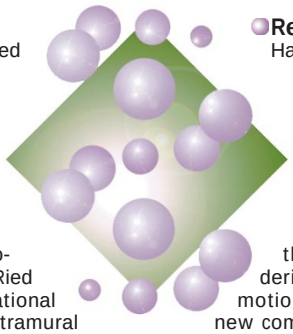
TOUCHING**base**

Filling in the C-CAPS



Identifying the precise breakpoints of translocated chromosomes is often a long and arduous task. The inception and development of fluorescence *in situ* hybridization (FISH) and spectral karyotyping (SKY) have helped, but at the end of the day, a workman is only as good as his tools, and genomic tools—as far as the deoxyribonucleic kind are concerned—can be difficult to obtain. To counter this obstacle, the National Cancer Institute (NCI) has launched the Cancer Chromosome Aberration Project (C-CAP), by Thomas Ried and Ilan Kirsch (of the intramural division of the National Institutes of Health (NIH)) and Grace Shen (of the extramural division). Its primary aim is to stock and maintain a clone repository of large-insert, ordered DNA clones that are mapped and suitable for FISH analysis. A pilot project is underway to test the current approach. Its aim is to generate FISH-mapped clones that mark 2-Mb intervals on chromosome 7—with over 30 STS-linked BAC clones, provided by Eric Green (NIH), mapped onto 7p in just over three months, it seems likely that the goal of 75 clones that span the entire chromosome will be reached by the end of September. Through collaboration with the Sanger Centre, chromosomes 1, 6, 20, 22 and X are next in line. The repository will also be useful for array applications: an array containing the BACs known to span an entire chromosome will help to localize regions of genomic amplification and deletion, as revealed by comparative genomic hybridization. The results of such independent investigations can be incorporated into the C-CAP database, which will be developed by the National Center for Biotechnology Information (NCBI) and will attempt to interrelate related BAC-based maps. The database (and the translocation archive published by Felix Mitelman in these pages early last year) will be hosted by C-GAP and should be ready for preview by the end of the year (http://www.ncbi.nlm.nih.gov/ncicgap/)—a resource to be reckoned with.

The Maine thing

For nearly 40 years—39 to be precise—The Jackson Laboratory has been running an annual summer course on mammalian genetics (known to many as the "Short Course"). Scientists, students, clinicians *et al.* descend on Bar Harbor, Maine, during the last weeks of July, to take in what is probably the most comprehensive course on mammalian genetics available in the United States. With the exception of the annual meeting of the American Society of Human Genetics, which is a different species of animal altogether, it is hard to imagine a convention which covers such a wide spectrum of genetic topics and—by virtue of its sterling speakers, all of whom are experts within their fields—covers them so well. In addition to supplying a solid introduction to mammalian genetics (and many of the mouse mutants that live at the Jackson Laboratory), the course was also notable for its communal lunches; a new feature this year, and one that promises to become a tradition. Formal seminars have their place; chinwagging in the sun while sharing a meal do too, and foster a different kind of discussion. The organizers of the course, Patsy Nishina, Jürgen Naggert, David Valle and Victor McKusick (the latter two from Johns Hopkins University), are to be congratulated, not only for putting the course together, but for their efforts to ensure that attendants get the most out of the course.The fortieth anniversary meeting promises additional food for thought; plans are afoot to invite six speakers to consider the current state of genetics and speculate about the future.

Victor McKusick terminates tea-time

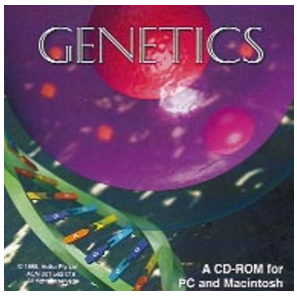
Ready to acCELERAte

Having recovered from the initial shock over the Venter/Perkin Elmer announcement in May to complete the sequence of the human genome faster and cheaper than the publicly sponsored Human Genome Project, geneticists are waiting to see how reliably the new generation of capillary sequencers work and how easy the shotgun strategy can be applied to complex genomes. The optimism of the founders, who recently christened the new company 'Celera' is unbroken—'celera' derives from the word 'celerity' which means swiftness of motion and is meant to "mirror the speed with which the new company intends to provide pharmaceutical companies and researchers the information contained in the complete human genome". The researchers keenest to see the first sequences being assembled are those working on *Drosophila*, as Celera is to use the fruit fly genome as an 'appetizer' to demonstrate its capabilities. They estimate that the fruit fly's 1.4×10^8-bp genome will be completed within the first four months of Celera's operation—that is, by April 1999. Successful completion of the *Drosophila* sequence would give a big boost to fly research, but is unlikely to convince skeptics who surmise that the shotgun strategy will not work on human DNA with its much longer stretches of repetitive sequences.

"God gave me the stubbornness of a mule and a fairly keen scent."

—Albert Einstein

Absolute beginners



With genetic research advancing more rapidly than 'scientific literacy' (see last month's editorial), the video and CD-ROM package released by Animated Biomedical Productions (ABP), aimed at teaching the basics of genetics to the novice, is welcome. The 60-minute video, created by a team at Westmead Neurological Centre, Australia, is neatly divided into conceptual bite-size pieces. The viewer is introduced to the internal workings of a cell and the 'stars' of the show, DNA and protein, and then taken on a historical journey from the first realization of hereditary processes to the technical revolution that has led us to current genetic models. A picture says a thousand words (or textbook phrases, in this case) and sophisticated computer graphics give the viewer a quick appreciation of the contents of the geneticist's 'toolbox', including PCR, restriction enzymes and recombinant DNA techniques. A section is dedicated to the ethical and legal implications of genetic research. While broad in scope, it faces the problem of many educational aids—that is, how to portray the issues in an unbiased way. For example, the use of germline therapy is contemplated from a negative perspective without balance by presentation of alternative views. Nevertheless, the ABP package serves as a valuable tool which teachers, clinicians, genetic counsellors—even geneticists—can use to convey advances of genetic research and their implications. For more information, visit ABP's web site (http://www.magna.com.au/~helke/).

"Cloning hasn't worked yet, but I'll be the first. The first human Dolly will be me."

—Martha Stewart (doyenne of the domestic front)