: A knot is a circle, S^1 , embedded in S^3 . We call two knots equivalent if they are isotopic in S^3 , but if we imagine the S^3 as the boundary of B^4 , new isotopies appear in B^4 . To clarify this relationship, we define knot concordance, an equivalence relation on knots. Under this equivalence relation, knots form a group, called the knot concordance group. In this talk, I will briefly describe knot theory, then talk about some properties of the knot concordance group, and my work trying to better understand it.

Adventures with the Gene Hunter: Categorical Traits and the Elimination Algorithm
Abra Brisbin

G'day, mates! I'm the Gene Hunter, and I'd like to show you some of the highlights from one of my recent adventures: tracking down the genes that contribute to traits that are categorical, such as diseases that can be mild, moderate, or severe. First I'll introduce you to one of my favorite tools, the elimination algorithm. It's a fast way of solving lots of problems in probability. Then I'll give you the skinny on how I'm using the elimination algorithm to find the varmints—that is, genes—that are giving some poor doggies hip dysplasia!

Persistence Homology and Gene Expressions
Aubrey HB

Abstract: The new area of mathematics, Persistence, can distinguish tiny, non-trivial trends from the noise found within large-scale, time-series data sets. The detection of genetic expression patterns from gene micro arrays is particularly challenging problem. The level of a particular gene expression, variability in rates of expression among genes, background noise are some of the variables complicating the classification of genetic expression patterns. This presentation focuses on the application of persistence homology to differentiate among the genetic expression patterns within an array. If time permits, recent research will be highlighted which shows the influence of one gene on the expression process of another gene.

Hadamard Conjugation and Splits Networks

Cayla Kuhs

Biologists have been interested in Phylogenetics, the study of evolutionary relatedness among various groups of organisms, for more than 140 years. In spite of this, it has only been in the last 40 years that advances in technology and the availability of DNA sequences have led to statistical, computational and algorithmic work on determining evolutionary relatedness between organisms. One method of determining historical relationships is to assume a group based evolutionary model and use Fourier calculus over a finite Abelian group. The 1993 paper Fourier Calculus on Evolutionary Trees by L.A. Székely, M.A. Steel and P.L. Erdős contains a theorem which relates information derived from a set of nucleotide sequences and applies a Fourier transform in order to obtain a set of splits corresponding to a phylogenetic tree. There are biological and statistical reasons for using networks as well as trees and by following the approach of Székely et al it is possible to prove a similar result for splits networks. I will provide an overview of the use of splits networks in displaying historical relationships between organisms as well as discuss the extension of Székely et al's result to splits networks.