Using "raw" online data derived from global gene expression experiments for postgraduate teaching activities

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Understanding published data and fine tuning thoughts and ideas pertaining to a scientific subject to perform a leap forward leading to original knowledge is a central task in scientific life. This is a key step for a PhD student in order to develop hypothesis for future work. Genomics has open interesting possibilities regarding the process of the interpretation of data generated in labs all over the world. On one side, final figures presented in publications are usually interpreted intuitively from the non-trained eye perspective. On the other side, the "raw" data that originated the final figure is available to be re-analyzed in a scientific or in a teaching context. The gap between the two sides mentioned represents a fertile ground to teaching activities. Reproducing the analysis pipeline usually enhances not only the interpretation of genomics results but the so much needed intuitive driving force of generating ideas when confronted with experimental results. This in turn will strengthen the student's expertise in relating and understanding the actual data generated and the interpretation of results through a chain of informatics processes applied to it. In addition, re-analysis, may lead into the exploration of perspectives the original authors left behind in their publication and also to deeper critique on the criteria used to process and select data to show to support the main conclusions obtained. The presentation will summarize four years of implementing postgraduate activities in genomics trying to show that the large sets of data available can be used to teach complex data analysis pipelines and stimulate intuitive and fact driven thinking in our postgraduate students.