



Pierre Luisi

Human Population Geneticist
Master in Public Health
PhD in Biomedicine
Engineer in Biostatistics

PERSONAL DETAILS

<i>Nationality</i>	French with permanent residence in Argentina
<i>Birth</i>	6th of July 1985
<i>Address</i>	Mza 10 Lote 6 S/N José de la Quintana, CP 5198 Córdoba Province, Argentina
<i>Phone</i>	+54 9 3547 638952
<i>E-Mail</i>	pierre.luisi@unc.edu.ar

ACADEMIC BACKGROUND

Postdoctoral Fellow 2020-Present
Psychological Research Institute, National University of Córdoba, Argentina
Supervisor: Dr. Pablo Barttfeld
Project: *Genetic bases of image-derived phenotypes*

Postdoctoral Fellow 2016-2019
Department of Ecology, Genetics and Evolution, University of Buenos Aires
Research and Development Center for Immunology and Infectious diseases, Córdoba, Argentina
Supervisor: Dr. Hernán Dopazo
Projects:

1. *Missing heritability of infectious phenotypes: genetic association strategies for understanding the etiology of immune susceptibility to pathogens.*
2. *Genetic structure and diversity in Argentina: towards a genomic knowledge for future biomedical studies in our country*

Postdoctoral Fellow 2015
Biology Department, Stanford University, California, USA
Supervisor: Dr. Hunter B. Fraser
Project: *Impact of natural selection on tissue-specific gene and isoform regulation in humans: application to infectious diseases.*

Ph.D. in Biomedicine 2009-2014
Institute for Evolutionary Biology (Pompeu Fabra University) (IBE-UPF), Barcelona, Spain
Supervisors: Pr. Jaume Bertranpetit y Dr. Hafid Laayouni
Thesis Title: *Positive selection in humans, from single genes to interaction maps.*
Graduated with *Excellent cum laude*

Master in Public Health, specialization in Genetics and Statistics

2008-2009

Paris-Sud XI University, Paris, France

Supervisors: Dr. Audrey Sabbagh y Dr. Emmanuelle Génin

Thesis Title: *Genetic differentiation among human populations and natural selection, application to polymorphisms of interest in pharmacogenetics.***Engineer in Mathematics and Modeling (Biostatistics)**

2003-2008

National Institute for Applied Sciences (INSA), Toulouse, France

JOBS, TRAINEESHIPS AND EXCHANGES

Scientific Consultant

Since August 2019

myDNAMap S.L.

Next-Generation Sequencing data analysis:

- Pipeline to generate Variant Call Format files
- Pipeline to estimate uniparental lineages and genetic ancestry proportions from millions of autosomal markers
- Methodological development for Polygenic Risk Scores for a wide range of diseases

Ten-Day Lab Visit

June 2019

Harvard Medical School, Harvard University, USA

Supervisor: Pr. David Reich

Project Title: *Ancient DNA studies in Argentina.***Three-Month Lab Visit**

2012

Human Genetics Department, Chicago University, USA

Supervisor: Pr. Anna Di Rienzo

Project: *Building a meta-dataset for human population genetics studies.***Biostatistics Engineer**

2008-2009

University Hospital Group of Northern Paris (**GHU-Nord**), Paris, France

Supervisor: Pr. France Mentré

Six-Month Internship

2008

University Hospital Group of Northern Paris (**GHU-Nord**), Paris, France

Supervisor: Pr. France Mentré

Thesis Title: *Biostatistics technician for a network of constitutional genomics laboratories.***Three-Month Internship**

2007

Gulbenkian Science Institute (**IGC**), Lisbon, Portugal

Supervisor: Dr. Lounès Chikhi

Thesis Title: *The confounding effects of population structure, genetic diversity and the sampling scheme on the detection and quantification of population size changes.*

SPECIALIZATION COURSES

Wellcome Genome Campus Advanced Course

September 2017

Genetic Analysis of Population-based Association Studies

Wellcome Genome Campus, Hinxton, United Kingdom

Passed

50 hours

CONAE Graduate Course

Nov.-Dic. 2017

Epidemiological Analyses of Environment-linked Diseases

National Comision of Spatial Activities, CONAE, Córdoba Province, Argentina

Passed

30 hours

CeGen Training Meeting

July 2011

Ascertaining the genetic architecture of diseases

Centro Nacional de Genotipado (CeGen), Barcelona, Spain

Passed

16 hours

Postgrade Courses of Barcelona University

September 2011

DNA Phylogeny and Genealogy: Reconstruction and Applications

Barcelona University, Barcelona, Spain

Passed

160 hours

PARTICIPATION TO CONSORTIUM AND SCIENTIFIC NETWORKS

PoblAR

Since 2015

Consortium in its building phase.

Main objective: Create a reference center to host a free-access Biobank for genomics biomedical research in Argentina.

Ancient DNA studies in Argentina

Since 2019

Directed by Dr. Rodrigo Nores, Instituto de Antropología de Córdoba, Argentina and Pr. David Reich, Harvard Medical School.

Main objective: Study the evolutionary history in human populations from Argentina and the region.

PUBLICATIONS

Articles Published in Peer-Reviewed Journals

19. Nathan Nakatsuka*, **Pierre Luisi***, Josefina M. B. Motti, Mónica Salemmé, Fernando Santiago, Manuel D. D'Angelo del Campo, Rodrigo J. Vecchi, Yolanda Espinosa-Parrilla, Alfredo Prieto, Nicole Adamski, Ann Marie Lawson, Thomas K. Harper, Brendan J. Culleton, Douglas J. Kennett, Carles Lalueza-Fox, Swapnil Mallick, Nadin Rohland, Ricardo A. Guichón, Graciela S. Cabana, Rodrigo Nores, David Reich
Ancient genomes in South Patagonia reveal population movements associated with technological shifts and geography. Nat Commun. 2020 Aug 3;11(1):3868.
* Co-first authors
18. **Pierre Luisi**, Angelina García, Juan Manuel Berros, Josefina Motti, Darío Demarchi, Emma Alfaro, Eliana Aquilano, Carina Argüelles, Sergio Avena, Graciela Bailliet, Julieta Beltramo, Claudio M. Bravi, Mariela Cuella, Cristina Dejean, José Edgardo Dipierri, Laura S. Jurado Medina, José Luis Lanata, Marina Muzzio, María Laura Parolin, Maia Pauro, Paula B. Paz Sepúlveda, Daniela Rodríguez Golpe, María Rita Santos, Marisol Schwab, Natalia Silvero, Jeremias Zubrzycki, Virginia Ramallo, Hernán Dopazo
Fine-scale genomic analyses of admixed individuals reveal unrecognized genetic ancestry components in Argentina. PLoS ONE. 2020. 15(7): e0233808.
17. María C. Ávila-Arcos, Kimberly F. McManus, Karla Sandoval, Juan Esteban Rodríguez-Rodríguez, Viridiana Villa-Islas Alicia R. Martín, **Pierre Luisi**, Rosenda I. Peñaloza-Espinosa, Celeste Eng, Scott Huntsman, Esteban G. Burchard, Christopher R. Gignoux, Carlos D. Bustamante, and Andrés Moreno-Estrada
Population History and Gene Divergence in Native Mexicans Inferred from 76 Human Exomes. Mol Biol Evol. 2020 Apr 1;37(4):994-1006.
16. Jacqueline Milet, Anne Boland, **Pierre Luisi**, Audrey Sabbagh, Ibrahim Sadissou, Paulin Sonon, Nadia Domingo, Friso Palstra, Laure Gineau, David Courtin, Achille Massougboji, André Garcia, Jean-François Deleuze, Hervé Perdry
First Genome-Wide Association Study of Non-Severe Malaria in Two Birth Cohorts in Benin. Hum Genet. 2019 Dec;138(11-12):1341-1357.

15. Guillem de Valles-Ibáñez, Jessica Hernández, Javier Prado, **Pierre Luisi**, Tomàs Marquès-Bonet and Ferran Casals
Genetic load of loss-of-function polymorphic variants in great apes. Genome Biol Evol. 2016 Feb 24. pii: evw040.
14. Marc Pybus*, **Pierre Luisi***, Giovanni M Dall'Olio*, Manu Uzkudun, Angel Carreño-Torres, Pavlos Pavlidis, Hafid Laayouni, Jaume Bertranpetit and Johannes Engelken
A machine-learning framework to detect and classify hard selective sweeps in human populations. Bioinformatics. 2015 Aug 26. pii: btv493.
* Equal contribution
13. Begoña Dobon, Hisham Hassan, Hafid Laayouni, **Pierre Luisi**, Isis Ricaño-Ponce, Alexandra Zhernakova, David Comas, Mihai G. Netea, and Jaume Bertranpetit
The genetics of human populations of the Sudanese region: a novel Nilotic component in the African landscape and signals of positive selection in the East-African. Sci Rep. 2015 May 28;5:9996
12. **Pierre Luisi***, David Alvarez-Ponce*, Marc Pybus, Mario A. Fares, Jaume Bertranpetit and Hafid Laayouni
Recent positive selection targets the center of the human protein-protein interaction network. Genome Biol Evol. 2015 Apr 2;7(4):1141-54.
* Equal contribution
11. Laure Gineau, **Pierre Luisi**, Erick C. Castelli, Jacqueline Milet, David Courtin, Blandine Patillon, Hafid Laayouni, Philippe Moreau, Eduardo A. Donadi and André Garcia
Balancing immunity and tolerance: genetic footprint of natural selection in the HLAG 5' upstream regulatory region. Genes Immun. 2015 Jan;16(1):57-70.
10. Blandine Patillon, **Pierre Luisi**, Estella Poloni, Sotiria Boukouvala, Pierre Darlu, Emmanuelle Génin
A homogenizing process of selection has maintained an 'ultra-slow' acetylation NAT2 variant in humans. Human Biology. Jul;86(3):185-214
9. Garima Juyal, Mayukh Mondal, **Pierre Luisi**, Hafid Laayouni, Peter Heutink, Jaume Bertranpetit, Ferran Casals and Thelma BK
Population and genomic lessons from genetic analysis of two Indian populations. Hum Genet. 2014 Oct;133(10):1273-87
8. Vincenza Colonna, Qasim Ayub, Yuan Chen, Luca Pagani, **Pierre Luisi**, Marc Pybus, Yali Xue, Chris Tyler-Smith, The 1000 Genomes Project Consortium
Human genomic regions with exceptionally high levels of population differentiation identified from 911 whole-genome sequences. Genome Biol. 2014 Jun 30;15(6):R88
7. Hafid Laayouni, Marije Oosting, **Pierre Luisi**, Mihai Ioana, Santos Alonso, Isis Ricaño-Ponce, Gosia Trynka, Alexandra Zhernakova, Theo Plantinga, Shih-Chin Cheng, Jos W.M. van der Meer, Thelma BK, Radu Popp, Ajit Sood, Cisca Wijmenga, Leo A.B. Joosten, Jaume Bertranpetit and Mihai G. Netea
Common evolutionary signals in European and Roma populations: convergent evolution exerted by plague on TLR1/TLR6/TLR10 pattern recognition system. Proc Natl Acad Scien U S A. 2014 Feb;111(7):2668-73
6. Audrey Sabbagh*, **Pierre Luisi***, Erick C. Castelli, Laure Gineau, David Courtin, Jacqueline Milet, Juliana D. Massaro, Hafid Laayouni, Philippe Moreau, Eduardo A. Donadi and André Garcia
Worldwide genetic variation at the 3' untranslated region of the HLA-G gene: balancing selection influencing genetic diversity. Genes Immun. 2013 Mar;15(2):95-106
* Equal contribution
5. Marc Pybus*, Giovanni M Dall'Olio*, **Pierre Luisi***, Manu Uzkudun*, Angel Carreño-Torres, Pavlos Pavlidis, Hafid Laayouni, Jaume Bertranpetit and Johannes Engelken
1000 Genomes Selection Browser 1.0: a genome browser dedicated to signatures of natural selection in modern humans. Nucleic Acids Res. 2014 Jan;42(Database issue):D903-9
* Equal contribution

4. Blandine Patillon*, **Pierre Luisi***, H  l  ne Blanch  , Etienne Patin, Howard M. Cann, Emmanuelle G  nin and Audrey Sabbagh
Positive selection in the chromosome 16 VKORC1 genomic region has contributed to the variability of anticoagulant response in humans. PLoS One. 2012;7(12):e53049
* Equal contribution
3. Giovanni M. Dall'Olio, Hafid Laayouni, **Pierre Luisi**, Martin Sikora, Ludovica Montanucci and Jaume Bertranpetit
Distribution of events of positive selection and population differentiation in a metabolic pathway: the case of asparagine N-glycosylation. BMC Evol Biol. 2012 Jun 25;12:98
2. **Pierre Luisi**, David Alvarez-Ponce, Giovanni M. Dall'Olio, Martin Sikora, Jaume Bertranpetit and Hafid Laayouni
Network-level and population genetics analysis of the insulin/TOR signal transduction pathway across human populations. Mol Biol Evol. 2012 May;29(5):1379-92.
1. Loun  s Chikhi, Vitor C. Sousa, **Pierre Luisi**, Beno  t Goossens and Mark A. Beaumont
The confounding effects of population structure, genetic diversity and the sampling scheme on the detection and quantification of population size changes. Genetics. 2010 Nov;186(3):983-95

4. Shyam Gopalakrishnan, Inge KC Lundstrøm, S. Sunna Ebenesersdóttir, Gordon Turner-Walker, **Pierre Luisi**, [40 authors], Eske Willerslev, Johannes Krause, Francois Balloux, Tomas Marques-Bonet, Carles Lalueza-Fox, Rasmus Nielsen, Kári Stefánsson, Agnar Helgason, M Thomas P Gilbert.
The population genomic legacy of the second plague pandemic. In revision.
3. Julian Prádo, Diego De Panis, **Pierre Luisi**, Hernán Dopazo, Esteban Hasson and Ignacio Soto
An indirect approach to study the genetic response to mescaline in humans. In preparation.
2. Angelina García, Rodrigo Nores, Josefina M. B. Motti, Maia Pauro, **Pierre Luisi**, Claudio M. Bravi, Mariana Fabra, Anna L. Gosling, Olga Kardailsky, James Boocock, Neus Solé-Morata, Elizabeth A. Matisoo-Smith, Darío A. Demarchi, David Comas.
Ancient and modern mitogenomes from Central Argentina: new insights into population continuity, temporal depth and migration in the Southern Cone of America. In preparation.
1. Rodrigo Nores, Angelina García, James Boocock, Josefina Motti, Claudio M. Bravi, **Pierre Luisi**, Darío A. Demarchi, Elizabeth Matisoo-Smith.
C4c haplogroup in an archaeological mitogenome of southern South America and its implication in the American peopling. In preparation.

Note: I am not aware of the totality of the communications in which my name appears.

Selected Oral Presentations

5. ** 5th meeting of the Spanish Society for Evolutionary Biology (SESBE), 18th-21st January 2015, Murcia, Spain
Natural selection in functional pathways: an approach to understand natural selection within the complexity of life.
4. ** XV Jornada Biología Evolutiva, Secció de Biología Evolutiva de la Societat Catalana de Biologia, 23rd June, Barcelona, Spain
The genetics of East African populations: a Nilo-Saharan component in the African genetic landscape.
3. EMBO Conference Series on Human evolution in the genomic era: origins, populations and phenotypes, 1st-4th April, Leicester, United Kingdom
Recent positive selection targets the center of the human protein-protein interaction network.
2. XIII Jornada Biología Evolutiva, Secció de Biología Evolutiva de la Societat Catalana de Biologia, 2nd July 2013, Barcelona, Spain
Impact of natural selection within the human interactome.
1. European Science Foundation Workshop on Population genetics modeling and habitat fragmentation, 19th-21st de Septiembre 2007, Instituto Gulbenkian de Ciencias (IGC), Oeiras, Portugal
The confounding effects of population structure, genetic diversity and the sampling scheme on the detection and quantification of population size changes.

Invited Seminars in Research Centers

8. Department of Genetics, Harvard Medical School, Boston, EE.UU. 23rd June 2019
Fine-scale genetic analyses reveal three Native American ancestry components in Argentina: Andean, Patagonian and Lowlander.
Invited by Dr. David Reich.
7. Medical Research Institute Mercedes y Martín Ferreyra, Córdoba, Argentina. November 3rd 2016
How to understand biological differences in infectious disease susceptibility? Basic genetic epidemiology toolkit
Invited by Dra. Melina Musri.
6. Virology Institute Dr. José María Vanella, Córdoba, Argentina. June 17th 2016
How to understand biological differences in infectious disease susceptibility? Basic genetic epidemiology toolkit
Invited by Dr. Guillermo Albreu.
5. Stanford University, California, USA, April 8th 2015
Positive Selection in Humans: from Single Genes to Interaction Maps.
Invited by the Center for Computational, Evolutionary and Human Genomics (CEHG).
4. Saint Justine Hospital , Montréal, Québec, Canada, September 19th 2014
Positive Selection in Humans: from Single Genes to Interaction Maps.
Invited by Dr. Luis Barreiro
3. Cornell University, Ithaca, New York, USA, September 16th 2014
Positive Selection in Humans: from Single Genes to Interaction Maps.
Invited by Dr. Philipp Messer
2. Mixte Research Unit (UMR-216; Institute of Research for Development - Paris Descartes University), Paris, France. 26th September 2013
Human Selection Browser 1.0: A genome browser dedicated to signatures of natural selection in the 1000 genomes data.
Invited by Dr. Audrey Sabbagh
1. GeoCenter, Copenhagen, Denmark, September 13th 2013
A Machine-Learning Framework to Detect and Classify Hard Selective Sweeps in Human Populations.
Invited by Prof. Tom Gilbert

Selected Posters

17. ** 2019 Congress of the Society of Molecular Biology and Evolution (SMBE2019). 21-25 Julio 2019, Manchester, Reino Unido
The population genomic legacy of the second plague pandemic in Trondheim, Norway.

16. IX Argentinian Congress of Bioinformatics and Computational Biology 9CAB2C. 20th-22nd November 2018, Mar del Plata, Argentina
Fine-scale human genetic structure reveals a Central-Patagonic and a Northern- Andean ancestry components throughout Argentina.
15. ** ISCB-LA, SOIBIO and EMBnet Joint Bioinformatics Conference, 5th-9th November 2018, Viña del Mar, Chile
Fine-scale human genetic structure reveals a Central-Patagonic and a Northern- Andean ancestry components throughout Argentina.
14. ** Annual Meeting of the International Genetic Epidemiology Society, 9th-11th Septiembre 2017, Cambridge, Reino Unido
Genome-wide association study of susceptibility to mild malaria in two cohorts of young Beninese children.
13. ** Cold Spring Harbour Laboratory meeting on the Biology of Genomes, 10th-14th May 2016 , Cold Spring Harbour, USA
Natural selection in functional pathways—An approach to evolutionary systems biology.
12. V IMPPC Annual Conference and 4DCellFate Workshop. 27th-28th March 2014, Barcelona, Spain
Recent positive selection targets the center of the human protein-protein interaction network.
11. 4th meeting of the Spanish Society for Evolutionary Biology (SESBE), 27th-29th November 2013, Barcelona, Spain
Recent positive selection targets the center of the human protein-protein interaction network.
10. ** 4th meeting of the Spanish Society for Evolutionary Biology (SESBE), 27th-29th November 2013, Barcelona, Spain
1000 Genomes selection browser 1.0: A genome browser dedicated to signatures of natural selection in modern humans.
9. ** 4th meeting of the Spanish Society for Evolutionary Biology (SESBE), 27th-29th November 2013, Barcelona, Spain
Genomics analysis of two Indian populations highlights the role demography shaping genetic variation.
8. ** 4th meeting of the Spanish Society for Evolutionary Biology (SESBE), 27th-29th November 2013, Barcelona, Spain
Positive selection analysis in european and romania populations identifies convergent evolution on TLR1/TLR6/TLR10 pattern recognition system.
7. 2nd Symposium of the Department of Experimental and Health Science. 26th November 2013, Barcelona, Spain
Recent positive selection targets the center of the human protein-protein interaction network.
6. The 1000 Genomes Project Community Meeting, 12th-13th July 2012, Ann Arbor, USA
A framework to detect genomic regions under natural selection in 1000 genomes data.
5. Cold Spring Harbour Laboratory meeting on the Biology of Genomes, 8th-12th May 2012 , Cold Spring Harbour, USA
Network-level and population genetics analysis of the insulin/TOR signal transduction pathway across human populations.
4. Cold Spring Harbour Laboratory meeting on the Biology of Genomes, 8th-12th May 2012 , Cold Spring Harbour, USA
A framework to detect genomic regions under natural selection in 1000 genomes data.
3. ** Annual Meeting of the International Genetic Epidemiology Society, 18th-20th September 2011, Heidelberg, Germany
Signatures Of Recent Positive Selection At The VKORC1 Gene Locus.
2. Symposium of the European Society for Evolutionary Biology (ESEB), August 20th-25th, Tübingen, Germany, 2011
Network-level and population genetics analysis of the insulin/TOR signal transduction pathway across human populations.

1. NuGOweek, August 31st -September 3rd 2010, Glasgow, United Kingdom
Network-level and population genetics analysis of the insulin/TOR signal transduction pathway across human populations.

TEACHING EXPERIENCE

- Invited Teacher** Since 2018
Ecology, Genetics and Evolution Department, University of Buenos Aires, Argentina
Graduate and Postgraduate chair: Evolution and Population Genomics
- Invited Teacher** April and May 2018
Judiciary of Córdoba province
Postgraduate workshop: Genetics variation in human populations
- Assistant Teacher** from March 2017
Philosophy and Humanities Faculty, National University of Córdoba, Argentina
Introduction to Bioanthropology within the Anthropology School's Bioanthropology chair
- R workshop** April 2016
Anthropology Institute of Córdoba (IDACOR), Argentina
Introduction to R for data management and statistical analysis
- Ad honorem associate teacher** from March 2016
Philosophy and Humanities Faculty, National University of Córdoba, Argentina
Human Population Dynamics within the Anthropology Grade School's Bioanthropology chair
- Training Workshop on Bioinformatics** June 2014 and 2015
Nogochi Memorial Institute for Medical Research (NMIMR), University of Ghana, Legon, Ghana
For clinicians, immunologists, biologists and ecologists. Postgraduate and graduate students
- IBE PhD Student Training Program** Jan 2013
Evolutionary Biology Institute (Pompeu Fabra University; IBE-UPF), Barcelona, Spain
Steps Towards a Classical Human Population Genetics Study
- Regular Private Teacher for High School Students** 2004-2008
Toulouse, France
Mathematics, Physics and Biology

FELLOWSHIPS, HONORS & AWARDS

- Postdoctoral fellowship** 2020-Present
Found for Science and Technology Research (FONCyT), Argentinean Minister of Science, Technology and Productive Innovation
- Travel grant** June 2019
Harvard Medical School. Covered 100 % of travel and stay expenses
- 1st Prize Poster Award** 20th-22nd Nov. 2018
IX Argentinian Congress of Bioinformatics and Computational Biology 9CAB2C
- 1st Prize Poster Award** 5th-9th Nov. 2018
ISCB-LA, SOIBIO and EMBnet Joint Bioinformatics Conference
- Travel grant** Sep.-Oct. 2017
DEANN-Developing An European American NGS Network . Covered 100 % of travel and stay expenses
- Postgraduate course fellowship** September 2017
Wellcome Genome Campus. Covered 50 % of inscription charges
- Postdoctoral fellowship** 2016-2018

National Council for Scientific Research and Technology (CONICET), Argentinean Minister of Science, Technology and Productive Innovation

PhD fellowship

Sept 2009-Aug 2014

Acción Estratégica de Salud, en el marco del Plan Nacional de Investigación Científica, Desarrollo e Innovación Tecnológica 2008-2011 from Carlos III Health Institute, Spanish Ministry of Economy and Competitiveness

Travel grant

Apr 2012-Jul 2012

Beca ayuda estancia from Acción Estratégica de Salud, en el marco del Plan Nacional de Investigación Científica, Desarrollo e Innovación Tecnológica 2008-2011 from Carlos III Health Institute, Spanish Ministry of Economy and Competitiveness

OUTREACH

3. Media coverage for Luisi et al. (2020) Plos One

List of interviews I delivered and articles I co-wrote and/or revised.

Blog article

11 Aug. 2020

Universidad nacional San Martin: *El genoma argentino y la clave de la nueva medicina.*

<http://noticias.unsam.edu.ar/2020/08/03/el-genoma-argentino-y-la-clave-de-la-nueva-medicina/>

Blog article

7 Aug. 2020

Agencia CTyS: *Caracterizan ascendencia genética de la población argentina.*

<https://www.ctys.com.ar/index.php?idPage=20&idArticulo=4137>

Radio Interview

4 Aug. 2020

Radio Nihuil: *Investigadores identificaron un componente novedoso en el ADN de la región de Cuyo.*

<https://radionihuil.com.ar/investigadores-identificaron-un-componente-novedoso-en-el-adn-de-la-region-de-cuyo/>

Newspaper article

31 Jul. 2020

Página 12: *Investigadores argentinos identificaron un componente novedoso en el ADN nacional.*

<https://mdzradio.mdzol.com/article/view?slug=investigadores-reconocieron-un-nuevo-componente-en-el-adn-argentino>

Radio Interview

31 Jul. 2020

MDZ Radio: *Investigadores reconocieron un nuevo componente en el ADN argentino.*

<https://www.pagina12.com.ar/281841-investigadores-argentinos-identificaron-un-componente-novedoso>

Newspaper article

20 Jul. 2020

Diario Web: *No, los argentinos no somos "descendientes directos" de europeos.*

<https://www.eldiarioweb.com/2020/07/no-los-argentinos-no-somos-descendientes-directos-de-europeos/>

Blog article

17 Jul. 2020

CONICET: *De dónde venimos para saber adónde vamos.*

<https://www.conicet.gov.ar/cde-donde-venimos-para-saber-adonde-vamos/>

Radio interview

21 June 2020

Radio LU17: *Entrevista con Pierre Luisi, genetista de poblaciones de la FFyH, UNC.*

<https://ar.radiocut.fm/audiocut/entrevista-con-pierre-luisi-genetista-poblaciones-ffyh-unc/>

Radio interview

12 Feb. 2020

Radio Universidad Córdoba: *El investigador Pierre Luisi sobre el estudio del genoma de los argentinos.*

<https://ar.radiocut.fm/audiocut/investigador-pierre-luisi-sobre-estudio-del-genoma-argentinos/>

Newspaper article

9 Feb. 2020

La Voz del Interior: *La historia del ADN. Científicos de todo el país se unieron en una investigación que busca dar con el perfil genómico de las ancestrías argentinas.*

<https://m.lavoz.com.ar/ciudadanos/genes-ancestrales-clave-para-mejorar-precision-medica>

2. Media coverage for Nakatsuka, Luisi et al. (2020) Nature Communications

List of interviews I delivered and written articles I co-wrote and/or revised.

Blog article

3 Aug. 2020

CONICET: *Reconstruyen seis mil años de historia de la Patagonia Austral a través del genoma de veinte esqueletos antiguos.*

<https://www.conicet.gov.ar/reconstruyen-seis-mil-anos-de-historia-de-la-patagonia-austral-a-traves-del-genoma-de-veinte-esqueletos-antiguos/>

1. Other outreach activities Outreach Team

March 12th-16th 2014

EspaiCiència: Education exhibition, Barcelona, España

Organization and animation of a stand: Exposition of IBE projects, answer questions about IBE activities and biological research in general

PARTICIPATION IN FUNDED RESEARCH PROJECTS

DNA Studies, family stories and identity reconfigurations: an interdisciplinary study in Córdoba Province, Argentina

Funded by Universidad Nacional de Córdoba (Consolidar 2018)

Genetic diversity and structure in Argentina: obtaining a genomic knowledge for future biomedical studies in the country

Funded by el Fondo Nacional para las Ciencias y Tecnologías (PICT 2016).

Investigador Responsable

The Argentinean Genome. Pointing to a genomic and statistical model of our populations

Funded by the Consejo Nacional de Investigaciones en Ciencias y Tecnologías (2016-2018)

Systematically pinpointing causal polymorphisms underlying complex diseases

Funded by Pew Foundation Scholar in the Biomedical Sciences (2011-2016)

Detecting and understanding natural selection footprints in human and primate genomes

Funded by Ministerio de Ciencia e Innovación (Science and Innovation Spanish Government) (2014-2016)

'Selección natural en redes moleculares funcionales' (Natural selection in functional molecular networks)

Funded by Ministerio de Ciencia e Innovación (Science and Innovation Spanish Government) (2011-2013)

'Factores de riesgo genético en malaria' (Genetic risk factors of Malaria)

Funded by Ministerio de Ciencia e Innovación (Science and Innovation Spanish Government) (2008-2010)

SKILLS

Languages

French: native speaker

English: fluent (reading, writing and speaking) with working experience

Spanish: fluent (reading, writing and speaking) with working experience

Data analysis

Expert statistician

- **Multivariate analysis:** lineal & non lineal models (including mixed and generalized ones), principal component analysis, discriminate analysis, factorial analysis, parametric and non parametric statistical testing, etc.
- **Machine learning:** SVM, genetic algorithms, decision trees, etc.

Advanced programmer for **big data management** and statistical analyses

– Advanced: PERL, R, BASH, LATEX

– Intermediate: MYSQL, PYTHON, AWK, C/C++, MATLAB, SAS, S-PLUS

OS

Linux, MacOS, Windows

REFERENCES

Dr. Hernán Dopazo (Postdoc supervisor)
Evolutionary and Population Genomics Lab, CONICET
Av. Gral Paz 5445
Escuela de Ciencia y Tecnología UNSAM
Edificio 21. INTI San Martín
CP. 1650. Buenos Aires. Argentina
E-Mail: hdopazo@gmail.com

Dr. Rolando Gonzáles-José (Collaborator)
Grupo de Investigación en Biología Evolutiva Humana
Instituto Patagónico de Ciencias Sociales y Humanas (CENPAT-CONICET)
Bv. Almirante Brown 2915,
Puerto Madryn, Chubut, Argentina.
E-Mail: rolando@cenpat-conicet.gob.ar

Dr. David Reich (Collaborator)
Department of Human Evolutionary Biology, Harvard University
26 Oxford Street
MCZ, Room 525
Cambridge, MA 02138, USA
E-Mail: reich@genetics.med.harvard.edu

Dr. Hunter B. Fraser (Postdoc supervisor)
Biology Department,
Gilbert Building, Room 109
371 Serra Mall
Stanford, CA 94305-5020
E-Mail: hbfrazier@stanford.edu

Prof. Jaume Bertranpetit (PhD supervisor and collaborator)
IBE, Institut de Biologia Evolutiva (UPF-CSIC)
CEXS-Universitat Pompeu Fabra-PRBB
Doctor Aiguader 88
08003 Barcelona, Catalonia, Spain
E-Mail: jaume.bertranpetit@upf.edu

Dr. Hafid Laayouni (PhD supervisor and collaborator)
IBE, Institut de Biologia Evolutiva (UPF-CSIC)
CEXS-Universitat Pompeu Fabra-PRBB
Doctor Aiguader 88
08003 Barcelona, Catalonia, Spain
E-Mail: hafid.laayouni@upf.edu

Dr. Audrey Sabbagh (Master supervisor and collaborator)
Institut de Recherche pour le Développement
UMR 216 Mère et enfant face aux infections tropicales
Université René Descartes
4 Avenue de l'Observatoire
75006 Paris, France
E-Mail: audrey.sabbagh@ird.fr

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