URL for web:
Database of Genomic Variants
http://projects.tcag.ca/variation

WEB WATCH

Uniting human variation

- http://projects.tcag.ca/variation

It's becoming increasingly clear that polymorphism in the human genome goes way beyond SNPs. More and more studies are now identifying large-scale genomic variants — which include inversions, deletions and copy-number variants — as important components of normal human genetic variation. The Database of Genomic Variants aims to put all the information from these studies in one place.

The database is continually updated with information from both experimental data produced in-house by the research groups that curate it and from published studies. Just pick a chromosome and you are presented with a list of known variants, organized by location. Alternatively, you can enter the name of your favourite gene or region of the genome and the database will tell you if any identified variants are associated with it.

Useful graphical representations allow you to visualize where each variant lies in relation to cytological bands, coding regions and segmental duplications. The database also tells you the frequency of each variant, the method that was used to identify it and the ethnic backgrounds of the individuals in whom it was located. Links to gene databases and original papers make further investigations straightforward.

Once you've identified a variant of interest, the database also allows you to access a genome browser that provides more information about the surrounding genomic region. Here you can look for a range of features, including CpG islands, gene deserts, SNPs and segmental duplications.

As it expands, the database should help to piece together the contribution of large-scale polymorphisms to the genetic individualities that make each of us different.

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