

## PERSONAL INFORMATION

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### Institutional Address:

Unidad de Bioinformática  
Institut Pasteur de Montevideo  
Mataojo 2020- CP11400  
Montevideo - URUGUAY.

## ACADEMIC BACKGROUND

- “Doctor en Ciencias Biológicas” (PhD in Biology-Genetics/Genomics) Facultad de Ciencias, PEDECIBA. 2004.
- “Licenciado en Ciencias Biológicas” (BSc Biology) Facultad de Ciencias. 1999.

## ACTUAL POSITION

- Head of Bioinformatics (**uBi**), Institut Pasteur de Montevideo.
- Associate Professor of Quantitative Genetics & Animal Breeding, Facultad de Agronomía – Universidad de la República.
- Professor of Bioinformatics, Facultad de Ingeniería, Universidad ORT.
- Researcher at PEDECIBA (Basic Sciences Development Program).
- Categorized researcher at SNI (National Researchers System), level II.
- Member of the Post-Graduation College, Facultad de Agronomía.

## PREVIOUS

- Special Visiting Professor, Universidade Federal da Bahia – Salvador (Brazil), 2012-2015.
- Member of the board of directors for the Master in Bioinformatics, PEDECIBA.

## TEACHING ACTIVITIES

### *Post-graduate*

- “Bioinformatics Algorithms”. PEDECIBA – Bioinformatics (2008-2010).
- “Linear Models in Quantitative Genetics”. CP-FAGRO.
- “Quantitative Genetics”. CP-FAGRO / PEDECIBA.
- “Introduction to Domestic Animals Genomics”. CP-FAGRO / PEDECIBA.

## **Undergrad**

- “Bioinformatics I”. Universidad ORT.
- “Bioinformatics II”. Universidad ORT.
- “Animal Breeding”. Universidad de la República.

## **RESEARCH LINES**

Our research focus involves functional and evolutionary genomics. In particular, we are interested in the application of quantitative methods derived from statistical genetics in the bioinformatics field. In addition, we have some ongoing research in the field of quantitative genetics. Recently we have started to analyze pathogenicity from the genomics point of view; we have developed some methods to search for changes in proteins associated with pathogenicity and have applied machine-learning methods to the prediction of pathogenicity. We have extended our interests in pathogenicity to understand the molecular bases of biofilm formation in *Leptospira*.

Finally, we started a research project to understand the human genomic variability in the Uruguayan population, particularly to understand the admixture process and to begin a genomic medicine program. In this sense, we are particularly interested in genomics applied to diagnostic in rare diseases, both of nuclear and mitochondrial origins.

## **PUBLICATIONS**

- [72] Guillén-Nepita AL, Negrete-Paz AM, Vázquez-Marrufo G, Cruz-Hernández A, Fresia P, **Naya H**, Vázquez-Garcidueñas MS (2018). “Sequencing and Annotation of the Genome of *Mycobacterium tuberculosis* MYC004, a Strain Causing Meningitis in Mexico”. *Genome Announc.* 6(25). pii: e00523-18. doi: 10.1128/genomeA.00523-18.
- [71] Spangenberg L, Graña M, Mansilla S, Martínez J, Tapié A, Greif G, Montano N, Vaglio A, Gueçaimburú R, Robello C, Castro L, Quijano C, Raggio V, **Naya H** (2018). “Deep sequencing discovery of causal mtDNA mutations in a patient with unspecific neurological disease”. *Mitochondrion.* pii: S1567-7249(18)30008-4. doi: 10.1016/j.mito.2018.09.004.
- [70] Gianola D, Cecchinato A, **Naya H**, Schön CC (2018). “Prediction of Complex Traits: Robust Alternatives to Best Linear Unbiased Prediction”. *Frontiers in Genetics* 9:195. DOI: 10.3389/fgene.2018.00195.
- [69] Naya DE, **Naya H**, White C (2018). “On the interplay among ambient temperature, basal metabolic rate and body mass”. *Am Nat* 192(4):518-524. doi: 10.1086/698372.
- [68] Robert AW, Angulski ABB, Spangenberg L, Shigunov P, Pereira IT, Bettes PSL, **Naya H**, Correa A, Dallagiovanna B, Stimamiglio MA (2018). “Gene expression analysis of human adipose tissue-derived stem cells during the initial steps of in vitro osteogenesis”. *Scientific Reports* 8(1):4739. doi: 10.1038/s41598-018-22991-6.
- [67] Lasserre M, Fresia P, Greif G, Iraola G, Castro-Ramos M, Juambeltz A, Nuñez A, **Naya H**, Robello C, Berná L (2017) “Whole Genome Sequencing of the monomorphic pathogen *Mycobacterium bovis* reveals local differentiation of cattle clinical isolates” *BMC Genomics* 19(1):2. doi: 10.1186/s12864-017-4249-6.
- [66] Iraola G, Forster SC, Kumar N, Lehours P, Bekal S, García-Peña FJ, Paolicchi F, Morsella C, Hotzel H, Hsueh PR, Vidal A, Lévesque S, Yamazaki W, Balzan C, Vargas A, Piccirillo

- A, Chaban B, Hill JE, Betancor L, Collado L, Truyers I, Midwinter AC, Dagi HT, Mégraud F, Calleros L, Pérez R, **Naya H**, Lawley TD (2017) “Distinct *Campylobacter fetus* lineages adapted as livestock pathogens and human pathobionts in the intestinal microbiota” *Nature Communications* DOI: 10.1038/s41467-017-01449-9.
- [65] Naya DE, **Naya H**, Cook J (2017). “Climate change and body size trends in aquatic and terrestrial endotherms: does habitat matter?” *PLoS ONE* 12(8):e0183051. doi: 10.1371/journal.pone.0183051.
- [64] **Naya H**, Peñagaricano F, Urioste JI (2017). “Modelling female fertility traits in beef cattle using linear and non-linear models”. *Journal of Animal Breeding and Genetics* 134(3):202-212. doi: 10.1111/jbg.12266.
- [63] Dallagiovanna B, Pereira IT, Origa-Alves AC, Shigunov P, **Naya H**, Spangenberg L (2017). “lncRNAs are associated with polysomes during adipose-derived stem cell differentiation”. *Gene* pii: S0378-1119(17)30082-3. doi:10.1016/j.gene.2017.02.004.
- [62] Luna F, **Naya H**, Naya DE (2017). “Understanding evolutionary variation in basal metabolic rate: An analysis in subterranean rodents”. *Comp Biochem Physiol A Mol Integr Physiol.* 206:87-94. doi: 10.1016/j.cbpa.2017.02.002.
- [61] Gianola D, Fariello MI, **Naya H**, Schön CC (2016). “Genome-wide association studies with a genomic relationship matrix: a case study with wheat and Arabidopsis”. *G3 (Bethesda)* 6(10):3241-3256. doi: 10.1534/g3.116.034256.
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- [58] Iraola G, Spangenberg L, Lopes-Bastos B, Graña M, Vasconcelos L, Almeida A, Greif G, Robello C, Ristow P, **Naya H** (2016). “Transcriptome sequencing reveals wide expression reprogramming of basal and unknown genes in *Leptospira biflexa* biofilms”. *mSphere* 10.1128/mSphere.00042-16.
- [57] Naya DE, **Naya H**, Lessa EP (2016). “Brain size and thermoregulation during the evolution of the genus Homo”. *Comp Biochem Physiol A Mol Integr Physiol.* 191:66-73. doi: 10.1016/j.cbpa.2015.09.017.
- [56] Sanchez AL, Urioste JI, Peñagaricano F, Neimaur K, Sienna I, **Naya H**, Kremer R (2016). “Genetic parameters of objectionable fibers and of their associations with fleece traits in Corriedale sheep”. *Journal of Animal Science* 94(1):13-20. doi: 10.2527/jas.2015-9619.
- [55] Gutiérrez V, Rego N, **Naya H**, García G (2015). “First complete mitochondrial genome of the South American annual fish *Austrolebias charrua* (Cyprinodontiformes: Rivulidae): peculiar features among cyprinodontiforms mitogenomes”. *BMC Genomics* 16(1):879. doi: 10.1186/s12864-015-2090-3.
- [54] Lasserre M, Berná L, Greif G, Díaz-Viraqué F, Iraola G, **Naya H**, Castro-Ramos M, Juambeltz A, Robello C (2015). “Whole-Genome Sequences of *Mycobacterium bovis* Strain MbURU-001, Isolated from Fresh Bovine Infected Samples”. *Genome Announc* 3(6). pii: e01237-15. doi: 10.1128/genomeA.01237-15.

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- [53] Gianola D, de Los Campos G, Toro MA, **Naya H**, Schön CC, Sorensen D (2015). "Do Molecular Markers Inform About Pleiotropy?" *Genetics* pii:genetics.115.179978.
- [52] Fernandez-Calero T, Garcia-Silva R, Pena A, Robello C, Persson H, Rovira C, **Naya H**, Cayota A (2015). "Profiling of small RNA cargo of extracellular vesicles shed by *Trypanosoma cruzi* reveals a specific extracellular signature". *Mol Biochem Parasitol*. pii: S0166-6851(15)00013-4. doi:10.1016/j.molbiopara.2015.03.003.
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- [50] Iraola G, Pérez R, **Naya H**, Paolicchi F, Pastor E, Valenzuela S, Calleros L, Velilla A, Hernández M, Morsella C (2014). "Genomic evidences for the emergence and evolution of pathogenicity and niche preferences in the genus *Campylobacter*". *Genome Biology and Evolution* 6(9):2392-405. doi: 10.1093/gbe/evu195.
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- [47] Urioste JI, Peñagaricano F, López-Correa R, **Naya H**, Kremer R (2014) "Incidence and relationships of black skin spots in the fleece area and pigmentation traits in commercial Corriedale flocks". *Small Ruminant Research* 120:64-70.
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- [44] Greif G, Iraola G, Berna L, Coitinho C, Rivas C, **Naya H**, Robello C (2013) "Complete genome sequence of *Mycobacterium tuberculosis* strain MtURU-001, isolated from a rapidly progressing outbreak in Uruguay". *Genome Announc* 2(1) pii:e01220-13 doi:10.1128/genomeA.01220-13.
- [43] Laporta J, Rosa G, **Naya H**, Carriquiry M (2013) "Liver functional genomics in beef cows on grazing systems: novel genes and pathways revealed". *Physiological Genomics* 46(4):138-47 doi:10.1152/physiolgenomics.00120.2013.
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- [41] Spangenberg L, Correa A, Dallagiovanna B, **Naya H** (2013) "Role of alternative polyadenylation during adipogenic differentiation: an in silico approach". *PLoS ONE* 8(10):e75578 doi:10.1371/journal.pone.0075578.
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- [38] Spangenberg L, Shigunov P, Abud AP, Cofré AR, Stimamiglio MA, Kuligovski C, Zych J, Schittini AV, Costa AD, Rebelatto CK, Brofman PR, Goldenberg S, Correa A, **Naya H**, Dallagiovanna B (2013) "Polysome profiling shows extensive posttranscriptional regulation during human adipocyte stem cell differentiation into adipocytes". *Stem Cell Res* 11(2):902-912.
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- [36] Espasandín AC, Urioste JI, **Naya H**, Alencar MM (2013) "Genotype x Production Environment Interaction for Weaning Weight in Angus Populations of Brazil and Uruguay". *Livestock science* 151(2): 264-270.
- [35] Naya DE, Spangenberg L, **Naya H**, Bozinovic F (2012) "How does evolutionary variation in basal metabolic rates arise? A statistical assessment and a mechanistic model". *Evolution* 67(5):1463-76.
- [34] Iraola G, Vazquez G, Spangenberg L, **Naya H**. (2012) "Reduced set of virulence genes allows high accuracy prediction of bacterial pathogenicity in humans". *PLoS ONE* 7(8):e42144.
- [33] Iriarte A, Sanguinetti M, Fernández-Calero T, **Naya H**, Ramón A, Musto H. (2012) "Translational selection on codon usage in the genus *Aspergillus*". *Gene* 506(1):98-105.
- [32] Trujillo AI, Peñagaricano F, Grignola MP, Nicolini P, Casal A, Espasandín AC, **Naya H**, Carriquiry M, Chilibruste P. (2012) "Using high resolution melting analysis to identify variation of NPY, LEP and IGF-1 genes in Angus cattle". *Livestock Science* 146:193-198.
- [31] Rego N, Bianchi S, Moreno P, Persson H, Kvist A, Pena A, Oppezso P, **Naya H**, Rovira C, Dighiero G, Pritsch O. (2012) "Search for an aetiological virus candidate in chronic lymphocytic leukaemia by extensive transcriptome analysis". *Br J Haematol* 157(6):709-17.
- [30] Naya DE, Spangenberg L, **Naya H**, Bozinovic F. (2012) "Latitudinal patterns in rodent metabolic flexibility" *Am Nat* 179(6):E172-9.
- [29] Gascue C, Tan PL, Cardenas-Rodriguez M, Libisch G, Fernandez-Calero T, Liu YP, Astrada S, Robello C, **Naya H**, Katsanis N, Badano JL. (2011) "A Direct Role of Bardet-Biedl Syndrome Proteins in Transcriptional Regulation" *J Cell Science* 125(Pt2):362-75.
- [28] Peñagaricano F, Zorrilla P, **Naya H**, Robello C, Urioste JI. (2011) "Gene expression analysis identifies new candidate genes associated with the development of black skin spots in Corriedale sheep". *J Appl Genet* 53(1):99-106.

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- [27] Spangenberg L, Battke F, Graña M, Nieselt K, **Naya H**. (2011) “Identifying associations between amino acid changes and meta information in alignments”. *Bioinformatics* 27(20):2782-9.
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- [25] Persson H, Kvist A, Rego N, Staaf J, Vallon-Christersson J, Luts L, Loman N, Jönsson G, **Naya H**, Höglund M, Borg A, Rovira C. (2010). “Identification of new microRNAs in paired normal and tumor breast tissue reveals a dual role for the ERBB2/Her2 gene”. *Cancer Res* 71(1):78-86.
- [24] Bianchi S, Moreno P, Landoni AI, **Naya H**, Oppezzo P, Dighiero G, Gabus R, Pritsch O. (2010). “IGHV-D-J gene rearrangement and mutational status in Uruguayan patients with chronic lymphocytic leukemia”. *Leukemia & Lymphoma* 51(11):2070-8.
- [23] Peñagaricano F, Urioste JI, **Naya H**, de los Campos G, Gianola D. (2010). “Assessment of Poisson, Probit and linear models for genetic analysis of presence and number of black spots in Corriedale sheep”. *J Anim Breed Genet* 128(2):105-13.
- [22] González-Recio O, Weigel KA, Gianola D, **Naya H**, Rosa GJM. (2010). “L2-Boosting algorithm applied to high dimensional problems in genomic selection”. *Genet Res* 92(3):227-37.
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- [20] Sabbia V, Romero H, Musto H, **Naya H**. (2009). “Composition profile of the human genome at the chromosome level”. *J Biomol Struct Dyn* 27(3):361-70.
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- [18] Romero H, Pereira E, **Naya H**, Musto H. (2009). “Oxygen and GC profiles in marine environments”. *J Mol Evol* 69(2):203-6.
- [17] de Los Campos G, **Naya H**, Gianola D, Crossa J, Legarra A, Manfredi E, Weigel K, Cotes JM. (2009). “Predicting Quantitative Traits with Regression Models for Dense Molecular Markers and Pedigrees”. *Genetics* 182(1):375-85.
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- [14] Rego N, **Naya H**, Lamolle G, Álvarez-Valin F (2008). “Evolutionary and comparative genomics of *Leptospira*”. *RECIIS* 1(2 Supl): 321-328. - NO ARBITRADA –

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- [11] Urioste JI, Chang YM, **Naya H**, Gianola D. (2007). "Genetic variability in calving success in Aberdeen Angus cows under extensive recording". *Animal* 1:1081-8.
- [10] Sabbia V, Piovani R, **Naya H**, Rodriguez-Maseda H, Romero H, Musto H. (2007). "Trends of amino acid usage in the proteins from the human genome". *J Biomol Struct Dyn* 25:55-9.
- [9] Musto H, **Naya H**, Zavala A, Romero H, Alvarez-Valín F, Bernardi G. (2006). "Genomic GC level, optimal growth temperature and genome size in prokaryotes". *Biochem Biophys Res Commun* 347:1-3.
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## SHORT COMUNICATIONS

- more than 50 national/international short communications.

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## RESEARCH PROJECTS

- “Identification of microRNAs regulating infection of human cells by *Listeria monocytogenes*”. PROGRAMMES TRANSVERSAUX DE RECHERCHE – PTR Institut Pasteur 2016/2018 Javier Pizarro-Cerdá (**H Naya**).
- “Strengthening technical and human capacities for genomic services exports”. Funded by IDB 2014/2016. **H Naya**.
- “Análisis transcripcional en *Leptospiras* formadoras de biofilms”. Funded by ANII 2013/2015. **H Naya**.
- “Investigação dos Mecanismos Genéticos e Moleculares em Biofilmes de *Leptospira*”. Funded by CAPES – Brazil 2012/2015. A Schnadelbach/P Ristow. Special Visiting Professor **H Naya**.
- “Genome-wide analysis of chromatin modifications and gene expression profiles in human adult stem cells”. Funded by Fiocruz-Pasteur 2011/2013. S Goldenberg, **H Naya**.
- “Data Quality Management for Model Improvement in GWAS”. Funded by Microsoft Research 2008. **H Naya**, R Ruggia.
- “High-Content High-Throughput Flow cytometry: Development of a multi-application technical platform”. ACIP 2008/2009. HKU-PRC, IPMon (**H Naya**), FING, IPP, IPD.
- “Merging, InduCing and Reasoning with Ontologies in BIOinformatics – The MICROBIO Project”. STIC-AMSUD 2007-2009. IPMont (**H Naya**), UdelaR (Uruguay), CNRS MoDyCO UMR7114, LORIA (Francia), UN Córdoba (Argentina), PUC Rio Grande do Sul (Brasil), U de Concepción (Chile).
- “Generación de capacidad de anotación de genomas”. Funded by grant FPTA-INIA 2007-2008. F. Alvarez-Valín, **H Naya**, F. Capdevielle.
- “Disminución de fibras pigmentadas en Corriedale por vías genéticas”. Funded by PDT 2005-2007. Facultad de Agronomía and Facultad de Veterinaria. JI Urioste.
- “Evaluación Genética de Reproductores ABERDEEN ANGUS” 2002-2005. Convenio ARU-SCAAU-Fac.Agronomía-INIA.
- “Mejoras al modelo de evaluación de leche en la raza Holando en Uruguay: corrección por heterogeneidad de varianzas”. JI Urioste **H Naya**. ARU-SCHU-Fac.Agronomía-INML-INIA 2002.

## EDITORIAL BOARDS

- Associate Editor of *Frontiers in Ecology and Evolution*.
- Member of the Editorial Board of *Frontiers in Livestock Genomics (Frontiers in Genetics)*.
- Member of the Editorial Board of *ISRN Biomathematics*.

## INVITED TALKS

- **Naya H** (2014). “Human pathogens emerging from harmless bacteria: A simple model based in NGS data”. I Congresso Paranaense de Microbiologia e Simposio Sul – Americano de *Escherichia coli*, August 5, Londrina, Brazil.



- **Naya H** (2012). “Human pathogens emerging from harmless bacteria: A hybrid theoretical-empirical model”. International Scientific Symposium on Unmet Medical Needs and Technological Innovations, September 24, Pangyo Technovalley, Institut Pasteur Korea, Seoul, Korea.
- **Naya H** (2012). “Ronald vs Ronald: are we doing McDonaldized science”. New paradigms in the relationship between Mathematics and the Applied Sciences: Learning Theory and Immunology, Conferencias Internacionales de Investigación Interdisciplinaria, April 12, Buenos Aires, Argentina.
- **Naya H**, Spangenberg L (2011). “AQuaMAn: Applying Quality to Meta-Analysis”. Sextas Jornadas Argentinas de Data Mining, October 27-28, Buenos Aires, Argentina.
- **Naya H**, Rego N (2011). “Next Generation Sequencing: Search for an etiological virus Candidate in chronic lymphocytic leukaemia by extensive transcriptome analysis”. Escuela Latinoamericana de Genética Humana, ELAG2011, Caxias do Sul, Brasil.
- **Naya H**, Rego N (2011). “Something like a needle in a haystack: Search for an etiological virus Candidate in chronic lymphocytic leukaemia by extensive transcriptome analysis”. Conferencia de la Asociación Argentina de Bioinformática y Biología Computacional, 2011 Córdoba, Argentina.
- **Naya H** (2006). “Comparative Methods in Genomics from a Bayesian MCMC Perspective”. Global Dialogues on Emerging Science and Technology, 2006 Petrópolis, Brasil.

## **ORGANIZER OF COURSES AND MEETINGS**

- « Introducción a la Genómica Médica », Organizer Hugo Naya. Montevideo, March 5-9, 2018.
- « Human Genome Tour 2016. From NGS technologies to Evolutionary and Medical Genomics », Organizer Hugo Naya. Montevideo, March 14-April 1st, 2016.
- « Analysis & Prediction of Complex Traits Using Whole-Genome Regression Methods », organizers : Hugo Naya, María Inés Fariello, Daniel Gianola. Teachers : Daniel Gianola & María Inés Fariello. Montevideo, 20-24 April 2015.
- « Hands on course on High Through-put Technologies on Sequencing data », organizers : Hugo Naya and Magnus Fontes. Montevideo 1-14 December 2014.
- Member of the Steering Committee, ISCB-LA 2012, Santiago de Chile, Chile.
- Member of the Steering Committee, ISCB-LA 2010, Montevideo, Uruguay.
- « Advanced Course on Bioinformatics and Comparative Genome Analysis », organizers: Fredj Tekaia, Edmundo Grisard, Alberto Davila, Hugo Naya. Universidade Federal de Santa Catarina, Florianópolis, Brazil. June 30 - July 12, 2008
- “Third Meeting STIC-AMSUD”, Taller de Bioinformática y Sistemas de Información Biológica”, organizers: Fernando Álvarez-Valin y Hugo Naya. Montevideo 21-23 November 2007.

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- “The First Joint Pasteur Institute/Wellcome Trust Course on Genomics in South America”. Montevideo 5-15 June, 2006. Institut Pasteur de Montevideo and Instituto de Higiene.

## **COURSES TAUGHT IN OTHER COUNTRIES**

- “First Tripartite Course in Bioinformatics”. Ribeirão Preto Medical School (FMRP/USP), 19-30th October 2015, Ribeirão Preto, Brazil. **Naya H**, Fontes M, Araújo da Silva W.

- “INDA Hands-on NGS-GWS course”. 10-19th September 2015, Saint-Louis, Senegal. **Naya H**, Fontes M, Loucoubar C.

- “Genômica de procariotos”. Pós-graduação em Genética, UFBA, Salvador, 1-27 November, 2013. **Naya H**, Spangenberg L.

- “Análise de dados de NGS e suas aplicações em vírus e procariotes”. Pós-graduação em Biologia Computacional, Instituto Oswaldo Cruz, Rio de Janeiro, 7-18 October, 2013. **Naya H**, Romero J.

- “Introdução à bioinformática para análise de genomas procariotos”. UFBA, Salvador, 3-7 junho, 2013. **Naya H**, Spangenberg L.

- “Ferramentas bioinformáticas para análises de expressão gênica”. Pós-graduação em Genética, UFBA, Salvador, 19-23 November, 2012. **Naya H**, Spangenberg L.

- “Bioinformatics Tools for new High Throughput Technologies – Short Course”. ELAG2011, Caxias do Sul, 14 April, 2011. **Naya H**.

- “Alineamiento de secuencias”. INTA-Castelar, Buenos Aires 12-17 May, 2008. **Naya H**, Romero H, Graña M.

- “Herramientas bioinformáticas para genómica comparativa de procariotas”. INTA-Castelar, Buenos Aires 23-28 April, 2007. **Naya H**, Romero H.

## **DEVELOPMENT OF SCIENTIFIC SOFTWARE**

- “OS, software para el estudio de Objetivos de Selección en ganado de carne”. (2015) Jorge I. Urioste, María Isabel Pravia, Gustavo Alvez, **Hugo Naya**, Lucía Spangenberg, Olga Ravagnolo, Juan Manuel Soares de Lima, Mario Lema.

- “BacFier” classification of bacterial pathogenesis from genomic composition. (2012) Lucía Spangenberg & **Hugo Naya**. Java software available at [googlecode](http://bacfier.googlecode.com) (<http://bacfier.googlecode.com>).

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- “bcool: Bringing to light significant Columns correlated with Organism Labels”. (2011) **Hugo Naya & Lucía Spangenberg**. R package available at CRAN (<http://cran.r-project.org/web/packages/bcool/index.html>).

- “bmaMCMAnalysis: Bayesian Model Average for the Bayesian Phylogenetic Mixed Model”. (2011) **Hugo Naya & Lucía Spangenberg**. R package available upon request.

## **CONSULTANT/ADVISOR**

- OPP-INEFOP (ICT4V). Informatics in Uruguay 2050. Responsible of bioinformatics' vertical. 2018-2019.

- GenLives (medical genomics). Startup incubated at Bioespinn (Institut Pasteur Montevideo). 2015-.

- Oxygene (microbial, clinical and environmental genomics). Startup incubated at Bioespinn (Institut Pasteur Montevideo). 2015-.

- CeTAE (clinical oncology). Consultant in medical genomics and HL7/SNOMED. 2012-2013.

## **STUDENTS**

- 6 graduation projects in Biology/Biochemistry finalized
- 1 graduation projects in Biology/Biochemistry currently working
- 1 graduation project in bioinformatics finalized (2 students)
- 3 graduation projects in Informatics finalized (6 students)
- 1 graduation project in Statistics finalized (2 students)
- 1 M.Sc thesis finalized (Bioinformatics)
- 1 M.Sc co-tutored thesis finalized
- 3 M.Sc students currently doing thesis + 2 M.Sc student co-tutored
- 1 PhD student in Biology/Bioinformatics thesis tutored, finalized
- 1 PhD student in Biology/Bioinformatics thesis co-tutored, finalized
- 1 PhD student in Mathematics/Biology thesis co-tutored, finalized