
Feasibility of particle genetics in humans

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Résumé

Our ability to predict the phenotype from the genotype is limited; even clonal cells grown in the same environment display cell to cell variability in their expression patterns. Clonal populations allow to identify and study the genetic determinant of stochastic variation after having eliminated environment and genetic interactions as confounding factors. We are exploring how the statistical properties of gene expression (distribution of single cell expression levels) are affected by the genotype using cell lines from different individuals. Using a dedicated R pipeline of single cell data analysis, we observed inter-cell line differences in CV (Coefficient of Variation) values suggesting intra variability within population. This approach provides a basis for the identification of genetic loci that influence the statistical distribution of protein expression levels.

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