



Computational Biology for Whole Metagenome Sequencing in Livestock

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Who Am I?

- Bachelor of Veterinary Science and Animal Husbandry
(Cuba; 2001-2006)



- MSc. Animal Breeding and Reproduction Biotechnology
at CIHEAM (Spain; 2007- 2009)



- PhD on Animal Genetics at Universitat Autònoma de
Barcelona (Spain; 2009 - 2013)



- **Mobility Project AgreeSkills (August 2013):**

“Computational Biology for Whole Metagenome Sequencing in Livestock”

Lab: INRA, UMR GABI; **Mentor:** Dr. Jordi Estellé; **Project:** METALIT (INRA-MEM)

- Microbes residing in the gut have a profound influence on host physiology and homeostasis (= **HEALTH**)

- **Challenge** = How to study microbiota if the great majority of gut bacteria are not cultivable?

Metagenomics is based on the NGS analysis of microbial DNA that is extracted directly from communities in environmental samples.



NGS = Big Data

Computational
biology tools

OBJETIVE: To implement tools and data analysis pipelines and to use them in the generation of metagenome catalogues for livestock species (e.g. pig).

Biological questions related to the gut microbiome

- Who is living there?
- What are they doing?
- How is the host interacting with “them”?
- Impact on animal health and production yield?

