SOFTWARE

WHY I BELIEVE IN TWIN STUDIES

4.04.2014

These are some pictures that I took roughly two years ago on twin meeting in Austria. Twin studies give us some unique opportunities like in this recent paper

> We performed a genome-wide study to investigate differences in (i) DNA methylation (using a custom tiled four-plex array containing tiled 50-mers 19,084 randomly chosen methylation sites), (ii) copy number variation (CNV) (with a chip including markers derived from the 1000 Genomes Project, all three HapMap phases, and recently published studies), and/or (iii) gene expression (by whole-genome expression arrays). Based on the results obtained from these three approaches we utilized quantitative PCR to compare the expression of candidate genes. Importantly, our data support consistent differences in discordant twins and siblings for the (i) methylation profiles of 60 gene regions, (ii) CNV of 10 genes, and (iii) the expression of 2 interferon-dependent genes.