

4th International Conference on

Plant Genomics

July 14-15, 2016 Brisbane, Australia

C2Pe: A new open source qPCR algorithm and web interface for raw data analysis

Juan Pablo Matte¹, J Padarian², R Siqueira³, N Wilson² and B Jones²¹Pontificia Universidad Catolica de Chile, Chile²The University of Sydney, Australia³University of Lausanne, Switzerland

The determination of transcript levels via quantitative polymerase chain reaction (qPCR) is now widespread and instrumental in research, medicine and a broad range of other areas. The standard method of analysis is delta Ct, that is simple to use, but has a high probability of deviating from the true value. Several alternative approaches that give more consistent results have been presented but they are all complex to use. The C2Pe method we have developed can improve on the delta Ct method by 51%, using the PCR curve to estimate the efficiency of each reaction. The main innovations are that the embedded equations use the second phase of the curve to add a quality value to the data to correct the information given by the exponential phase. We have also incorporated revised statistics to improve the robustness of the analysis and constructed a web-based interface to give a straightforward, streamlined qPCR experience.

Biography

Juan Pablo Matte has studied both, Forestry Engineering and Biological Science degree in the Pontificia Universidad Catolica de Chile. He has completed his PhD in 2013 and Postdoctoral studies in 2015 from The University of Sydney, Australia. Currently he is an Associate Researcher at the Pontificia Universidad Catolica de Chile, under the PAI project number 82140040 from CONICYT.

jpmatte@uc.cl**Notes:**