PHILOSOPHY

FAIL BETTER

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I truly liked the recent Sjoblom study while a new Science letter now raises heavy criticism:

… put into stark reality the challenges facing the Human Cancer Genome Project (HCGP). One wonders about the merits of such high-cost, low-efficiency, and ultimately descriptive-type “brute force” studies. Although previously unknown mutated genes were unearthed, the functional consequences of most of these and their actual role in tumorigenesis are unknown, and even with that knowledge we are a long way from identifying new therapeutic targets.

This seems to be the open wound of modern biology: all these high throughput driven genotyping / expression profiling / metabolome scanning approaches are mainly money & impact & activity driven – parameter or hypothesis-free has become a fashionable buzz phrase while only a few years ago it would have been an affront to every serious research-er.

Funny to see also the new Nature initiative opentextmining.org as nobody wants to read the results of these studies. So at least computers should be able to do that. Fail better…

Addendum

Similar criticism of the Neanderthal studies but a different argument

However, although such comparisons are of interest, it is not the static genome but rather the dynamic proteome that determines the phenotype of an organism. Salient examples include the caterpillar and the tadpole, which share
genomes with the butterfly and frog, respectively, but which have very different proteomes making them into very different organisms.
Thus, rather than performing untargeted comparisons of sizable genomes, we suggest that it might be more useful to address this question using a standard hypothesis-driven approach.