



Mathematical 2013 Congress of the Americas

PLENARY SPEAKERS

STATE AUDITORIUM

AUGUST 5 - 9, 2013

5007-11-340

James G Arthur* (arthur@math.toronto.edu), Department of Mathematics, Bahen Centre,
6th Floor, 40 St. George Street, Toronto, Ontario M5S 2E4, Canada. *Classification of
Representations.*

Automorphic forms are matrix coefficients of automorphic representations. But they are also eigenfunctions of natural families of commuting linear operators. Their simultaneous eigenvalues govern fundamental objects of number theory and arithmetic geometry, according to the Langlands program. We shall review these matters. We shall then describe a recent classification of the automorphic representations of classical matrix groups, which is a consequence of a complex comparison of trace formulas. (Received May 13, 2013)

5007-37-591

Artur Avila* (artur@math.jussieu.fr). *Poincaré series and renormalization.*

* (Received May 15, 2013)

5007-11-416

Manjul Bhargava* (bhargava@math.princeton.edu). *Rational points on elliptic and hyperelliptic curves.*

Given a random elliptic or hyperelliptic curve of genus g over \mathbb{Q} , how many rational points do we expect the curve to have? In this talk, we give an overview of recent conjectures and theorems giving some answers and partial answers to this question. (Received May 14, 2013)

5007-00-648

Luis Caffarelli*, University of Texas at Austin, Department of Mathematics, Austin, TX

78712-1082. *Some segregation models: local and long range.*

Segregation problems arise in several circumstances: When different particles annihilate on contact, species cannot coexists, or in equipartition problems where we are asked to split a domain in several optimal shapes. I will describe several results on the geometric properties of solutions when segregation occurs on contact and also when segregation occurs at some long range. (Received May 16, 2013)

MCA2013-01

Ingrid Daubechies* (susan@math.northwestern.edu). *Computational differential geometry with biological applications.*

At present, biological scientists using physical traits to study evolutionary relationships among living and extinct animals analyze data extracted from carefully defined anatomical correspondence points (landmarks). Identifying and recording these landmarks is time consuming and can be done accurately only by trained morphologists; this renders these studies inaccessible to non-morphologists and causes phenomics to lag behind genomics in elucidating evolutionary patterns.

This motivated a team of mathematicians and biologists to propose new ways of defining "similarity distances" between morphological surfaces. Unlike many other algorithms presented for morphological correspondences, the new approaches do not require any preliminary marking of special features or landmarks by the user. It also differs from other seminal work in computational geometry in that the algorithms are polynomial in nature and thus faster, making pairwise comparisons feasible for significantly larger numbers of digitized surfaces.

The talk will present the motivation, the new mathematical constructions, and directions for future work.

The work reports on joint work with Yaron Lipman, Jesus Puente, Reema Al-Aifari, Tingran Gao, Doug Boyer, Liz St.Clair and Gabriel Yapuncich.