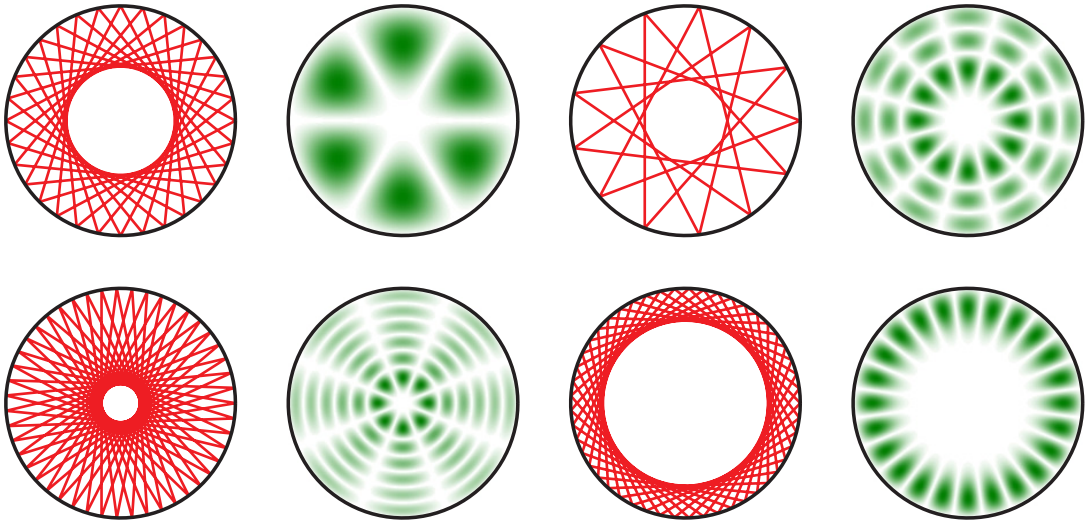
International Association of Mathematical Physics

News Bulletin

April 2013



International Association of Mathematical Physics News Bulletin, April 2013

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Cover picture: Circle billiards; see the article of Anantharaman and Bäcker in this issue

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ISSN 2304-7348
News Bulletin (International Association of Mathematical Physics)

Nine Lessons of my Teacher, Arthur Strong Wightman
A Talk at Princeton University, 10 March 2013

by Arthur Jaffe (Cambridge (MA), Basel, and Zürich)

At Harvard University, Arthur Jaffe is the Landon T. Clay Professor of Mathematics and Theoretical Science. He is currently on sabbatical leave at the University of Basel and at the ETH, Zürich. He has worked in several fields of mathematical physics. Arthur Jaffe received his doctorate in physics from Princeton as a student of Arthur Wightman, after studying mathematics as a Cambridge undergraduate and chemistry as a Princeton undergraduate. He has served as president of IAMP, and also as president of the American Mathematical Society.

Preamble.
All of us here today have been students of Arthur Wightman. But his thirty-six formal doctoral students form a very special club, which I represent on this part of today's program. A few members appear in this 1965 snapshot of Arthur Wightman's seminar in Palmer 301, with Arthur smiling benevolently in the center.

Postdoctoral fellows and other visitors to Princeton surround the students during those exciting times some 48 years ago. To the best of my knowledge, here is the complete, wide-ranging list of graduate students:

Arthur Wightman's student club

Silvan Samuel Schweber 1952
Richard Ferrell 1952
Douglas Hall 1957
Oscar W. Greenberg 1957
Huzihiro Araki 1960
John S. Lew 1960
William Stanley Brown 1961
James McKenna 1961
Peter Nicholas Burgoyne 1961
E. James Woods 1962

John Dollard 1963
Eduard Prugovecki 1964
David Shelupsky 1965
Arthur Jaffe 1966
Oscar Lanford, III 1966
Anton Capri 1967
Robert Powers 1967
Lawrence Schulman 1967
Christian Gruber 1968
Jerrold Marsden 1968

Gerald Goldin 1969
Eugene Speer 1969
George Svetlichny 1969
Barry Simon 1970
Charles Newman 1971
Stephen Fulling 1972
Robert Baumel 1979
Alan Sokal 1981
Vincent Rivasseau 1982
Rafael de la Llave Canosa 1983

Steven Bottone 1984
Thea Pignataro 1984
Jan Segert 1987
Jay Epperson 1988
Marek Radzikowski 1992
Jan Westerholm 1996

Pictures amplify words, so I passed through Cambridge for one day while travelling from Basel and Zürich (where I am currently on sabbatical) to Princeton. Most of Thursday I waded into the piles of boxes in my attic. This mining operation yielded a random and quite incomplete sample of images—for life provides too little time for the things we want to do. The photos are not all from Princeton, nor do they all include Arthur Wightman. Important periods, places, and people remain temporarily buried in my attic. But I did turn up a few gems—including this seminar image—that relate in some way to our beloved, departed friend. I project them independently from my talk, and you can view some 100 other images, including a few courtesy of Ludmilla. Eventually these photos can be viewed on the Princeton physics department web site.

Let me proceed with a very personal story, woven between those photographs that provide some interesting glimpses into the past. My remarks reflect a student's perspective, and are entitled Nine Lessons of my Teacher, Arthur Strong Wightman. Some lessons

are quotes; others are inferences. These lessons frustrate a humble student's attempt at emulation. Hopefully these remarks will resonate with others here.

Lesson I. Modesty.
In retrospect it seems quite improbable that a science undergraduate in the 1950's could spend four years at Princeton without ever encountering—or even hearing the name—Arthur Wightman. Yet that happened. Even though those years were spent mainly in Frick Laboratory, all my roommates, and many other friends were in physics or mathematics. I attribute this to Arthur's lack of self-promotion or self-aggrandizement. In today's world filled with primadonnas, such modesty is extraordinary—and very special. Arthur was always speaking of the work of others—rarely of his own. Luckily Arthur had many advocates who admired what he achieved.

My first impression of Arthur came as a student in Cambridge. I had gone to learn mathematics and physics—British style—with the encouragement of my undergraduate mentors Donald Spencer and Charles Coulston Gillispie. In spite of Cambridge being a hotbed of analyticity and S-Matrix theory in perturbation theory, a couple of my friends (including John Challifour) recommended reading Arthur's paper on the axioms. And someone there had an early copy of the 1960 Les Houches lectures. The refreshing appeal of Arthur's approach lit my desire to return to Princeton as a graduate student, and I was not alone. Thus began my personal encounter with Arthur Wightman's scientific adventures.

So even as a student, I discerned that Arthur Wightman's work received wider recognition and appreciation in Europe, than it did at home—a familiar theme of heroes not being recognized in their own back yard. For in Europe, Arthur Wightman was a well-deserved super-star. He remains so in our memories.

Interlude.
During the summer of 1961, before returning to Princeton at age 23, I made my way as an official "observer" to a summer school in Hercegnovi, not far from Dubrovnik. My main goal motivating that trip was to encounter another personal hero, Kurt Symanzik. Also Tullio Regge was there as well, and complex angular momentum was a concept I had been trying to understand. The physicist B. Jakšić organized that remarkable meeting. Exhausted from the train from London to Paris, I made my way through the crowded hallway of the Simplon-Orient Express with great despair, as there seemed to be no remaining seat. Finally I spotted what must have been the last open place in the train; what a pleasure to discover that I was sitting next to Maurice Jacob, who in fact was heading to the same place. Our resulting conversation led to a lifetime friendship.

The Hercegnovi lectures were outside in the warm climate, with the help of a small, portable blackboard. Many informal discussions took place in an open coffee area shielded from the sun by trees and an arbor; many more developed over dinner in one of the local restaurants. There I met and became friends with several other students, including Klaus Hepp, David Ruelle, Derek Robinson, Angus Hurst from Adelaide, and Edward Prugovecki from Belgrade (who like me was about to make his way to Princeton to study with Arthur Wightman). I became familiar with some of the teachers as well:

not only Jacob, Symanzik and Regge, but also André Martin, Walter Thirring, and the experimentalists Jack Steinberger and Valentine Telegdi.

The Zürich theorists in Hercegnovi were emissaries of their mentor Res Jost. This lineage continued when Hepp became an ETH professor. His students: Robert Schrader, Konrad Osterwalder, and Jürg Fröhlich, along with some of their students, became four generations of mathematical physicists who, along with Edward Nelson and Barry Simon, continued the Princeton-ETH and eventually Harvard connection.

Lesson II. Work on Big Problems.
Arthur Wightman's modesty was personal. It had nothing to do with scientific direction. Arthur towered over problems by his physique, and also by his persistence and strength—in science as well as in his middle name. He bent over backward to avoid the pedestrian. Arthur extolled work he held in high esteem, and his private evaluations of others could be severe. He aspired to think about perplexing things. So it was natural that Arthur suggested problems to his students that were important, but often they were impossible to solve.

What could be more fundamental than to understand the compatibility of relativity with quantum theory? They were the two most fruitful advances in 20th century physics. During the 40's, physicists developed rules for predicting consequences of the quantum field equations of Maxwell and Dirac. Today the measurements and calculations have evolved to 14-decimal place accuracy, with 23 Nobel laureates along that path. So one of the most fundamental questions in 1950 was: does it all make sense?

At the time, most physicists thought that a non-perturbative, mathematical theory of non-linear fields was impossible. But Arthur took up the challenge resulting in the Wightman axioms embodying quantum theory, covariance, stability, and locality. Pauli, Schwinger, Lüders, and Zumino understood spin and statistics and PCT in certain contexts. It appeared amazing that both results were simply consequences of the fundamental Wightman axioms, the latter work relying on the Bargmann-Hall-Wightman theorem and work of Res Jost.

The full proof of this, as well as studying further consequences of the axioms, led to much new mathematics, including Arthur's collaboration with Lars Gårding. These gave insights into the theory of several complex variables, domains of holomorphy, representation theory, linear and non-linear analysis, operator algebras, the theory of distributions, and partial differential equations. And I was lucky to arrive in Princeton about the time that Ray Streater came for a year to write together with Arthur their famous exposition, "*PCT, Spin and Statistics, and All That*."

Arthur wanted to find examples of field theories satisfying the axioms. As an early attempt, he began the herculean program of analyzing representations of an infinite-dimensional Weyl algebra, and the corresponding anti-commutation algebra. Perhaps that would lead to insight into possible interactions. Arthur's students Schweber, Lew, Araki, Woods, and later Powers (and others) made major advances in understanding the representations. Again it led to new frontiers both in mathematics and in statistical physics. But the multiplicity of possibilities clouded the original goal of giving insight into relativistic interactions, their equations of motion, or their Lagrangians.

Arthur then asked whether mathematical analysis could be used to find solutions to certain specific Lagrangian field theories, using perturbative or non-perturbative analysis. This effort came to be known as constructive quantum field theory. Oscar Lanford and I had problems in this domain as thesis topics. The three of us wrote a joint paper on our early work. But it took almost ten additional years after we received our degrees, before complete examples of interacting quantum fields in two and in three-dimensional space-time were shown to exist, to satisfy all the Wightman axioms, and more. In the two-dimensional case, one also proved that the fields describe particles and their scattering. This follows from the existence of isolated single particle states, and using Haag-Ruelle theory to obtain the existence of an S-matrix.

Arthur Wightman was the spirit behind this effort, which had major contributions from many persons here today, including my teacher Ed Nelson in its early stages. I am extremely grateful for my long and fruitful collaboration on these problems with Jim Glimm, as well as work with many students, postdoctoral fellows, and collaborators. To list at this point the names of all those persons whose work was crucial for establishing Arthur's dream about this topic would take too long—so I only mention Jürg Fröhlich, Barry Simon, and Tom Spencer who are here today.

Lesson III. Distinguish 'What you Know' from 'What you Think you Know'.
In his lecture on Hilbert's sixth problem, Arthur insisted, "A great physical theory is not mature until it has been put in a precise mathematical form." Physics based on mathematics had been the norm for Newton, Maxwell, and Einstein. This attitude can be traced through the history of modern physics, including the history of statistical physics and non-relativistic quantum theory.

Arthur was among a small minority of scientists who insisted that in spite of its difficulty, relativistic quantum physics (and specifically quantum field theory) should be put on the same solid footing! Arthur spread this view with missionary zeal. Arthur was a fanatic about detail. This is necessary if one wants everything to be correct, and Arthur did just that. But detail is not enough, and unfortunately we still do not know the complete answer.

Arthur was fascinated by Polynesian head-shrinkers, for which he found an analog in our world. Arthur sometimes joked that the 'world's greatest head-shrinkers are the publishers of books.' When he received the galleys of the Streater-Wightman book, he gave copies to Oscar Lanford and me; we then competed to see who could find more typos (or other small problems). Arthur relished every one we found.

Lesson IV. Do not ignore what physicists think.
This was Arthur's mantra. He constantly emphasized that mathematical physics is a part of both physics and mathematics. If physicists believe they understand something, one should get to the bottom of it. Ignore it at your peril, even if at first sight it appears to be nonsense. And you need to look in all mathematical directions. For example: if you work in constructive quantum field theory, you need to incorporate whatever is known from the perturbative analysis of renormalization, renormalization group flows, or the mathematics of phase-cell analysis or of functional integrals.

I took that lesson to heart, and always tried to have contact with persons outside mathematical physics—both in physics and in mathematics. The natural interchange brought about by casual conversation had a profound effect on my own scientific direction. Curt Callan once joked that 'mathematical physicists try to solve difficult problems, while particle physicists try to avoid them.' But in my mind 'avoiding' a problem is the first step to solving that problem.

Lesson V. Do not ignore the past.
Arthur was also adamant about careful citation of the work of others. He taught us to read the literature and to understand it. We have heard of his great knowledge; Arthur appreciated the history of his subject, and he respected it.

For this Arthur relied heavily on the wonderful Princeton library. This torus-shaped domain on the top of Fine Hall was replete with wood paneling, book cases built into appealing nooks, and files where one could even find copies of unpublished reports or notes available nowhere else. Arthur loved that library, which was the charge of a remarkable woman Ann Kenny, who had been originally trained as a mathematician. Arthur and Ann got along famously; he often told coworkers and students how he argued to protect the library from budget cuts or other administrative problems.

Lesson VI. Teach Well.
Arthur told us that in a lecture you should, "tell them what you are going to do; do it; then tell them what you have done." Yes, Arthur's lectures were wonderful from a student's point of view. But Arthur's legacy as a teacher extends far beyond pedagogy.

Arthur's interests were so broad. They spanned quantum mechanics, the foundation of quantum fields, representation theory, renormalization, symmetry and symmetry breaking, the physics of higher spin particles, continuum mechanics, statistical physics, ergodic theory, dynamical systems, transport theory; the list goes on and on. Arthur put many of these topics into his courses. Others appeared in summer schools or workshops that he organized.

But beyond conveying knowledge of the past, Arthur was so generous with his ideas about research directions and the future. Arthur inspired thirty-six students, countless collaborators, and many colleagues. Perhaps the most important knowledge a teacher can impart on a student is to explain what others know and what they do not know—and to tell which research questions are really important. Arthur did that so splendidly!

As a student I recall being interrupted while in Arthur's office by a string of telephone calls and other visitors to his open door. Everyone seemed to desire Arthur's wisdom or guidance. I recall thinking to myself how selfless he was; perhaps Arthur should make himself less available to others, in order to keep more time to work on his own research.

Lesson VII. Create a Congenial Working Atmosphere.
I could talk at length about the atmosphere in the department for students, or Arthur and Anna-Greta's sociable evenings at their home. But your eyes see the whole story in the expressions on people's faces in the 1965 photo of Arthur's seminar, the first of the photos in the collection. (I believe the speaker was Klaus Hepp.) People and the quality of their personal interaction meant a great deal to Arthur. It stimulated good work.

When Arthur went to Madison for the summer, he included a bevy of students in his party. When Arthur spent his 1963–64 sabbatical starting the mathematical physics program in Bures, he took Oscar Lanford and me along.

At Princeton, life in the department was unbureaucratic. Courses were to enjoy and not to be graded. Administrators were to be conversed with and not to be bombarded with forms. And Arthur's door was always open. Where can one find that simple life now?

Lesson VIII. Be a Good Citizen.
Arthur also worked in so many ways to improve Princeton and the world. He argued for a rational policy for the admission of science undergraduates. He spent countless hours working for the Princeton Press. He encouraged the founding of *Communications in Mathematical Physics* and later served for years as an editor there and with other journals. He helped found the Department of Applied Mathematics at Princeton, and recruit its original members. He was involved in the transition from Palmer and Fine to Jadwin and the New Fine Hall. The list is endless, and Arthur showed his students that unusual citizenship should be the norm.

Lesson IX. What Next?
Being Arthur's student could be frustrating. After meeting with Arthur to discuss a successful new idea or result, inevitably Arthur moved the conversation from achievements (for they were the past) to ask about the future. Predictably, out would come the exclamation and question, "What Next?" (Like the Elliott Carter opera with that title.) Arthur seemed never satisfied with knowledge; Arthur always wanted more.

Today we still do not know the answer to many of Arthur's simple questions. Does four-dimensional quantum field theory makes sense? Abdus Salam remarked privately in 1969 that one could not hope to find the answer in the 20th century. And he was right! Hopefully the 21st century will provide insight into that conundrum.

Moreover, to understand confinement in QCD, or the mass gap in Yang-Mills theory, one will need new insights both into physics as well as into mathematics. And who will supply those ideas? Certainly Arthur would be overjoyed if both the physics advances and the mathematics advances originated from the same mathematical physicist!

In any case, I am sure that whenever any big problems in mathmatical physics like these are solved, Arthur will be with us in spirit—smiling benevolently from heaven.

Quantum ergodicity and beyond. With a gallery of pictures.

by Nalini Anantharaman and Arnd Bäcker (Orsay, France, and Dresden, Germany)

Nalini Anantharaman completed her PhD in 2000 at Université Paris 6, under the supervision of François Ledrappier, on the fine periodic orbit structure of Anosov dynamical systems. From 2001 to 2006 she was Maître de conférences at École Normale Supérieure de Lyon when she discovered the relevance of ergodic theory in the study of the linear wave equation and the Schrödinger equation. In 2006 she obtained a position at the French Centre National de la Recherche Scientifique (CNRS) and a Hadamard professorship at École Polytechnique. Since 2009 she has been a professor at Université Paris-Sud, Orsay. She has received the 2010 Salem Prize and the 2012 Henri-Poincaré Prize.

Arnd Bäcker received his PhD in 1998 at the Universität Ulm under the supervision of Frank Steiner, on classical and quantum chaos in billiards. After a postdoc at the university of Bristol from 1999-2001, working on systems with a mixed phase space, he became assistant at the TU Dresden in 2002. In 2007 he did his Habilitation and subsequently obtained a faculty position in 2009. His current main research interests are nonlinear dynamics, quantum properties of systems in which regular and chaotic dynamics coexist and the dynamics of higher–dimensional systems.

The vibrations of a guitar string, electromagnetic waves, seismic waves, or states of quantum systems: all these physical phenomena are described by mathematical equations belonging to the family of *wave equations*. The results we describe here deal with *linear* wave equations in a *closed* cavity. Apparently simple equations, such as the d'Alembert equation $\frac{\partial^2\psi}{\partial t^2} = \Delta\psi$ or the Schrödinger equation $\frac{\partial\psi}{\partial t} = i\Delta\psi$ are still at the heart of active research. One major challenge is to understand the "scar" phenomenon, namely, the possibility for stationary waves (or waves evolved over a long time) to stay localized in the vicinity of periodic billiard trajectories, or periodic geodesics. The interpretation of scars is controversial: simple heuristic arguments suggest that it is difficult for a wave to follow an *unstable* billiard orbit for a long time, while [56, 26, 24] give a reasoning in favor of the enhancement along unstable orbits. In numerical computations such as shown in Figures 1 and 2, some stationary waves do have a slightly higher intensity around unstable periodic orbits in billiards.

The series of papers by Anantharaman and co-workers [2, 12, 11, 14, 72, 4, 6] eradicates

the possibility of *strong scars* in the case of negatively curved manifolds (leaving open the possibility of *partial scars*, as explained later). This answered a long-standing open question, and also constituted a progress towards the Quantum Unique Ergodicity conjecture of Rudnick and Sarnak [75, 74]. This conjecture, formulated for negatively curved manifolds, predicts that the stationary solutions of the Schrödinger equation should occupy phase space uniformly, in the small wavelength limit. Quantum Unique Ergodicity would imply the absence of scars, but has not been proved rigorously except in a specific "arithmetic" setting [63, 80], quite remote from the physical models. On the contrary, the ideas introduced in [2, 12] could in principle apply to very general geometries.

One of the novelties in this work is the use of a concept from ergodic theory, the Kolmogorov-Sinai entropy, to study the qualitative behaviour of solutions of linear wave equations. Ergodic theory was born at the beginning of the twentieth century, with the foundational works of Poincaré and Birkhoff, and has been developed over the years to provide tools to study the large time behaviour of solutions of Ordinary Differential Equations, from a statistical point of view. Ergodic theory usually deals with finite-dimensional, non-linear systems. It is well suited for the study of classical mechanics. On the other hand, wave mechanics is described by Partial Differential Equations which require working with infinite dimensional function spaces. The notions of "chaos", "entropy"... that have been developed in ergodic theory do not apply naturally to these non-commutative dynamical systems. In our work we used the semiclassical approximation as a bridge between quantum dynamics and classical ergodic theory. This circle of ideas is usually referred to as "quantum chaos", where "quantum" just means "wave mechanics", and chaos refers to the classical theory of chaos in ergodic theory.

When trying to understand the large time behaviour of waves, it is clear that the answer depends on the ambient geometry. Figure 3 shows snapshots of the propagation of an initial "gaussian wave packet" in a half cardioid, and gives an idea of the complexity of the phenomenon. The movie suggests that an equilibrium regime is reached, in which the wave fills uniformly all the space at its disposal. Of course, the simulation only runs over a finite time, and one may imagine that the wave packet later comes back to its original state, if one waits long enough. Although this is difficult to believe, there is today no mathematical result ruling out this possibility. In particular, in certain situations, like integrable systems, the occurence of revivals has been observed in numerical investigations and are also rigorously proved for specific examples. The origin of such revivals are specific relations among the eigenvalues. Something like this is not expected for chaotic systems leading to the common belief that there are no such revivals (but also see [83]).

In a closed domain, there are countably many stationary waves, that is waves that oscillate in a stationary manner. These correspond to eigenfunctions of the laplacian,

$$\Delta\psi_n = -k_n^2\psi_n,$$

i.e. the Helmholtz equation, with the physically relevant boundary conditions. Figures 1 and 2 display samples of consecutive laplacian eigenfunctions in a stadium-shaped domain and in a cardioid with Dirichlet boundary conditions, i.e. $\psi_n(x, y) = 0$. Numerically the eigenvalues have been computed using the boundary element method (see e.g. [21] and

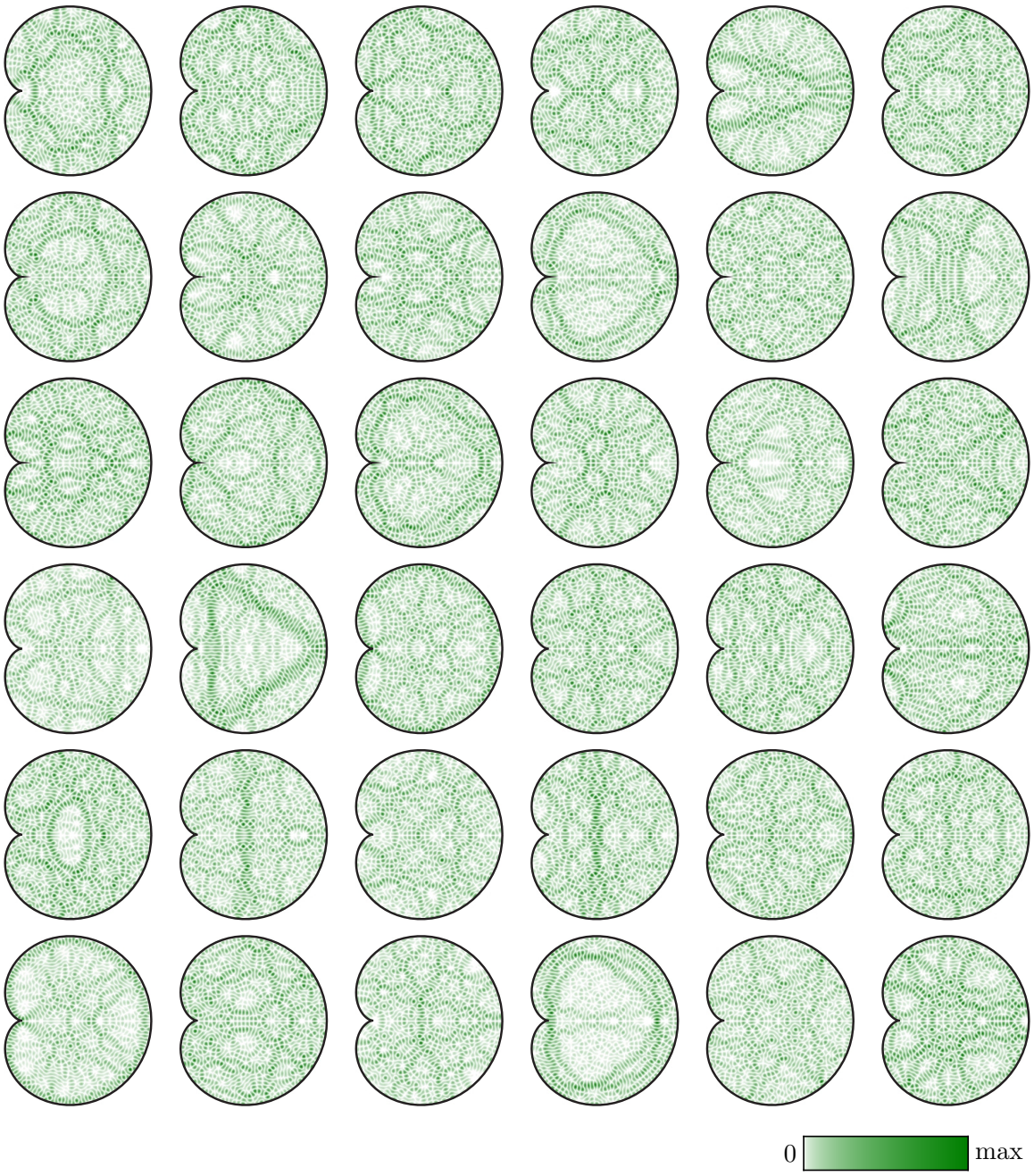

Figure 1: Plot of $|\psi_n(x,y)|^2$ for the cardioid billiard with odd symmetry, for consecutive states starting from $n = 700$.

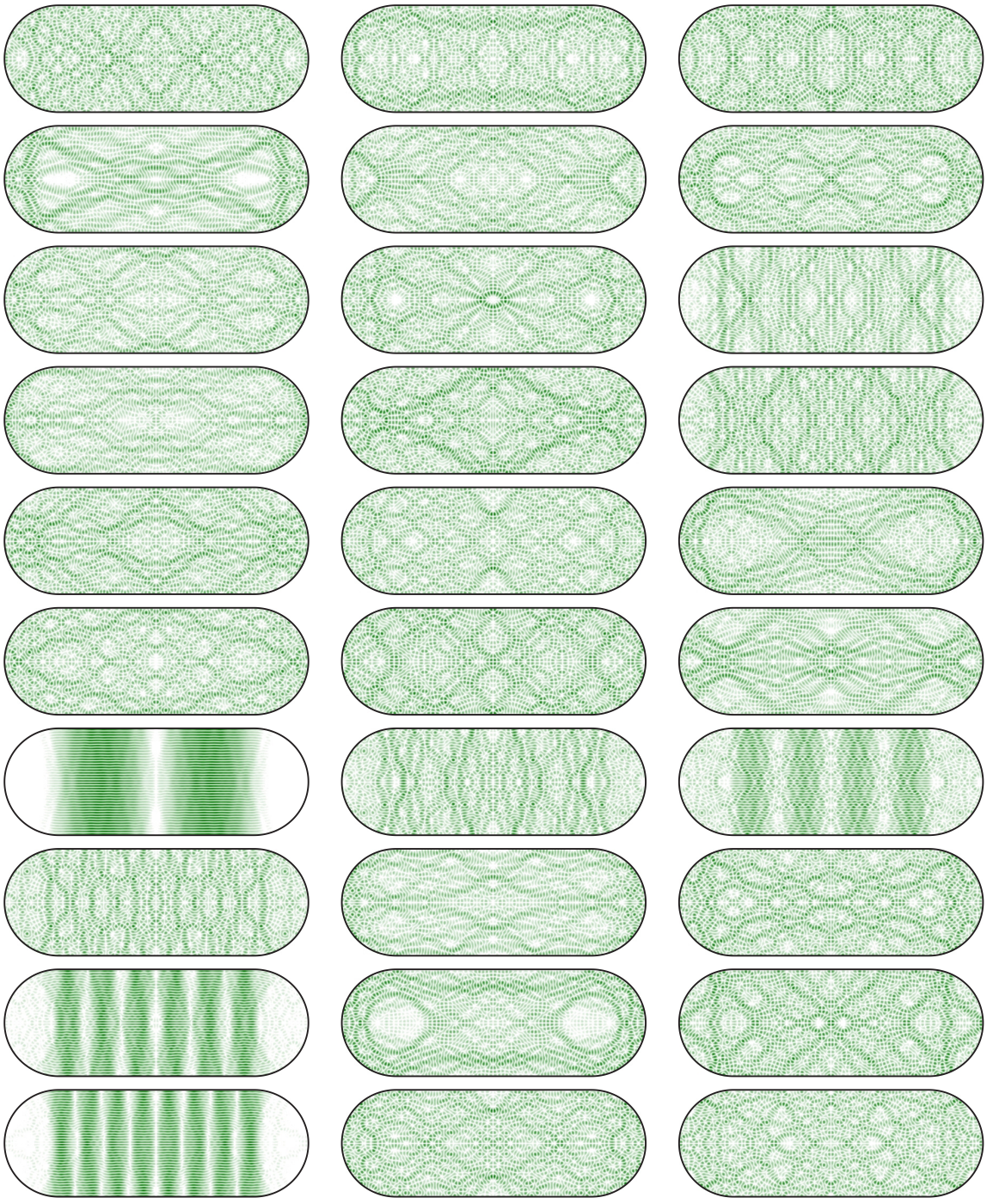

Figure 2: Plot of $|\psi_n(x,y)|^2$ for the stadium billiard with odd-odd symmetry, for consecutive states starting from $n = 758$.

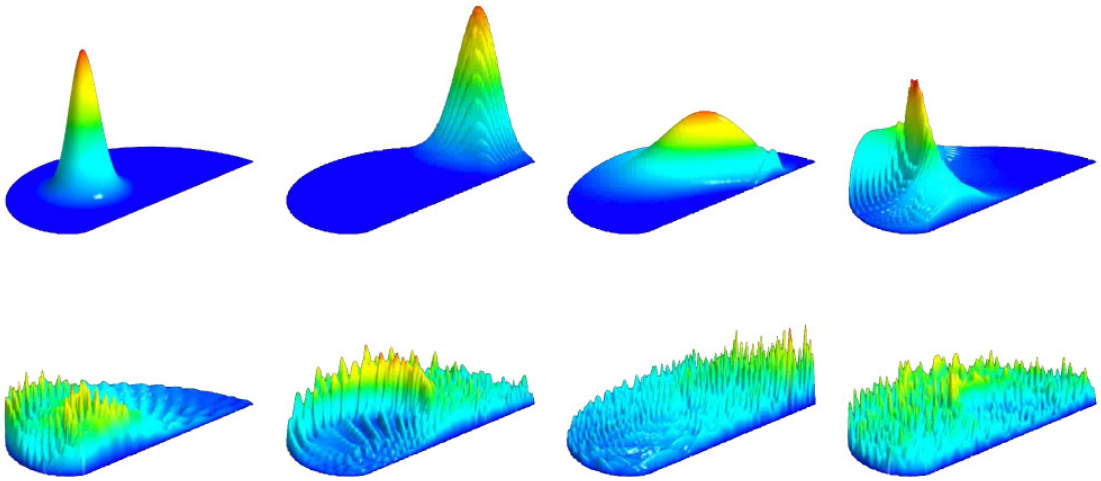

Figure 3: Time evolution of a wave-packet in the desymmetrized cardioid billiard with Dirichlet boundary conditions.

references therein) in the case of the stadium billiard and by means of the conformal mapping technique for the cardioid billiard [73]. From the eigenvalues, together with the corresponding normal derivative function along the billiard boundary, one can reconstruct the eigenfunction at any point inside the billiard.

Since we deal with linear wave equations, the propagation of any wave can be written as a superposition of stationary waves. For the Schrödinger equation, solutions are of the form

$$\psi(t,x) = \sum_n a_n e^{-itk_n^2} \psi_n(x)$$

where the coefficients a_n can be expressed in terms of the initial conditions. For the numerical computation leading to Figure 3 the first 2000 eigenstates of the cardioid billiard have been used.

Thus, in principle everything boils down to understanding the eigenfunctions ψ_n and the eigenfrequencies k_n of the laplacian. However, this statement is mostly of theoretical interest: one of the difficulties we meet is the fact that the eigenfunctions and eigenvalues are not given by explicit expressions. It is difficult to lay hands on individual eigenfunctions otherwise than by numerical methods, that give visual pictures without explaining: for instance, the interesting geometric patterns of Figures 1 and 2 are only very partially understood ! Here, we will mostly discuss the phenomenon called "scarring", namely enhancement of an eigenstate in the vicinity of a periodic trajectory, see Figures 4 and 5. The "bouncing ball modes" of the stadium also want an explanation; and the *nodal lines* (places where the eigenstates vanish) also form a very beautiful and mysterious lace.

Working with explicit models is sometimes possible, but one rapidly runs into delicate problems of number theory. As an example, let us consider the solutions of

$$\Delta\psi = -k^2\psi$$

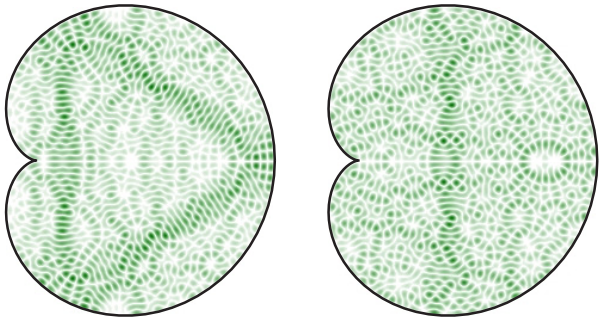

Figure 4: Selected states in the cardioid showing higher intensity ("scarring") around unstable periodic orbits.

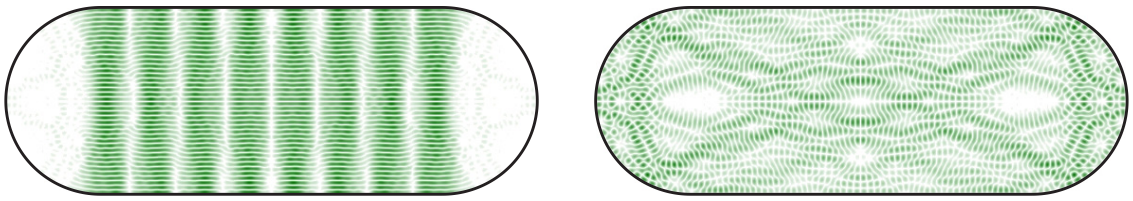

Figure 5: Selected states in the stadium showing a bouncing–ball mode and an eigenstate with slightly higher intensity ("scarring") around an unstable periodic orbit.

in the cube $[0,\pi]^d$, with Dirichlet boundary conditions. Of course, k^2 must be an integer, and a general solution can be expanded into Fourier series as

$$\psi(x) = \sum_{(k_1,\dots,k_d)\in\mathbb{N}^d\setminus(0,\dots,0),k_1^2+\dots+k_d^2=k^2} c_{k_1,\dots,k_d}\sin(k_1x_1+\dots+k_dx_d).$$

The sum involves all the possible ways of writing k^2 as a sum of d squares : describing and counting these constitutes a notoriously difficult problem in number theory. Thus, even in a cube, the study of the Schrödinger equation is a rich subject, at the frontier between harmonic analysis, number theory, and the analysis of partial differential equations [28, 27, 29, 60, 59, 32, 33, 34, 9, 1, 7]. For instance, proving the impossibility of scars in a (2-dimensional) square is easy, but in cubes of higher dimensions this requires some elaborate Fourier analysis and/or discussion of the geometric properties of integer points lying on a sphere [27, 60, 9, 1].

Coming back to a general setting, an interesting approach to understand the propagation of waves is to use the *semiclassical approximation*. In this approximation the wavefronts propagate like in a billiard: in straight lines as long as the movement is free, and bouncing on obstacles in the usual way (angle of incidence = angle of reflection). Figures 6 and 7 show individual billiard trajectories for several well known billiards. Figure 8 shows the emission of a beam of trajectories in a small angular interval. According to the semiclassical approximation, the wave emitted by one point source will disperse

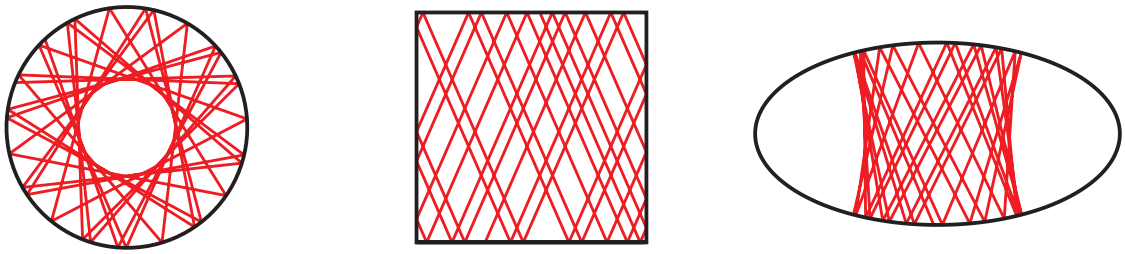

Figure 6: The billiards in a circle, square and ellipse examples for integrable dynamics. The resulting orbits show regular dynamics.

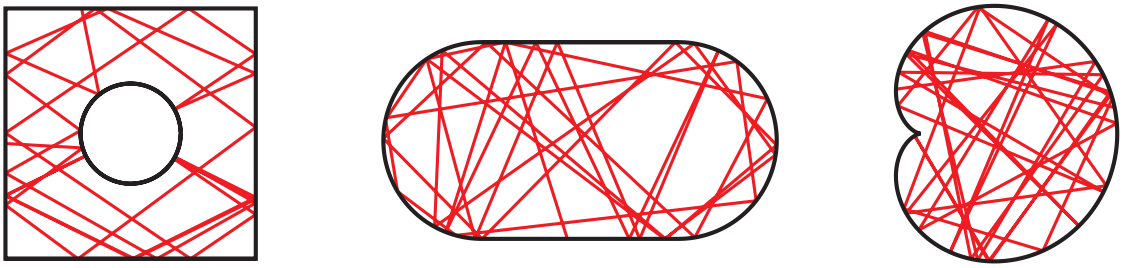

Figure 7: The billiards in a square with a circular scatterer (so-called Sinai-billiard), in a stadium shaped boundary and in the cardioid are examples for chaotic dynamics, more precisely, they are proved to be ergodic, mixing, K–systems and Bernoulli. The resulting orbits show irregular dynamics.

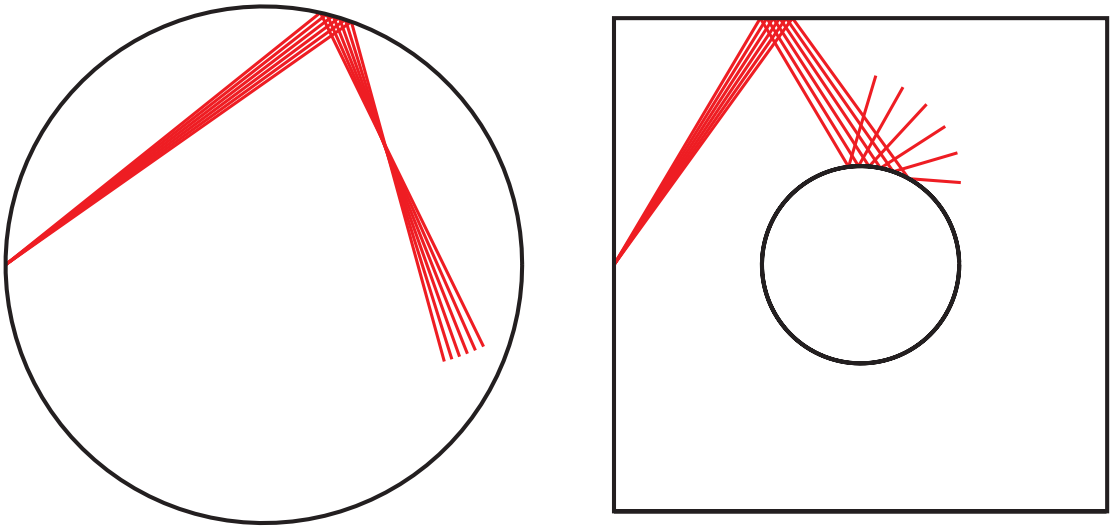

Figure 8: Trajectories started at the same point but with different initial angles stay close to each other in the case of integrable dynamics while for the chaotic systems a strong defocusing occurs. This is the origin of the chaotic properties and illustrates the exponential sensitivity on the initial conditions in such systems.

in the same way. However, as the name indicates, this is only an imperfect description of what actually happens. The dispersion of rays explains only the initial dispersion of the wave-packet. The smaller the wavelength, the smaller the error: the semiclassical approximation is well-adapted to describe the propagation of waves with small wavelength and large frequency. This approximation gives for instance the link between Huygens' wave theory of light and the geometric optics of Descartes. The mathematical technique that allows this to be formalized is a sophisticated version of Fourier analysis, called *microlocal analysis* or *semiclassical analysis*, developed to a point of extreme refinement by Lars Hörmander and his school [55].

The semiclassical approximation gives a fair account of the first four snapshots of the movie of Figure 3: we indeed observe that the center of the wave packet moves along a straight line and effectively bounces on the boundary like a ball. Later, the wave-packet starts dispersing, interferences occur, and we are out of the range of usefulness of the semiclassical approximation. This happens at a time called the Ehrenfest time, which (for chaotic systems) typically grows like $\log k_n$ when the frequency k_n goes to infinity [46, 41, 86, 25, 35]. Beyond that time, the complicated interference effects are described by sums of oscillatory terms known as "exponential sums". These are in general impossible to cope with, except for certain explicit models where number theory can help.

Research has focused on *completely integrable* billiards on the one hand, Figure 6, and *chaotic* billiards on the other hand, Figure 7. For the integrable case, Figure 9 shows in green, a few stationary waves in the disc; in red, the trajectory of a billiard ball with approximately the same angular momentum as the eigenfunction directly on its right. In a disc, the trajectory of the ball is organized in a very simple way: the angle of reflection on the boundary is always the same, and the trajectory is tangent to an inner disc called the caustic. As beside the energy, the angular momentum is an independent conserved quantity, this is a *completely integrable system*, the most ordered class of systems in the theory of dynamical systems. The images of stationary states offer a certain visual similarity. This is of course expected, as in the semiclassical limit the quantum states should resemble more and more the corresponding classical dynamics. [1]

In a chaotic system, on the other hand, the ball thrown at random (typically) follows a chaotic trajectory and eventually visits uniformly all the space at its disposal (Figure 7). Chaotic billiards also have countably many hyperbolic periodic trajectories, which occupy a dense set of measure zero in phase space (Figure 10). The global orbit structure is thus extremely rich and complex. Here again, this is reflected in the variety of patterns in Figures 1 and 2.

Up to now our discussion has been based on intuition and the observation of pictures, without any rigorous mathematical formulation. Let us focus on the chaotic case, and state a few theorems whose proofs are based on the semiclassical approximation and require overcoming the difficulties mentioned above.

[1] More explicitly, according to the semiclassical eigenfunction hypothesis [71, 23, 84], one expects that quantum states concentrate on those regions in phase space, which a typical orbit explores in the long time limit. For integrable systems these invariant regions are the regular tori, while for chaotic systems one expects a uniform distribution on the energy shell. Note: In the latter case this follows [19] from the quantum ergodicity theorem, with the restriction to a subsequence of density 1.

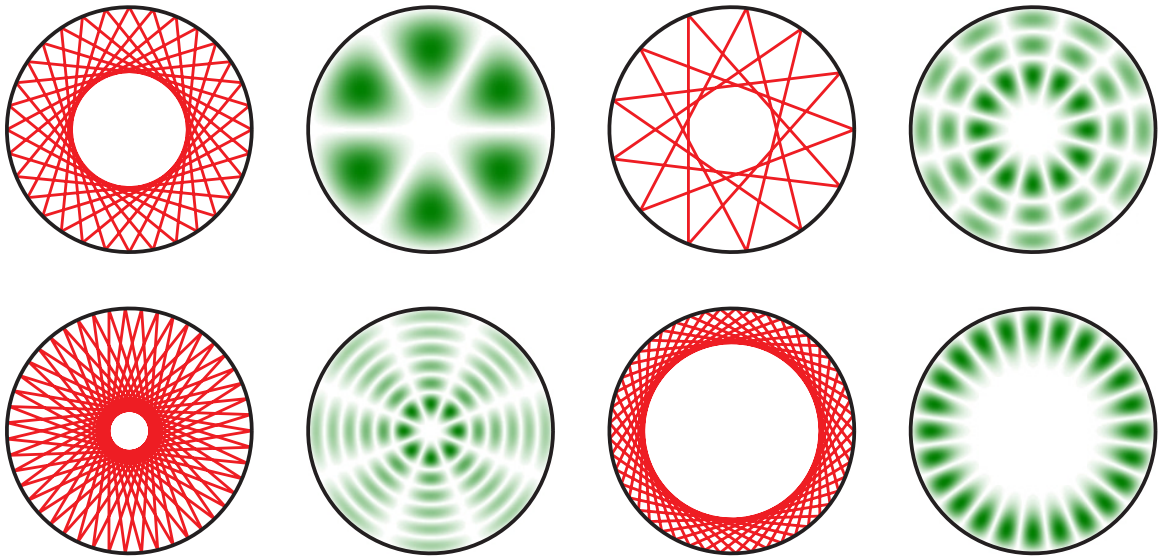

Figure 9: Plot of $|\psi_{nm}(x,y)|^2$ for selected states in the circle billiard.

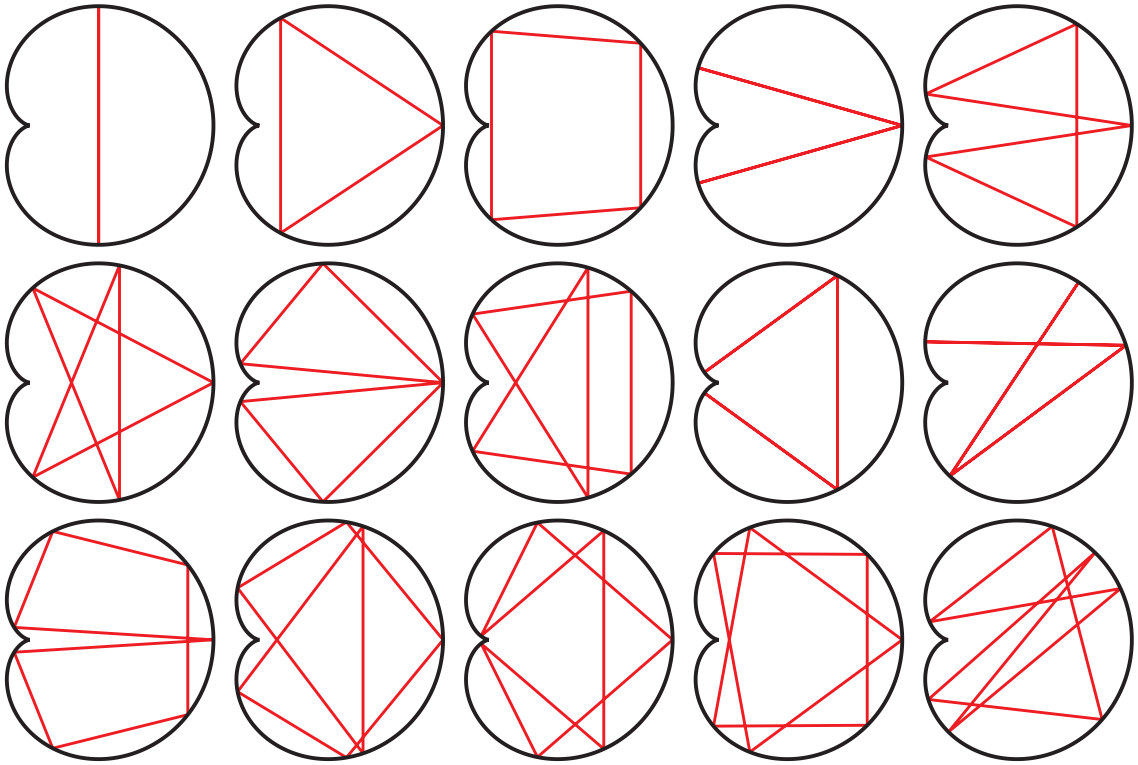

Figure 10: Periodic orbits in the cardioid billiard. For this system a proved symbolic dynamics exists [18, 17, 45] such that periodic orbits can be determined in a systematic way.

The "quantum ergodicity theorem" (Shnirelman, Zelditch, Colin de Verdière [79, 89, 42, 54]) deals with the case of "ergodic" systems and has been extended to the case of billiards [49, 87]. Classical ergodicity means that a ball thrown in a random direction will visit phase space uniformly: for almost all initial conditions, the average time spent in a given region is proportional to the volume of that region. The Sinai billiard, stadium billiard and cardioid billiard are known to be ergodic [78, 37, 85, 65]. The quantum ergodicity theorem proves a correspondence between the ergodicity property of a billiard table and the behaviour of waves: it establishes that a typical stationary wave will occupy phase space uniformly.

For a precise formulation of the theorem, we let (X, g) be a compact Riemannian manifold (the billiard table). We denote by T^*X the cotangent bundle over X, and $S^*X \subset T^*X$ the unit cotangent bundle. An element of S^*X is denoted by (x, θ), where $x \in X$ and $\theta \in S^*_x X$ is a vector of norm 1; x represents "position", whereas θ represents "velocity", or "momentum". The phase space S^*X is endowed with the Liouville measure, $\mathrm{Vol}(dx)d\sigma_x(\theta)$, where Vol is the Riemannian volume element and $d\sigma_x(\theta)$ is the uniform measure on the sphere $S^*_x X$.

Theorem 1. *[79, 89, 42] Assume that the geodesic motion (billiard motion) on S^*X is* **ergodic** *for the Liouville measure.*

Let $(\psi_n)_{n\in\mathbb{N}}$ be an orthonormal basis of the Hilbert space $L^2(X)$, formed of eigenfunctions of the Laplacian ($\Delta\psi_n = -k_n^2\psi_n$, with $k_n \leq k_{n+1}$).

Let A be a pseudodifferential operator of order 0. Then, there exists a subset $\mathcal{S} \subset \mathbb{N}$ of density[2] *1, such that*

$$\langle \psi_n, A\psi_n \rangle \underset{\substack{n\to\infty,\\ n\in\mathcal{S}}}{\longrightarrow} \int_{S^*X} \sigma(A)(x,\theta)\,\mathrm{Vol}(dx)d\sigma_x(\theta) \tag{1}$$

where $\sigma(A)$ stands for the principal symbol of A.

In other words, the convergence (1) holds, except possibly on a "negligible" subsequence.

The principal symbol $\sigma(A)$ is a function on S^*X. In quantum mechanical terms, it is the "classical observable" corresponding to the "quantum observable" A. The quantum ergodicity theorem can be interpreted as saying that almost all eigenfunctions become uniformly distributed over the phase space S^*X, both in the "position" variable x and in the "momentum" variable θ. An interesting special case is when $a(x)$ is a function on X and A is the operator of multiplication by a; in that case, equation (1) simply reads

$$\int_X a(x)|\psi_n(x)|^2\,\mathrm{Vol}(dx) \underset{\substack{n\to\infty,\\ n\in\mathcal{S}}}{\longrightarrow} \int_X a(x)\,\mathrm{Vol}(dx).$$

Thus in position space almost all eigenstates converge (in the weak sense) to a constant. For an introduction to the quantum ergodicity theorem for physicists see [20].

[2] $\mathcal{S} \subset \mathbb{N}$ being of density 1 means that $\frac{\sharp\{n\in\mathcal{S}, n\leq N\}}{N} \underset{N\to+\infty}{\longrightarrow} 1$, i.e. the complement of $\mathcal{S}$ is "negligible".

The quantum ergodicity theorem is in agreement with the idea that the semiclassical approximation allows a qualitative description of the spreading of waves. It proves that most eigenfunctions in Figures 1 and 2 occupy space uniformly. However, the stadium-shaped billiard is extremely mysterious: numerical simulations [56, 70, 66] show the existence of infinitely many "bouncing ball modes", like the one shown in Figure 5. These modes bounce back and forth between the two parallel walls, without visiting the bends. In agreement with the quantum ergodicity theorem, eigenfunctions of this type are extremely rare, their number is negligible in the collection of eigenfunctions. Nevertheless, they seem to exist. In [82, 19, 64] their number has been investigated numerically and theoretically, giving arguments in favor of $N_{\rm bb}(E) \sim E^{3/4}$. The existence of bouncing-ball modes was only proved mathematically around 2008 by Andrew Hassell [52]. To be more specific, consider the one-dimensional family of stadia, obtained by varying the width of the inner rectangle, while the height is fixed. What Hassell proved is that, for "almost all" stadia, there is a sequence of eigenfunctions that concentrate partially on the bouncing-ball trajectories. The proof is not constructive, and thus does not allow one to predict for which stadia and which frequencies these "bouncing ball modes" will be observed.

The work of Anantharaman and Anantharaman–Nonnenmacher deals with the eigenfunctions shown in Figures 4 and 5, which are enhanced in a neighbourhood of an unstable periodic billiard trajectory. This phenomenon named *scarring* [56] generally means, for physicists, a visual enhancement. Mathematicians are more cautious: they want a precise definition of the word *enhanced* ; and they require the existence of infinitely many such eigenfunctions to speak about "scarring". With their restricted definition, mathematicians tend to think that scarring on an unstable periodic trajectory cannot occur. Anantharaman and Nonnenmacher give a diplomatic answer: "scarring" on an unstable orbit, if it ever occurs, can only be partial. This means that part of the energy of oscillation must be localized away from the unstable orbit.

To state rigorous results, we will restrict our study to the case of *negatively curved* manifolds, closed and without boundary[3]. In addition to ergodicity, the classical dynamics (namely the motion of a particle along geodesics) is extremely chaotic: strong mixing properties, exponential instability,... Although the dynamics is deterministic, it has the property of being a *Bernoulli system*, meaning that the long time behaviour of the particle is as random as if it were flipping coins to decide where it is going. All this is already true for the above billiards [40], but the geodesic motion on negatively curved manifolds is, in addition, a *uniformly hyperbolic* dynamical system : this is a tame form of chaos, that has been studied very early on and is now well understood [57, 58, 53, 15].

For such systems, it is generally believed that the convergence (1) takes place for the whole sequence of eigenfunctions (i.e. $\mathcal{S} = \mathbb{N}$ in Theorem 1); in other words, there is no exceptional subsequence. This is the Quantum Unique Ergodicity conjecture of Rudnick

[3]Some of these results have also been proved for the "cat-map" on a torus [47, 36]. In principle the same results could also be proved rigorously for certain types of billiards, but this would be extremely technical work and has not been done yet. The adaptation to *non-positively curved* surfaces is already a technical challenge [72].

and Sarnak [75, 74]. Numerical computations already indicated [16] that there is no such scarring for an explicit example of a system on a surface of constant negative curvature. Up to now, the conjecture has only been proved by E. Lindenstrauss for the so-called "arithmetic" surfaces (for instance, the modular surface obtained as the quotient of the hyperbolic plane $\mathbb{H}^2$ by $SL(2,\mathbb{Z})$), and for simultaneous eigenfunctions of the laplacian and the Hecke operators [63, 31, 80]. Since these arithmetic surfaces are somehow more explicit than the other hyperbolic surfaces, this is again one case where number theory can come to the rescue – in a very elegant manner. By contrast, the work of Anantharaman *et al* deals with general negatively curved manifolds, for which even the phenomenon of "scarring" is not fully understood. But we now need a mathematical definition of scarring.

Let $B \subset \mathbb{N}$ be an infinite subset such that, for any pseudodifferential operator A of order 0,

$$\langle \psi_n, A\psi_n \rangle \underset{\substack{n\to\infty,\\ n\in B}}{\longrightarrow} \int_{S^*X} \sigma(A)(x,\theta) d\mu(x,\theta) \tag{2}$$

for some probability measure μ. We will say that the sequence of eigenfunctions $(\psi_n)_{n\in B}$ exhibits *strong scarring* if μ is a measure that is *entirely* supported on periodic classical trajectories. We will say that the sequence of eigenfunctions $(\psi_n)_{n\in B}$ exhibits *partial scarring* on a periodic classical trajectory γ if $\mu(\gamma) > 0$. In the case of an ergodic geodesic flow (in particular, on negatively curved manifolds), the quantum ergodicity theorem implies that such a set B must have zero density.

What is proved in various contexts in [2, 12, 11, 3, 14, 72, 36, 4, 6] is that, if such a convergence as (2) occurs, then the measure μ must have a high "dynamical complexity" (measured thanks to the notion of Kolmogorov-Sinai entropy). This rules out the possibility of strong scarring but leaves open the possibility of partial scarring. If partial scarring occurs, our result implies that $\mu(\gamma)$ cannot be too large. This means that the "scars" that one is tempted to see in Figures 4 and 5 are never very sharp. We stress the fact that partial scarring has been observed in certain examples of chaotic systems [61, 48]; thus we do not completely exclude the possibility of partial scarring on negatively curved manifolds.

To finish, let us go back to our simplest example, the cube. As alluded to earlier, in a euclidean cube, scarring is impossible, due to the following result. Let us take any sequence $(u_n)_{n\in\mathbb{N}}$ such that $\int_{[0,\pi]^d} |u_n(x)|^2 dx = 1$. After extracting a subsequence, one can always assume that there is a probability measure μ on $[0,\pi]^d$ such that

$$\int_{t=0}^{1} \int_{[0,\pi]^d} a(x) |e^{it\Delta} u_n(x)|^2 dx dt \underset{n\to+\infty}{\longrightarrow} \int_{[0,\pi]^d} a(x) d\mu(x)$$

for any continuous observable $a(x)$. It is shown in [30, 60] (with techniques from number theory) and [9] (with dynamical techniques) that μ must have a density: $d\mu(x) = \rho(x)dx$ (thus excluding the possibility of scars). Moreover, for any open set $\Omega \subset [0,\pi]^d$ there exists $c_\Omega > 0$, independent on the initial conditions (u_n), such that $\int_\Omega \rho(x)dx > c_\Omega$. This means that the solutions of the Schödinger equation must spend some uniform

proportion of time within Ω. Using the spectral degeneracies it is easy to build examples where $\rho(x)dx$ is not the uniform measure. However, obtaining more precise information on the density ρ is a subtle issue.

In recent work, techniques from ergodic theory have also been used to study the spectrum of the damped wave equation on negatively curved manifolds [5] or in the square [8] and to characterize the controllability of the Schrödinger equation in various geometries [9, 13, 10]. These ideas have also helped to understand the resonance spectrum of *open* systems [68, 69, 77, 38]. We stress the fact that the mathematical work described here deals with $|\psi_n(x)|^2$ as being a density: in expressions such as (2) we look at the average of this density over sets of finite, fixed sizes. This approach misses many features seen in numerics : nodal lines, fluctuations of eigenfunctions around their "typical" statistical bevaviour, estimates of L^p norms and description of the "peaks" of eigenfunctions, value distribution, restriction of eigenfunctions to submanifolds... Another challenge is to understand generic systems in which one has a coexistence of regular and chaotic motion. Even classically, this numerically observed coexistence has only been established rigorously in few cases. Quantum mechanically one expects that in the semiclassical limit eigenstates either concentrate on regular tori or within the chaotic regions. However, the convergence to this limit can be extremely slow and many important physical effects are relevant away from the semiclassical limit: e.g. dynamical tunnelling [43, 62] partial barriers [67], deviations from universal spectral statistics [22], ...

To learn more: We refer the reader to the lecture notes [3] for details about the work of Anantharaman–Nonnenmacher. The survey papers [88] and [76] and books in quantum chaos [50, 81, 51] offer a more detailed and exhaustive presentation of the various aspects of the subject.

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Algebraic tools for evolutionary biology

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Algebraic statistics is a new discipline which, among other applications, is being used to study the evolution of species. Here we present the problems evolutionary biologists deal with, and explain how to address them from the algebraic statistics point of view and using tools from algebraic geometry. At the same time, we present new mathematical challenges that have resulted from this interdisciplinary interaction.

1 Introduction

Based on Darwin's theory of natural selection, the evolution of species is usually modeled on a *phylogenetic tree*: the contemporary species are represented by its leaves, the root represents the common ancestor to all the species, and each split into branches represents a speciation process (see figure 1). Nowadays, due to the genome sequencing of a huge amount of species (publicly available at www.ensembl.org, for example), the study of the evolutionary history of a group of species is carried out via the relationship of DNA molecules attached to them (normally corresponding to genes). Thanks to the double helix structure, each DNA molecule can be thought of as a sequence of nucleotides (adenine `A`, cytosine `C`, guanine `G`, and thymine `T`), and thus as a sequence on the characters `A`, `C`, `G`, `T`. The aim of computational evolutionary biology or *phylogenetics* is to reconstruct the ancestral relations among species, i.e. the phylogenetic tree, from the given

[1] Partially supported by Ministerio de Economìa y Competitividad MTM2009-14163-C02-02 and Generalitat de Catalunya, 2009 SGR 1284. Part of this report had been inspired by the report by the same author presented in Spanish in *La Gaceta de la Real Sociedad Matemática Española*.

DNA sequences. The reconstruction of the phylogenetic tree is not only relevant to the evolutionary history, but also to the genetics and physiology of the species.

Mathematically speaking, a phylogenetic tree is an acyclic connected graph whose leaves are labeled with the contemporary species names, and (possibly) with a given interior node called *root*. The length of an edge on a phylogenetic tree represents the *evolutionary distance* between both ends and is called *branch length*. The *topology* of a phylogenetic tree means the topology of the labeled graph (without taking into account the branch lengths). It specifies the species groups that are created at each step of the evolutionary process (for instance, the trees in figure 1 have the same topology as graphs but distinct topology in terms of phylogenetics, i.e. as labeled graphs). A phylogenetic tree of a set of species is specified by its topology and the corresponding branch lengths.

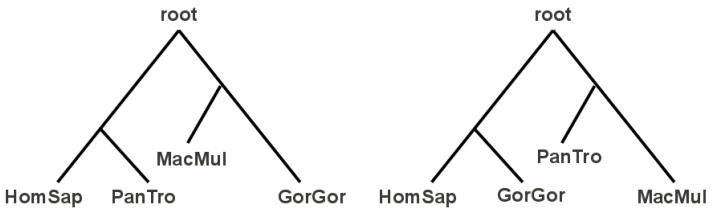

Figure 1: Two phylogenetic trees on the set of species *Homo Sapiens* (human), *Pan Troglodytes* (chimpanzee), *Gorilla Gorilla* (gorilla), and *Macaca Mulatta* (macaque) with distinct topology.

In order to reconstruct the phylogenetic tree of a group of contemporary species (both the tree topology and the branch lengths), one usually models evolution by mathematical models of nucleotide substitution (see next section). Then, the goal is to answer to following questions:

- What is the evolutionary model that best fits the given DNA sequences?
- What is the tree topology that best fits the data? What are the corresponding branch lengths?
- Is it actually possible to identify the phylogenetic tree from the DNA sequences? That is, are the parameters of the chosen evolutionary model *identifiable*?

Although one tends to think that biologists would consider only evolutionary models with an affirmative answer to the last question, this is not true in practice: biologists create more and more complex models of evolution without knowing whether its parameters can be recovered. For example, it is now well known that the root of a phylogenetic tree is not identifiable. Indeed, one cannot place the root having only information of the DNA sequences at the leaves, and an extra species acting as an outgroup is needed to determine its position. In other words, the common ancestral species cannot be placed in time only from the information of the contemporary species. This explains why phylogenetic trees

are unrooted, although we will use a root for clarity in exposition. Once unrooted trees are considered, the model parameters of the most commonly used evolutionary models are identifiable. However, for more complex models, identifiability is an important issue. Biologists do not know whether the parameters are identifiable or not and base their decisions on tests performed on simulated data, but mathematicians have tools which could solve this problem.

As far as the first question is concerned, biologists often make a heuristic choice of the evolutionary model depending on the the group of species under consideration, and even more often they just use the model set by default in phylogenetic software. However, inaccurate model selection completely conditions the phylogenetic tree inferred (see for example [RS08]). Therefore, the problem of selecting the most suitable model for the given data is also crucial.

Several mathematical areas such as combinatorics, dynamical systems, computer science, and statistics, play a role in phylogenetics nowadays. In the last decade, the new discipline of *algebraic statistics* (coined by Riccomagno, Pistone and Wynn in [PRW00]) has emerged and is becoming more and more used in computational biology [PS05]. In algebraic statistics one uses tools from algebraic geometry and commutative algebra on algebraic statistical models (that is, parametric statistical models where the distributions can be written as polynomials in the parameters). In 1987, the biologists Cavender, Felsenstein and Lake were the first to realize that certain polynomials can play an important role in phylogenetic reconstruction. But it has not been until the new century that mathematicians have turned their attention to this application of algebraic geometry and have started studying the varieties involved to give a better understanding of phylogenetic reconstruction. These tools have now been applied to model selection (cf. [KDGC12]), to solve identifiability issues (see discussion below and [AR06]), and to deduce ancestral divisions among groups of species [San90]. The reader interested in a deeper explanation on the applications of algebraic geometry in phylogenetics is referred to the book chapter [AR07].

In this paper we introduce the reader to the usage of algebraic statistics in phylogenetics, while proposing new mathematical challenges. In the next section we present evolutionary models as discrete-time hidden Markov processes on trees. In section 3, we introduce the tools needed to handle these models as algebraic varieties, and we discuss how to use these varieties in different phylogenetic problems. In section 4 we present the most used phylogenetic reconstruction methods, and we compare them to methods using algebraic geometry. Finally, we end the report with several conclusions.

2 Evolutionary models

Due to several processes of mutation, insertion and deletion of nucleotides along evolution, the DNA sequences of the same gene in different species are not identical: they contain similar parts, but also parts that cannot be compared. Even more, as the genomes of different species contain different numbers of chromosomes and nucleotides, it is difficult to find these similar regions of the same gene. However, it is important to know which

Gorilla Gorilla	AACTTCGAGGCTTACCGCTG
Homo Sapiens	AACGTCTATGCTCACCGATG
Pan Troglodytes	AAGGTCGATGCTCACCGATG

Table 1: A multiple sequence alignment of DNA sequences of *Homo Sapiens* (human), *Pan Troglodytes* (chimpanzee) and *Gorilla Gorilla* (gorilla).

parts of the genomes of contemporary species come from the same part of the genome of their common ancestor. This information is collected in a multiple sequence *alignment* that is, a table whose rows are the species DNA sequences and whose columns correspond, theoretically, to nucleotides that have evolved from the same nucleotide of the common ancestor to all sequences (see table 1). The problem is to obtain a "good" alignment for the given DNA sequences, that is an alignment where the majority of columns come indeed from the same nucleotide of the common ancestor (without having a priori any other knowledge than the DNA sequences of the species, given separately). In this paper, as most of biologist working in phylogenetics do, we will not deal with this problem, as we will assume that the alignment is already given. To simplify, we shall only consider mutation events (as most biologist do), that is, we avoid considering deletion and suppression of nucleotides.

In order to model evolutionary processes one usually gives a statistical model under the following hypotheses:

(i) Mutations in a DNA sequence occur randomly.

(ii) Evolutionary processes on different lineages only depend on their common node.

(iii) Each nucleotide in a DNA sequence evolves independently of the other nucleotides and all of them evolve according to the same process.

Due to this last hypothesis, it is enough to model the evolution of a single position in the DNA sequences. Assume we are given a tree, for instance the one in figure 2 (a). Then we represent the statistical model on the tree as in figure 2 (b). We associate a discrete random variable X_i taking values in the set of four nucleotides $\{\mathtt{A}, \mathtt{C}, \mathtt{G}, \mathtt{T}\}$ to each vertex i. Random variables on the leaves of the tree represent nucleotides observed at the contemporary species (for example, X_1 displays nucleotides in *Gorilla Gorilla* in figure 2). As each column of an alignment can be though of as an observation of the random vector $X = (X_1, X_2, X_3)$, the random variables X_i at the leaves are called "observed" variables. On the other hand, as we do not know the genome of the ancestral species, the random variables at the interior nodes of the tree are called "hidden" variables.

Following a Markov process, a *substitution matrix* (or *transition matrix*) S_e is associated to each directed edge e. Its entries are the conditional probabilities $P(x|y, e)$ of a nucleotide y at the parent node of e being substituted by a nucleotide x at its child, during the evolutionary process along branch e.

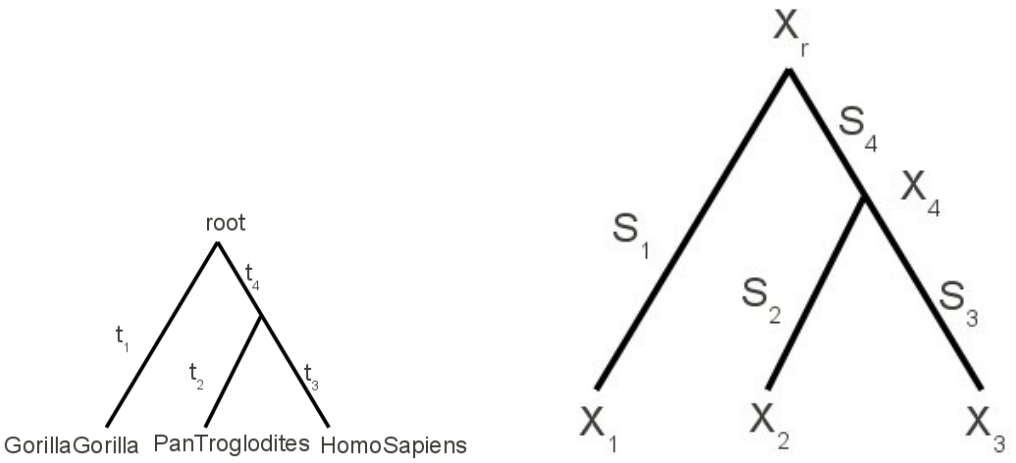

Figure 2: (a) *left* Phylogenetic tree of *Gorilla Gorilla, Pan troglodytes* and *Homo Sapiens* (magnitudes t_i denote branch lengths). (b) *right* Statistical model on a rooted phylogenetic 3-leaved tree.

$$S_e = \begin{array}{c} \\ \mathtt{A} \\ \mathtt{C} \\ \mathtt{G} \\ \mathtt{T} \end{array} \begin{array}{c} \begin{array}{cccc} \mathtt{A} & \mathtt{C} & \mathtt{G} & \mathtt{T} \end{array} \\ \begin{pmatrix} P(\mathtt{A}|\mathtt{A},e) & P(\mathtt{C}|\mathtt{A},e) & P(\mathtt{G}|\mathtt{A},e) & P(\mathtt{T}|\mathtt{A},e) \\ P(\mathtt{A}|\mathtt{C},e) & P(\mathtt{C}|\mathtt{C},e) & P(\mathtt{G}|\mathtt{C},e) & P(\mathtt{T}|\mathtt{C},e) \\ P(\mathtt{A}|\mathtt{G},e) & P(\mathtt{C}|\mathtt{G},e) & P(\mathtt{G}|\mathtt{G},e) & P(\mathtt{T}|\mathtt{G},e) \\ P(\mathtt{A}|\mathtt{T},e) & P(\mathtt{C}|\mathtt{T},e) & P(\mathtt{G}|\mathtt{T},e) & P(\mathtt{T}|\mathtt{T},e) \end{pmatrix} \end{array}.$$

The entries of S_e are unknown and, jointly with the distribution of nucleotides $(\pi_{\mathtt{A}}, \pi_{\mathtt{C}}, \pi_{\mathtt{G}}, \pi_{\mathtt{T}})$ at the root of the tree, form the *parameters* of the model. According to the values given to these parameters, there will be more or less substitutions along branch e, and therefore its length (measured as evolutionary distance) will vary. Actually, the branch length is usually measured in terms of the amount of substitutions per nucleotide that occurred along branch e, and it can be approximated by $-\frac{1}{4}\log\det S_e$ [BH87].

Depending on the amount of freedom allowed in these matrices, we have different evolutionary models. For example, if no restriction is given, we have the most *general Markov model GMM* (cf. [Ste94, BH87]):

$$S_e = \begin{pmatrix} a_e & b_e & c_e & d_e \\ e_e & f_e & g_e & h_e \\ j_e & k_e & l_e & m_e \\ n_e & o_e & p_e & q_e \end{pmatrix}$$

If one imposes $\pi_{\mathtt{A}} = \pi_{\mathtt{T}}$, $\pi_{\mathtt{C}} = \pi_{\mathtt{G}}$ and $j_e = h_e$, $k_e = g_e$, $l_e = f_e$, $m_e = e_e$, $n_e = d_e$, $o_e = c_e$, $p_e = b_e$, $q_e = a_e$, then one obtains the *Strand symmetric model* whose name is attributed to the fact that it reflects the double strand symmetry of a DNA molecule (cf. [CS05]). If

we impose uniform root distribution $\pi_{\mathtt{A}} = \pi_{\mathtt{C}} = \pi_{\mathtt{G}} = \pi_{\mathtt{T}} = 1/4$ and substitution matrices of type

$$S_e = \begin{pmatrix} a_e & b_e & c_e & d_e \\ b_e & a_e & d_e & c_e \\ c_e & d_e & a_e & b_e \\ d_e & c_e & b_e & a_e \end{pmatrix},$$

then we obtain the algebraic version of the *Kimura 3-parameter model* (cf. [Kim81]). Imposing also $b_e = d_e$, we obtain the algebraic *Kimura 3-parameter* model (cf. [Kim80]), and restricting to $b_e = c_e = d_e$, one obtains the algebraic version of the *Jukes-Cantor (JC)* model (cf. [JC69]):

$$S_e = \begin{pmatrix} a_e & b_e & b_e & b_e \\ b_e & a_e & b_e & b_e \\ b_e & b_e & a_e & b_e \\ b_e & b_e & b_e & a_e \end{pmatrix}.$$

Therefore, the parameter a_e in these last models stands for the probability that nucleotides remain the same throughout the evolutionary process. All these models are instances of the so-called *equivariant* models (see [DK09, CFS11]). Obviously, the root distribution and the row sums of the transition matrices add to 1, so that the actual number of free parameters is smaller than the quantity of letters given (for example, for the general Markov model there are three free parameters at the root and 12 free parameters in each substitution matrix).

Hypothesis **(iv)** implies that the probability that the alignment in table 1 has been produced following an evolutionary process on the tree T of figure 2 equals

$$(p^T_{\mathtt{AAA}})^4 * p^T_{\mathtt{CCG}} * p^T_{\mathtt{TGG}} * (p^T_{\mathtt{TTT}})^3 * (p^T_{\mathtt{CCC}})^4 * p^T_{\mathtt{GTG}} * p^T_{\mathtt{GTT}} * (p^T_{\mathtt{GGG}})^3 * p^T_{\mathtt{TCC}} * p^T_{\mathtt{CAA}},$$

where p^T_{xyz} stands for the probability of observing nucleotides x, y, z at the leaves *Gorilla gorilla* (X_1), *Homo sapiens* (X_2) and *Pan troglodytes* (X_3) of the tree T respectively:

$$p^T_{xyz} = \mathrm{Prob}(X_1 = x, X_2 = y, X_3 = z \mid T).$$

Under the Markov process (hypothesis **(ii)**) on the tree of figure 2, the probability p^T_{xyz} can be expressed in terms of the entries of the substitution matrices as follows:

$$p^T_{xyz} = \sum_{x_r, x_4 \in \{\mathtt{A},\mathtt{C},\mathtt{G},\mathtt{T}\}} \pi_{x_r} S_1(x_r, x) S_4(x_r, x_4) S_2(x_4, y) S_3(x_4, x), \tag{3}$$

where $\pi = (\pi_{\mathtt{A}}, \pi_{\mathtt{C}}, \pi_{\mathtt{G}}, \pi_{\mathtt{T}})$ is the distribution of nucleotides at the root.

For example, under the Jukes-Cantor model we obtain

$$p^T_{\mathtt{AAA}} = \frac{1}{4}(a_1a_4a_2a_3 + 3b_1b_4a_2a_3 + 3b_1a_4a_2a_3 + 3a_1b_4a_2a_3 + 6b_1b_4b_2b_3),$$

$a_i + 3b_i = 1$ for $i = 1, 2, 3, 4$.

As a consequence, under the evolutionary models we have described above, the joint distribution of nucleotides at the root of the tree can be expressed as a polynomial function in the parameters (see equation (3)). Models that share this property are called *algebraic statistical models* and are the kind of models algebraic statistics deals with.

3 Phylogenetic invariants

From now on, T will denote a phylogenetic tree *topology* on a set of n species. Given an evolutionary model $\mathcal{M}$ as above with d free parameters on the tree topology T, the following polynomial map sends each set of parameters to the joint distribution $(p^T_{x_1\dots x_n})_{x_1,\dots,x_n}$ (see equation (3)) of nucleotides at the leaves:

$$\begin{array}{rcl} \varphi^{\mathcal{M}}_T : \mathbb{R}^d & \longrightarrow & \mathbb{R}^{4^n} \\ \theta = (\theta_1, \dots, \theta_d) & \mapsto & p^T = (p^T_{\mathtt{AA\dots A}}, p^T_{\mathtt{AA\dots C}}, p^T_{\mathtt{AA\dots G}}, \dots, p^T_{\mathtt{TT\dots T}}). \end{array} \tag{4}$$

For instance, the Jukes-Cantor model on the tree topology of figure 2 corresponds to the following polynomial map:

$$\begin{array}{rcl} \varphi^{JC}_T : \mathbb{R}^4 & \longrightarrow & \mathbb{R}^{64} \\ (a_1, a_2, a_3, a_4) & \mapsto & p^T = (p^T_{\mathtt{AAA}}, p^T_{\mathtt{AAC}}, p^T_{\mathtt{AAG}}, \dots, p^T_{\mathtt{TTT}}). \end{array}$$

Although the parameters of the model represent probabilities and therefore lie in $[0, 1]$, in order to apply tools from algebraic geometry, one often forgets about this restriction and considers polynomial maps defined over $\mathbb{R}^d$ or $\mathbb{C}^d$.

The image $\operatorname{Im}\varphi^{\mathcal{M}}_T$ contains all joint distributions of nucleotides that have been generated by some set of parameters in the model $\mathcal{M}$ on the tree topology T. We denote by $V_{\mathcal{M}}(T)$ the smallest *algebraic variety* containing $\operatorname{Im}\varphi^{\mathcal{M}}_T$. An algebraic variety is the set of solutions to a system of polynomial equations: $V_{\mathcal{M}}(T) = \{p \in \mathbb{R}^{4^n} \mid f_1(p) = 0, \dots, f_r(p) = 0\}$ for some polynomials $f_1, \dots, f_r$. The image set itself $\operatorname{Im}\varphi^{\mathcal{M}}_T$ is not in general an algebraic variety, but it forms a dense subset in the smallest algebraic variety containing it, $V_{\mathcal{M}}(T)$, when we stick to the complex numbers field.

On the other hand, it is well known that given any subset S in $\mathbb{R}^{4^n}$, the set $I(S)$ of polynomials vanishing on all the points in S forms an ideal (called the *ideal of* S). The Hilbert basis theorem implies that this ideal will have a finite set of generators. We are interested in the ideal $I(\operatorname{Im}\varphi^{\mathcal{M}}_T)$, which will be denoted as $I_{\mathcal{M}}(T)$. If a polynomial f lies in $I_{\mathcal{M}}(T)$, then f is a relation among the theoretical probabilities $p^T_{x_1,\dots,x_n}$, no matter which set of parameters of the model produced them (so f is somehow "invariant"). In the eighties, biologists Cavender, Felsenstein and Lake propose the following definition (cf. [CF87], [Lak87]):

Definition 1. Given a tree topology T on n leaves and an evolutionary model $\mathcal{M}$, the polynomials in $I_{\mathcal{M}}(T)$ are called *invariants of* T. If f is a polynomial in $I_{\mathcal{M}}(T)$ which does not belong to $I_{\mathcal{M}}(T')$ for any other tree topology T' on n leaves, then f is called a *phylogenetic invariant of* T.

Example 2. There are three distinct unrooted tree topologies on the set of leaves $\{1, 2, 3, 4\}$:

Let T be one of these tree topologies, and let $p^T = \varphi^{JC}_T(\theta)$ be a point in $V_{JC}(T)$ (JC stands for the Jukes-Cantor model). Then the following equalities, which can be easily deduced from the symmetry of the transition matrices, lead to invariants of T:

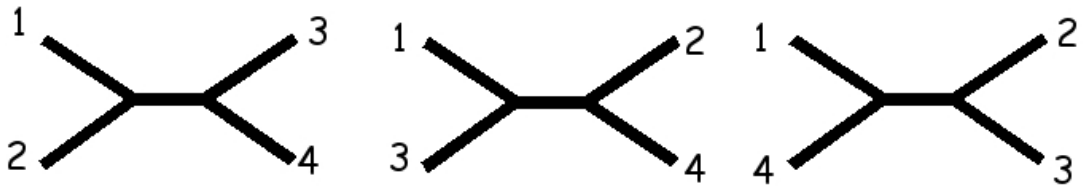

Figure 3: The three different unrooted tree topologies on four leaves are denoted as 12|34, 13|24, and 14|23 respectively.

$$p^T_{\texttt{AAAA}} = p^T_{\texttt{CCCC}} = p^T_{\texttt{GGGG}} = p^T_{\texttt{TTTT}}$$
$$p^T_{\texttt{AAAC}} = p^T_{\texttt{AAAG}} = p^T_{\texttt{AAAT}} = \cdots = p^T_{\texttt{TTTG}}.$$

However, as they hold for any tree topology on four trees as above, they are not *phylogenetic* invariants. To give phylogenetic invariants, we consider the following 16×16 matrix:

$$flat_{12|34} = \begin{array}{c} \\ states \\ leaves \\ 1,2 \end{array} \begin{array}{c} \overset{states\ at\ leaves\ 3\ and\ 4}{} \\ \begin{pmatrix} p_{\texttt{AAAA}} & p_{\texttt{AAAC}} & p_{\texttt{AAAG}} & \cdots & p_{\texttt{AATT}} \\ p_{\texttt{ACAA}} & p_{\texttt{ACAC}} & p_{\texttt{ACAG}} & \cdots & p_{\texttt{ACTT}} \\ p_{\texttt{AGAA}} & p_{\texttt{AGAC}} & p_{\texttt{AGAG}} & \cdots & p_{\texttt{AGTT}} \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ p_{\texttt{TTAA}} & p_{\texttt{TTAC}} & p_{\texttt{TTAG}} & \cdots & p_{\texttt{TTTT}} \end{pmatrix} \end{array}.$$

If $p = \varphi^{GMM}_T(\theta)$ for some parameters θ on the general Markov model, then this matrix has rank less than or equal to four when T is the tree 12|34 of figure 3. On the contrary, if $T = 13|24$ or $T = 14|23$ and $p = \varphi^T_{GMM}(\theta)$, then this matrix has rank 16 (for parameters θ general enough). That is, the order five minors of this matrix are phylogenetic invariants for $T = 12|34$ (they belong to $I_{GMM}(12|34)$ but not for $I_{GMM}(13|24)$ or $I_{GMM}(14|23)$).

The set of phylogenetic invariants is different for each tree topology and therefore can be used to recover the tree topology in phylogenetics as follows. Given an alignment on n species, let $\rho_{x_1 \ldots x_n}$ be the relative frequency of the n-tuple $x_1, \ldots, x_n$ occurring as column of the alignment. If the given alignment had been produced according a phylogenetic tree T under one of the models above, then the phylogenetic invariants of T would vanish over the vector of relative frequencies $\rho = (\rho_{\texttt{A}\ldots\texttt{A}}, \ldots, \rho_{\texttt{T}\ldots\texttt{T}})$ (although we would need an infinite alignment!) or, equivalently, ρ would be a point of the corresponding algebraic variety. In practice, genomes do not evolve under any mathematical evolutionary model nor on a phylogenetic tree but, if the evolutionary model considered fits the data well, then phylogenetic invariants of the "correct" tree topology evaluated at the vector of relative frequencies of columns of the alignment should be close to zero. That is, theoretically phylogenetic invariants can be used to infer the tree topology the data comes from (see

[Eri05] and [CGS05] for different approaches to this tree topology reconstruction using phylogenetic invariants).

One could ask whether it is easy to obtain phylogenetic invariants or whether a complete set of generators of the ideal is needed. The generators of $I_{\mathcal{M}}(T)$ could be obtained, in theory, using computational algebra software (such as `Singular` [GPS03] or `Macaulay2` [GS]). But computational algebra requires huge memory capacity and, in practice, this is not even possible for trees on three leaves. For example, for the strand symmetric and the general Markov models, this type of software does not allow the computation of $I_{\mathcal{M}}(T)$ for $n = 3$ (and actually a whole set of generators is still unknown for these models). Actually, providing a set of generators of the ideal of a 3-leaved tree under the general Markov model has become a challenge for the community working in this field and it is known as the *salmon problem* (as E. Allman has offered a personally caught salmon as prize, see http://www.dms.uaf.edu/ eallman/Papers/salmonPrize.pdf).

We are a bit more lucky when dealing with Jukes-Cantor, Kimura 2 and 3-parameter models because a certain change of variables (a discrete Fourier transform) converts $\varphi_T^{\mathcal{M}}$ into a monomial parameterization. In this case, software devoted to toric varieties allows the computation of generators of $I_{\mathcal{M}}(T)$ up to $n = 5$ leaves (the interested reader can find them at the webpage [GP]). To have an idea of what we are talking about, the ideal $I_{\mathcal{M}}(T)$ for four leaves and the Kimura 3-parameter model has 8002 generators.

Obviously, biologists are not happy with five species trees and we need to provide them phylogenetic invariants for any number of species. The following theoretical result allows one to compute the invariants for trees on n leaves from the invariants of three-leaved trees and the minors of certain matrices associated to the edges of the tree (as in example 2).

Theorem 1 ([DK09], [AR08], [SS05], [CS05])**.** *Let T be a phylogenetic tree of n species evolving according to one of the equivariant models $\mathcal{M}$ above. There exists an algorithm to obtain a set of generators of $I_{\mathcal{M}}(T)$ from the invariants of a 3-leaved tree and the minors of certain matrices associated to the edges of T (the so-called edge invariants).*

It is worth pointing out that a complete list of invariants for a tree on three leaves is not easy to obtain. As we mentioned above, such a list does not exist for the general Markov model or the strand symmetric model. This means that the previous theorem cannot be used in practice.

Nevertheless, one would hope that such a complete list of invariants is not needed, whereas suitably selected invariants should be enough for phylogenetic reconstruction purposes. For example, one only needs to consider those polynomials that define the variety $V_{\mathcal{M}}(T)$ at the points that correspond to distributions (this idea was explored in [CFS08] for the Kimura 3-parameter model and decreased the amount of 8002 invariants mentioned above to 48, for instance). On the other hand, if one is interested in just recovering the tree topology (not the substitution parameters or branch lengths), the focus should be on *phylogenetic* invariants. The following result proves that phylogenetic invariants are actually the edge-invariants presented above.

Theorem 2 ([CFS11]). *Let T be a phylogenetic tree of n species evolving under an equivariant evolutionary model as above. Then, for phylogenetic reconstruction purposes it is enough to consider only edge-invariants of T.*

Although its proof is quite technical, this result could have been easily expected. Indeed, there is a result in combinatorics guaranteeing that any tree can be reconstructed by only knowing the bipartitions it induces on its set of leaves. A *bipartition* of a set L is a pair of supplementary non-empty subsets (for example, $\{\{1,2\},\{3,4\}\}$ is a bipartition of $L=\{1,2,3,4\}$). Two bipartitions $\{A_1,A_2\}$ and $\{B_1,B_2\}$ of the same set are said to be *compatible* if at least one of the four intersections $A_1\cap B_1$, $A_1\cap B_2$, $A_2\cap B_1$, $A_2\cap B_2$ is not empty. If T is an unrooted tree whose leaves are labeled by the set L, then each edge in T induces a bipartition on L, corresponding to the two subsets of leaves split by that edge. It turns out that the set $bi(T)$ of $2n-3$ bipartitions induced by the edges of T is composed of pairwise compatible bipartitions. The following result is attributed to Buneman and is the combinatorial version of Theorem 2 above:

Theorem 3 (Buneman, [Bun71]). *Let L be a set of n elements and S a collection of $(2n-3)$ bipartitions of L. Then S is formed by pairwise compatible bipartitions if and only if there exists an unrooted tree T with leaves labeled on L such that $bi(T)=S$. In this case, the tree T is unique.*

4 Phylogenetic reconstruction methods

4.1 Maximum likelihood

One of the most common phylogenetic reconstruction methods is the maximum likelihood estimate. Given an alignment D and an evolutionary model $\mathcal{M}$, one wants to obtain the tree topology T_0 and the substitution parameters $\hat{\theta}$ which maximize $Prob(D|\mathcal{M},T,\theta)$ among all possible tree topologies and substitution parameters. To this end, the maximum likelihood estimate of the substitution parameters is obtained separately for each tree topology T using some of the available optimization methods and then one chooses the tree topology and the parameter estimates which maximize the likelihood among all tree topologies.

This method has a clear drawback: the number of (unrooted) tree topologies on n leaves is $(2n-5)!!$, which grows factorially in n, so that it becomes unfeasible to do an exhaustive search through all tree topologies for more than 15 leaves. The vast majority of phylogenetic reconstruction software (such as the widely used PHYLIP [Fel] or PAML [Yan97]) uses some branch and bound algorithm and not all tree topologies are considered. On the other hand, numerical optimization methods do not guarantee a global maximum in general and, even more, it is unknown whether there is a unique local maximum for biologically relevant parameters.

4.2 Neighbor-Joining

By far, the most used phylogenetic reconstruction method is Neighbor-Joining (it has more than four million entries in google!). This is a *distance-based method*, that is,

all the information from an alignment on a set of species $\{1,\dots,n\}$ is condensed into a *dissimilarity function* $d : \{1,\dots,n\} \times \{1,\dots,n\} \longrightarrow \mathbb{R}_{\geq 0}$ (symmetric and with zero diagonal entries). This dissimilarity function is intended to approximate the evolutionary *distance* (without the triangular inequality) between pairs of species or, in other words, it should account for the amount of mutations that separate both species. Obviously, not all mutations that have occurred during evolution can be observed in the contemporary species sequences (for instance, there may be an `A` mutating to `T` and finally coming back to `A` in the nowadays species) and the dissimilarity function has to take this into account. For example, the *Jukes-Cantor distance* between two DNA sequences defined as $-\frac{3}{4}\ln(1-\frac{4}{3}f)$, where f is the fraction of different nucleotides in both sequences, approximates the amount of mutations (observed and unobserved) if the species have evolved under the Jukes-Cantor model.

Given a dissimilarity function d, the first step in the Neighbor-Joining algorithm chooses two species x and y minimizing the function $D_{x,y} = d(x,y) - \frac{1}{n-2}\sum_z (d(x,z) + d(y,z))$. These two species are joined on a cherry (that is, two leaves joined by two edges and an interior node) and the interior node is treated as a new species substituting the former x and y. In this way the number of species is decreased at each step and the function D is redefined accordingly.

This algorithm produces the correct phylogenetic tree if the sequences actually come from a tree and the distances used are the corresponding lengths of the edges. However, when dealing with biological sequences, their estimated distances do not correspond to the branch lengths of any particular tree, and the tree constructed by Neighbor-joining algorithm may not have a realistic biological interpretation. In spite of this, it is thought to be a highly reliable method and, as there is no need to search through the whole space of tree topologies, it is used to produce phylogenetic trees for large numbers of species.

4.3 Phylogenetic reconstruction based on invariants

Phylogenetic reconstruction methods based on invariants can be found in [Eri05], [CFS07], and [CFS10]. The method tested in [CFS07] considers a set I_T of generators of the corresponding ideal for each 4-leaved tree topology T as in Figure 3 and, given an alignment corresponding to a point $p \in \mathbb{R}^{4^4}$, uses the function $c(T) = \sum_{f\in I_T} |f(p)|$ as a *cost* for the topology T. The topology which reaches the lowest cost is estimated as the correct topology. Whereas the results obtained with this method are slightly worse than those obtained by maximum likelihood or neighbor-joining, it is worth pointing out that the evolutionary models described here are much more general than the models considered in these widely used methods.

Indeed, the Markov processes are usually considered in continuous time, that is, the substitution matrices are of type $S_e = exp(Qt_e)$ where Q is an instantaneous mutation rate matrix and t_e denotes the amount of substitution events occurring along edge e. In most common applications the matrix Q is the same for all the edges in the tree and the evolutionary process is said to be *homogeneous*. This kind of process is used to model the evolution of species which evolve approximately at the same rate. This hypothesis is violated by most groups of species (for example, even inside the group of mammals,

rodents evolve faster than primates). The parameters for the models we have considered in this paper are the entries of the substitution matrices S_e, and therefore they account for non-homogeneous evolutionary processes. In [CFS07] it is proven that methods based on phylogenetic invariants outperform common phylogenetic reconstruction methods when dealing with non-homogeneous data. For example, the phylogenetic tree of primates, rodents, bovids, canids and elephants is drawn in figure 4(a), but this tree is incorrectly reconstructed by neighbor-joining and maximum likelihood (which reconstruct the tree in 4(b)). Methods based on invariants should reconstruct the phylogenetic tree of this set of species correctly.

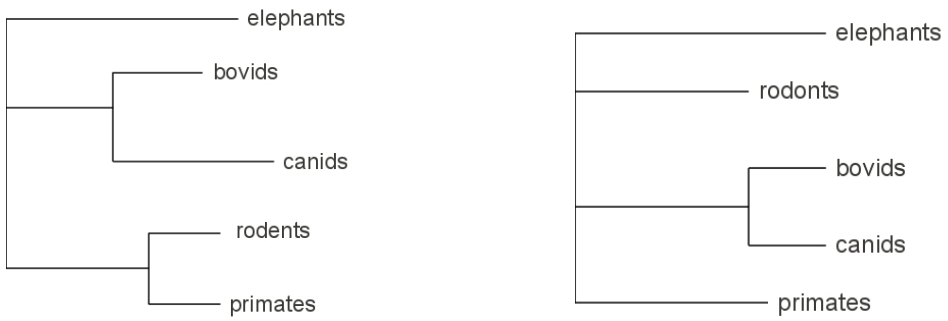

Figure 4: (a) *left* Correct phylogenetic tree of primates, rodents, bovids, canids and elephants. (b) *right* Incorrect tree reconstructed by neighbor-joining and maximum likelihood.

Although we have shown in Theorem 2 that the invariants which really matter for the reconstruction of the tree topology are the edge-invariants, there is no phylogenetic reconstruction method based solely on edge-invariants. In any case, the number of edge invariants grows exponentially in n, so that not all them should be used for large sets of species. Moreover, the number of unrooted tree topologies ($(2n-5)!!$ as mentioned above) makes it impossible to use a different set of invariants for each tree. A reasonable approach could be combining phylogenetic invariants with other existing methods. For instance, if a good inference method based on invariants is provided for quartet trees, then it could be incorporated into *quartet-based methods* (see [RG01]).

5 Conclusions

Presenting evolutionary models as polynomial maps allows one to relate phylogenetic questions to problems in algebraic geometry. We have seen that computational algebraic tools are not of much help in this case, but we have shown that theoretical results can indeed be used in phylogenetic reconstruction. The applications of algebraic geometry in evolutionary biology do not end here. For example, they can be applied to deal with identifiability issues of complex evolutionary models such as *phylogenetic mixtures*. Phylogenetic mixtures take into account the possibility that distinct parts of the genome have evolved in different ways (for example genes are not likely to mutate whereas other

regions of the genome mutate easily). DNA sequences are said to be a phylogenetic mixture on r trees if we can split the corresponding alignment into r pieces such that each of them comes from a particular phylogenetic tree (the r trees can have the same or different topology). Biologists do not know what is the maximum number of phylogenetic mixtures that one should use (i.e. the maximum r for which the parameters can be identified from the alignment) and they recommend (without any mathematical basis) not to use more than four or five. But an alignment from a phylogenetic mixture on trees $T_1, \ldots, T_r$ is just a point on a linear variety generated by points in the varieties $V_{\mathcal{M}}(T_i)$. In this way, advanced tools in algebraic geometry dealing with secants and joins of varieties can be used to determine the maximum number of phylogenetic mixtures to use.

On the other hand, we have already mentioned that the techniques introduced here have also been applied to other problems. However, there are still many other areas to explore using these tools. In any case, there is a long way to go in convincing biologists to use them. Indeed, these tools are often not directly applicable to real situations and should be used together with statistics, combinatorics and computational tools. Using a multidisciplinary point of view we could give back to biology all the knowledge we got from it in the shape of mathematical problems. Exactly as Joel E. Cohen says in [Coh04]: "Mathematics Is Biology's Next Microscope, Only Better; Biology Is Mathematics' Next Physics, Only Better".

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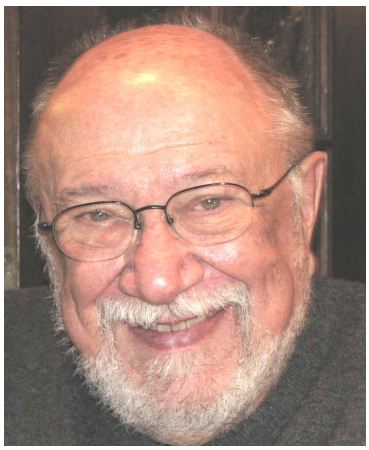
Editorial remark. This article was published first in the News Letters of the European Mathematical Society No.86, December 2012. We are thankful to Lucia Di Vizio (Editor-in-Chief) and Marta Casanellas for permission to reproduce the article in the framework of the IAMP News Bulletin – News Letters of the EMS exchange programme.

Gérard Gustav Emch (1936–2013)



With great sadness we note the passing of Gérard Gustav Emch, at the age of 76. He was born on July 21, 1936 in Geneva, Switzerland, and died suddenly, in his home in Gainesville, Florida, on March 5, 2013.

Gérard obtained his PhD in Theoretical Physics in 1963 under Josef Jauch at the University of Geneva. His thesis, 'Mécanique Quantique Quaternionienne et Relativité Restreinte', was a notable product of the school in the foundations of quantum mechanics which Jauch created in Geneva. But Gérard changed fields several times, in part from his postdoctoral training in the US, first at Princeton University (1964-65) with Valentine Bargmann as mentor, and then at the University of Maryland (1965-66) in the group of Elliott Montroll. Montroll brought Gérard with him when they moved to the physics department of the University of Rochester in 1966.

From his postdoc at Maryland, Gérard's work in statistical physics flourished, but the influence of his stay at Princeton was perhaps more profound. He arrived in Princeton early in the development of the C^*-algebraic framework of many-body physics, which expanded greatly after the influential paper in 1964 by Rudolph Haag and Daniel Kastler. This program used to good effect the functional analysis of operators on Hilbert spaces, based on the mathematical modeling of quantum mechanics beginning with Dirac and greatly expanded by John von Neumann, George Mackey and refined by Irving Segal. This allowed the inclusion of standard physical models of quantum theory, first in relativistic quantum field theory and then in nonrelativistic statistical physics. Gérard made an important early contribution in this program with his first book, 'Algebraic Methods in Statistical Mechanics and Quantum Field Theory' (1972), which was widely used and cited – a worthy successor to those of von Neumann, Mackey and Jauch.

Gérard published many papers on a variety of subjects. His series on K-flows was perhaps the best received. But his influence was also felt through less standard paths,

from the long chapters in books, including the one on C*-algebra methods in the first volume of the Domb and Green series, published lectures (including the Boulder Summer Schools of 1964 and 1965), authorship of several books, and from the environment he created, first in the physics and mathematics departments at the University of Rochester (he obtained a joint appointment in mathematics in 1971) and then in the second half of his career, at the University of Florida. Thirteen of his 16 PhD students were trained in Rochester (1966-86). He was recruited by Florida in 1986 to guide and develop the mathematics department. First as Chairman, and continuing afterwards, he accomplished this by encouraging significant faculty expansion in mathematical physics, geometry and dynamical systems.

In Florida, Gérard again changed fields, first into geometric quantization and gravitation, then into the history and philosophy of science. During this phase, he wrote two books: 'Mathematical and Conceptual Foundations of 20th Century Physics' and 'The Logic of Thermostatistical Physics' (coauthored with Chuang Liu). This phase continued after his retirement in 2005; in fact, he was well into an ambitious project on the history of calculus at the time of his death.

He received a number of honors, including the Gauss Professorship of the Academy of Science at Göttingen for 1985 and a Visiting Fellowship at All Souls College of the University of Oxford in 2002. There was a special session organized in his honor at the XXV Workshop on Geometric Methods in Physics, held in Bialowieza, Poland, in 2006 after his retirement, and a book: 'Contributions in Mathematical Physics: A Tribute to Gérard G. Emch' was published following the meeting.

Gérard was an important influence on many of us, and he will be remembered fondly. In particular, memories of his very special sense of humor and acerbic wit will always be with us.

S. Twareque Ali, Charles Radin, Kalyan B. Sinha

News from the IAMP Executive Committee

New individual members

IAMP welcomes the following new members

1. Dr. Serena Cenatiempo, Department of Mathematics and Physics, Università degli studi Roma 3, Roma, Italy
2. Prof. Dirk-André Deckert, Mathematics Department, University of California at Davis, USA
3. Prof. Bobby Gunara, Faculty of Mathematics and Natural Sciences, Institut Teknologi Bandung, Indonesia
4. Ms. Marwa Nasrallah, Mathematics Department, Aarhus University, Aarhus, Denmark
5. Dr. Jonathan Touboul, Mathematical Neuroscience Laboratory, College de France and INRIA, Paris, France

Recent conference announcements

Mathematical Physics of Disordered Systems

May 13-17, 2013, Fernuniversität Hagen, Germany

organized by
Werner Kirsch, Boris Khoruzhenko, Peter Müller.

Web page http://www.fernuni-hagen.de/pasturfest2013/

The Wednesday afternoon of the conference is dedicated to Prof. Leonid Pastur's 75th birthday.

Quantum Spectra and Transport

June 30 – July 4, 2013, The Hebrew University of Jerusalem, Israel

organized by
Jonathan Breuer, Omri Gat and Yoram Last

Web page `http://math.huji.ac.il/~avronfest/`

The conference is held on the occasion of Professor Yosi Avron's 65th birthday.
For further information please write to avronfest@math.huji.ac.il.

This conference is partially funded by the IAMP.

Mathematics and Quantum Physics

July 8–12, 2013, Accademia Nazionale dei Lincei, Roma, Italy

organized by
Corrado de Concini, Alberto De Sole, Sergio Doplicher, Giovanni Gallavotti, Alessandro Giuliani, Tommaso Isola, Giovanni Jona-Lasinio, Gerardo Morsella, Gherardo Piacitelli, Giuseppe Ruzzi.

Web page http://cmtp.uniroma2.it/13MQP/

This conference is partially funded by the IAMP.

The 8th Symposium on Quantum Theory and Symmetries

August 5 – 9, 2013, El Colegio Nacional, Mexico City

organized by
Kurt Bernardo Wolf, Octavio Novaro, Roelof Bijker, Octavio Castaños, Roco Jáuregui, Renato Lemus.

Web page http://www.fis.unam.mx/symposiaqts

This conference is partially funded by the IAMP.

QMath12: Mathematical Results in Quantum Physics

September 10 – 13, 2013, Humboldt-Universität, Berlin, Germany

organized by
Volker Bach, Michael Demuth, Pavel Exner, Wolfgang König, Alexander Mielke, Hagen Neidhardt, Reinhold Schneider.

Web page http://www.qmath12.de

This conference is partially funded by the IAMP.

Quantum Integrable Systems and Quantum Information Theory

August 18 – 24, 2013, Lawler's Hotel, Dungarvan

organized by Tony Dorlas (STP-DIAS, Dublin, Ireland)
Alexander Stolin (Chalmers University, Gothenburg, Sweden)

The school is aimed at postgraduate students and young researchers, as well as at higher level undergraduate students with an interest in quantum systems and/or quantum information theory.

For more information on the School, including registration, please visit its webpage http://www.dias.ie/summerschool2013 or contact Mary Brennan at DIAS, 01-6140122.

Mathematical Statistical Physics

July 29 – August 3, 2013, Yukawa Institute for Theoretical Physics, Kyoto, Japan

organized by: H. Tasaki, T. Deguchi, T. Hara, H. Hayakawa, M. Oshikawa, K. Sakai, T. Sasamoto

Web page http://www2.yukawa.kyoto-u.ac.jp/~mathstat/

The deadline for registration is May 31, 2013.

This will be one of the satellite meetings of STATPHYS25.

Open positions

Professorship in Mathematical Physics at Heidelberg University

The Departments of Mathematics/Computer Sciences and Physics/Astronomy of Heidelberg University invite applications for a tenured Professorship (W3) in Mathematical Physics. This professorship has been established within the framework of the German Excellence Initiative, and it is to play a major role in connecting research in the two departments.

Applicants should have made important, internationally recognized contributions to mathematical physics. All subfields of mathematical physics will be considered. Special attention will be given to candidates who can demonstrate their ability to enhance and complement the existing ties between mathematics and physics at Heidelberg University, for instance, in mathematical aspects of string theory or of complex physical systems.

The new professor will be a member of the Department of Mathematics/Computer Science or the Department of Physics/Astronomy depending on his/her profile and preferences, and will be co-opted to the respective other department. The successful candidate is expected to be able to teach in German after some initial period on all levels in his/her department and to contribute specialized courses aimed at students of both departments.

Applications (hardcopy and electronic) with curriculum vitae, description of scientific interests, list of publications (no reprints), and record of teaching activities should be submitted to Dekan der Fakultät für Mathematik und Informatik, Universität Heidelberg, Im Neuenheimer Feld 288, D-69120 Heidelberg, Germany, and in electronic form (preferably as a single pdf file) to dekanat@mathi.uni-heidelberg.de. Applications should include an exposé, which describes concepts for interdiciplinary cooperation and a research plan.

The deadline for applications is May 17, 2013.

Postdoctoral position in mathematical physics at University of Nijmegen

This is a 3-year position, starting October 1, 2013.

Applicants should have a PhD in theoretical physics, mathematical physics, or mathematics and should be thoroughly familiar with quantum physics and its mathematical methods (preferably including quantum spin systems, exactly solvable models, and operator algebras). A strong interest in relating theory to experiment is also mandatory.

The initial aim of this position is to adapt the remarkable "Flea on the Elephant" instability phenomenon in the theory of Schrödinger operators in the semiclassical limit (discovered by Jona-Lasinio, Martinelli, and Scoppola in 1981, named as such by Barry Simon in 1985, renamed as the "Flea on Schrödinger's Cat" and applied to the measurement problem by Landsman and Reuvers in 2013) to quantum spin systems in the thermodynamic limit. This possibility is predicated on the close mathematical analogy between the semiclassical limit and the thermodynamic limit, as well as on the groundbreaking work of Koma and Tasaki (1994) on (pre-)symmetry breaking in large (but finite) systems. Subsequently, dynamical aspects of this instability (including time-dependent perturbations and time-evolution of the perturbed ground state) should be analysed. Last but not least, theoretical groundwork should be done for the design and preparation of experiments testing the consequences of the theory for the (im)possibility of macroscopic superpositions (to be carried out at the Department of Materials of Oxford University).

This position is part of the innovative project Experimental Tests of Quantum Reality, in which the University of Oxford, Princeton University, and the Radboud University Nijmegen collaborate. This project will be funded by the Templeton World Charity Foundation. The PI of this project is Andrew Briggs (Oxford), with co-PI's Hans Halvorson (Princeton), Klaas Landsman (Nijmegen), and Andrew Steane (Oxford).

At the Radboud University Nijmegen, the position is embedded in the Department of Mathematical Physics, which is part of the Institute for Mathematics, Astrophysics, and Particle Physics (IMAPP) within the Faculty of Science. IMAPP is a lively institute performing fundamental research at the frontiers of science. Apart from Klaas Landsman (Mathematical Physics), the other full professors of mathematics are Ben Moonen (Algebra, starting 1-9-2013), Eric Cator (Applied Stochastics), Erik Koelink (Analysis), Gert Heckman (Geometry), and Spinoza Laureate Ieke Moerdijk (Topology). On the faculty, among (currently) ten other mathematicians one also finds mathematical physicists Hans Maassen, Michael Müger, and Walter van Suijlekom. Recently, the Department of Theoretical High-Energy Physics of IMAPP started a new group in quantum gravity led by Prof. Renate Loll. The Department of Experimental High-Energy Physics of IMAPP was closely involved in the discovery of the Higgs boson. The neighbouring Institute for Molecules and Materials (IMM) of the Faculty of Science hosts a strong group in theoretical condensed matter physics, led by the renowned graphene specialist Prof. Micha Katsnelson (who will act as consultant on this project).

Please apply by sending a CV including a list of publications, a short letter of motivation, and the names and email addresses of two or three referees to Klaas Landsman, landsman@math.ru.nl (from whom also further information may be obtained).
The deadline for applications is May 1st, 2013.

Postdoctoral positions in Mexico

Postdoctoral Positions in Mathematical Physics. The National Autonomous University of Mexico (UNAM) offers postdoctoral positions (Becas posdoctorales DGAPA-UNAM) for one year, with the possibility of extension for a second one. Applications are accepted twice a year, usually in September (to start the following March) and June (to start the following September). People interested in applying to work in Spectral and Scattering Theory, Quantum Mechanics, Quantum Field Theory, Quantum Information, and Quantum Optics, in collaboration with researchers of the Department of Mathematical Physics of the Institute for Research in Applied Mathematics and Systems (IIMAS) and who would like more information are welcomed to contact Dr Ricardo Weder, weder@unam.mx, or the Academic Secretary of IIMAS, Dr Ricardo Berlanga, berlanga@unam.mx. In order to have time to prepare the required documents please write sufficiently earlier than the application deadline.

More job announcements are on the job announcement page of the IAMP

http://www.iamp.org/page.php?page=page_positions

which gets updated whenever new announcements come in.

Manfred Salmhofer (IAMP Secretary)

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