A perspective on systems biology applications in livestock species

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- o The human genome sequence project over 20 years ago signified a massive boost to other species-specific biotechnology studies, including non-model organisms such as livestock.
- o Since then, high-throughput gene expression technologies have been a popular choice. They evolved from microarray assays in the 2000's to next-generation sequencies in the 2010's.
- However, soon we realized that isolated lists of differentially expressed (DE) genes which, by simply comparing genes to themselves, have the pitfall of taking molecular information out of context.
- The need for systems-level explanations of biological phenomena prompted us to adopt gene network approaches and to analyse rigorously the connectivity patterns within the network.
- We present algorithms developed by our group to reverse-engineer and analyse gene networks including: PCIT (partial correlation and information theory), RIF (regulatory impact factors) and AWM (association weight matrix) and provide examples within the realms of growth, reproduction, and disease resistance in livestock studies.



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Bioinformatics, Volume 24, Issue 21, 1 November 2008, Pages 2491–2497,



Normalization Statistical Significance Microarray $f(y; \Phi_k) = \sum_{i=1}^{k} \pi_i \phi(y; \mu_i, V_i)$ FDR < 1% DE Genes Transcription Factors Vaquerizas *et al.* (2009) Differentially PIF Genes Regulators Targets Co-Expression RIF1 Regulators consistently differentially wired with abundant DE genes Regulatory Impact Cond. B: r < 0 Cond. A: r > 0Factors RIF2 Regulators with altered ability to predict the abundance of DE genes Samples Samples

Progesterone signalling in broiler skeletal muscle is associated with divergent feed efficiency

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Bottje et al. BMC Systems Biology (2017) 11:29 DOI 10.1186/s12918-017-0396**BMC Systems Biology**



PNAS $\bigcirc \bigcirc$





PLoS One. 2009 Oct 1;4(10):e7249.

Inferring the transcriptional landscape of bovine skeletal muscle by integrating co-expression networks.

Hudson NJ, Reverter A, Wang Y, Greenwood PL, Dalrymple BP.



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