Pipettes and CPUs

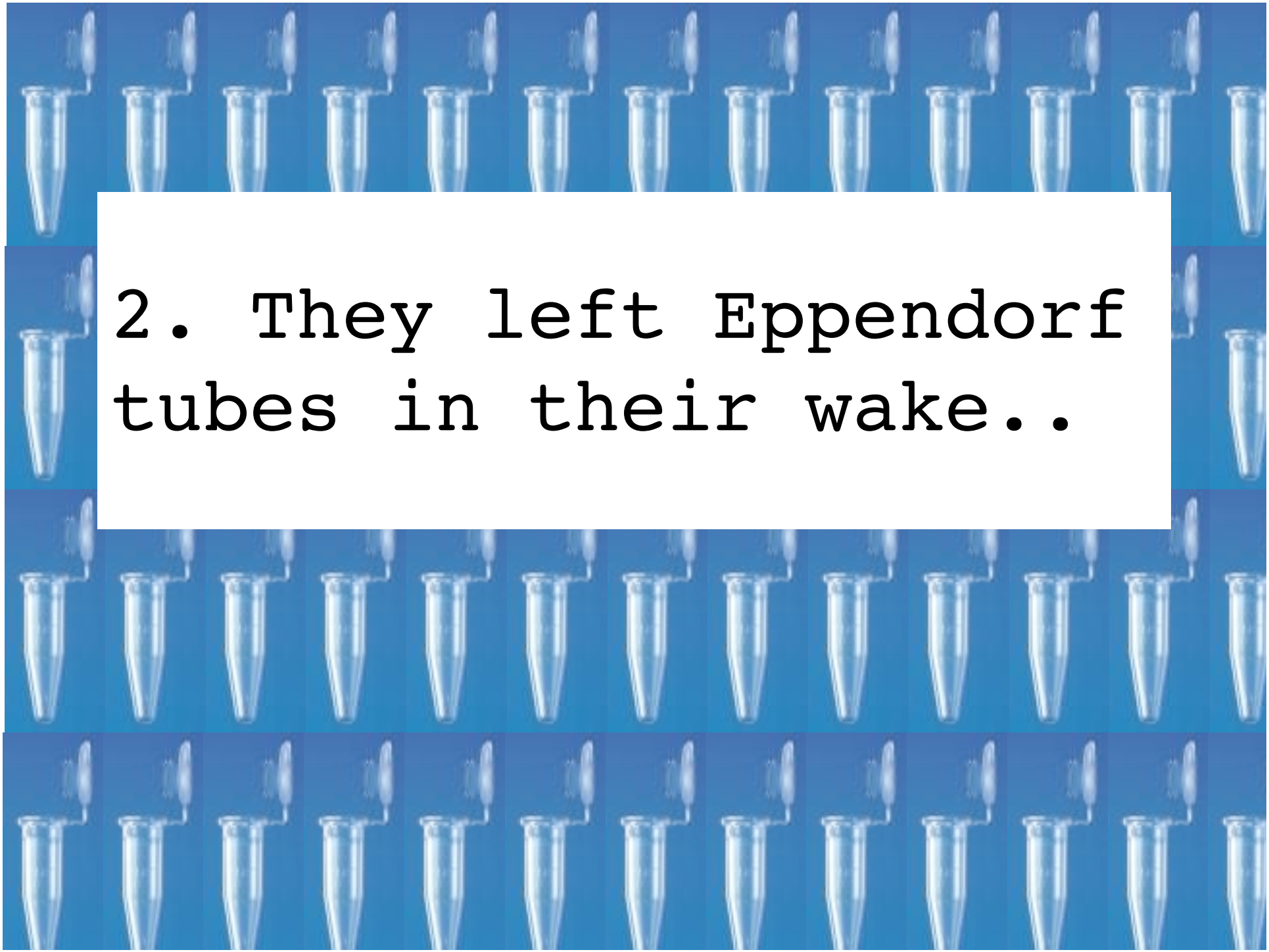
the Ying and Yang of modern biology

CSC

Once upon a time there was a new scientific discipline called molecular biology...

Molecular biologists could be identified by three criteria:

1. They carried pipettes..


2. They left Eppendorf tubes in their wake..

3. They dressed in jeans & tacky T-shirts.

In short, they were the coolest guys on the block.

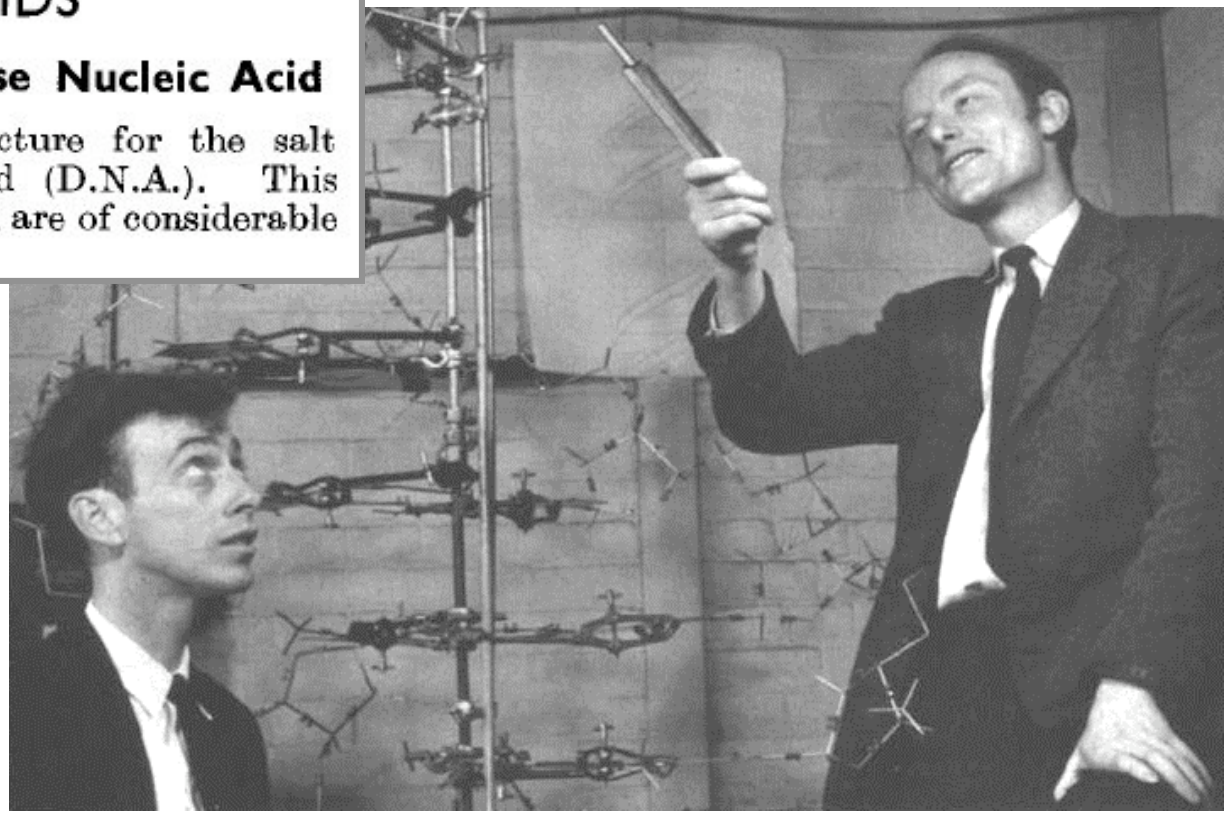
After a while,
molecular biologists
ruled the universe.
Or at least that's
what they thought.

They solved important problems..

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.



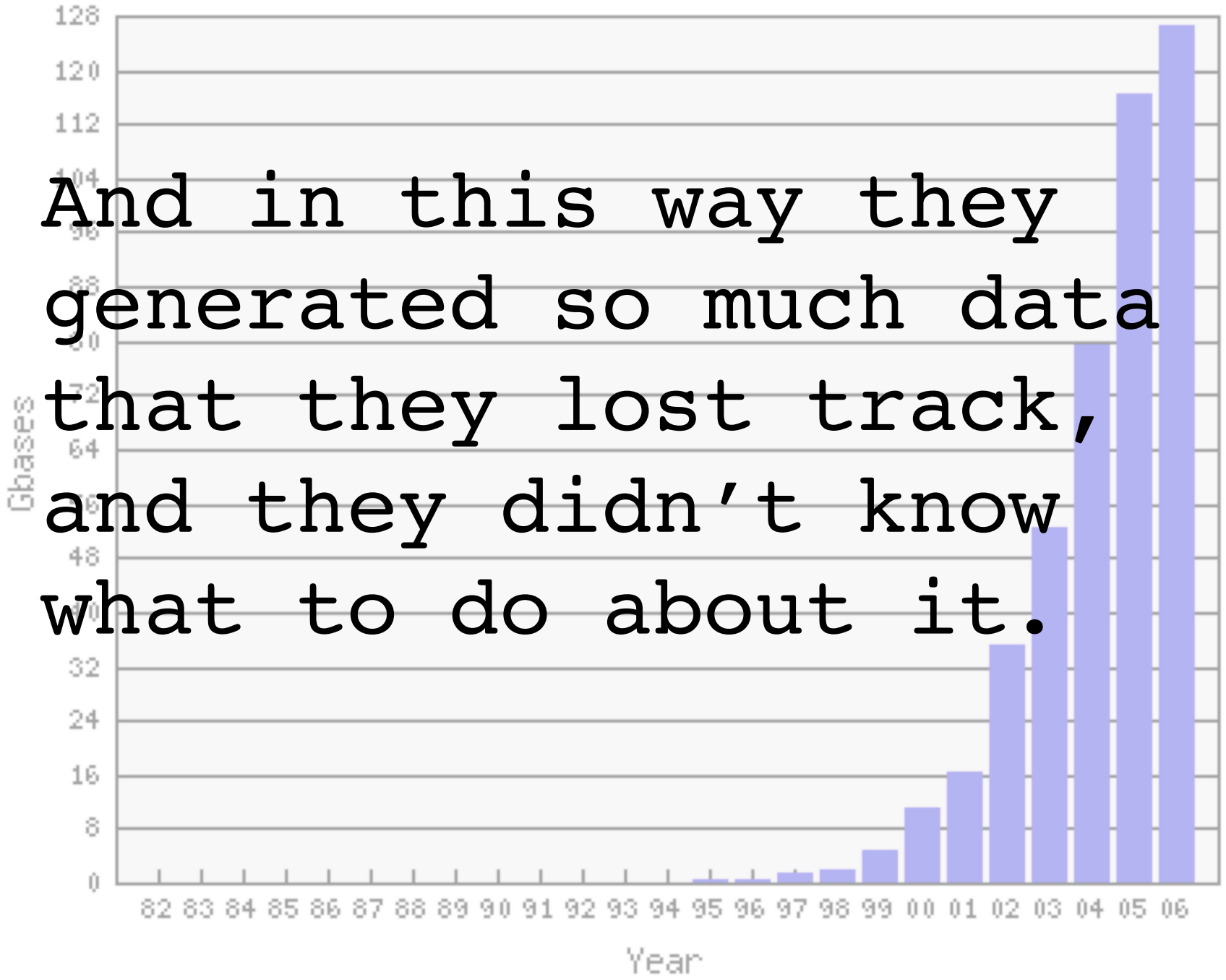
they started new companies..

and they got to meet
the King of Sweden.

But eventually they became the victims of their own success:

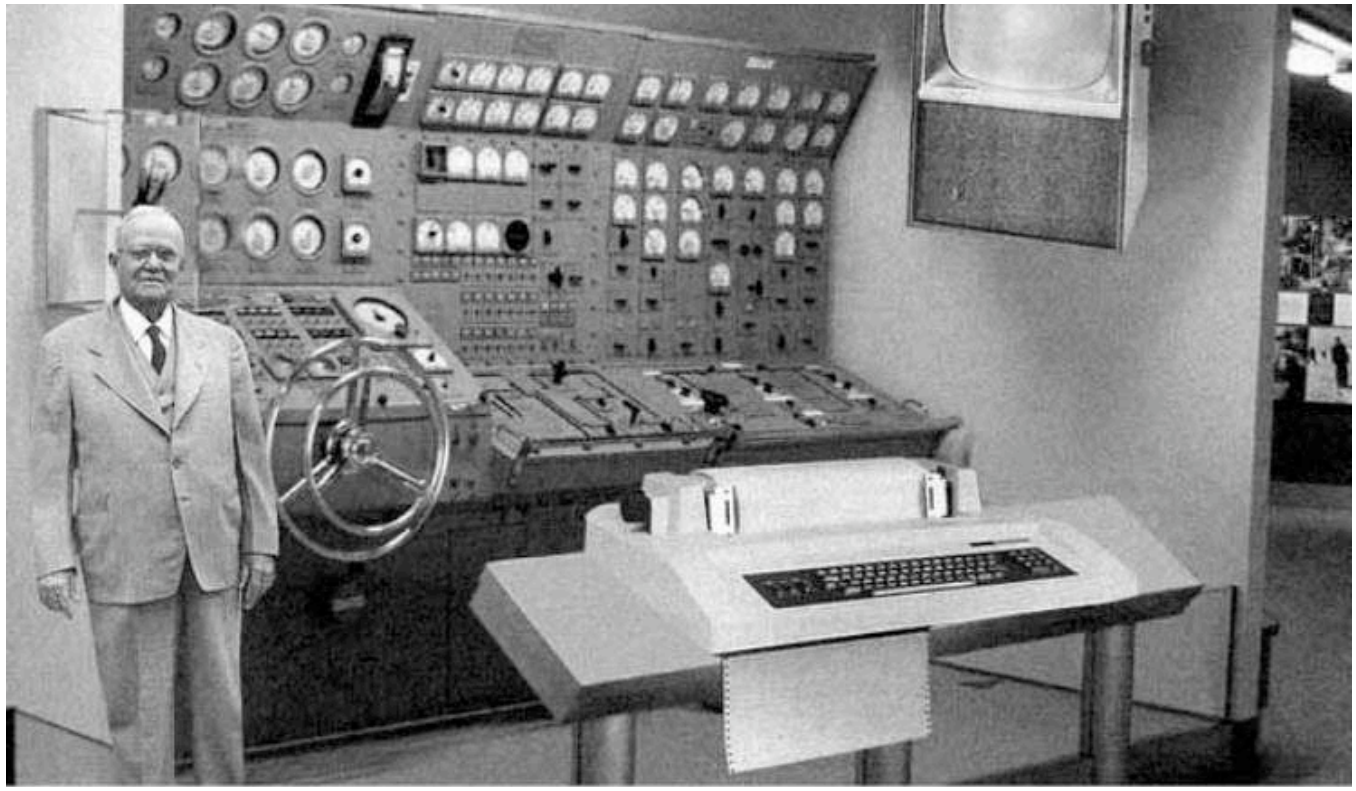
They became so good
with their pipettes
and Eppendorf tubes
that the only way they
could compete with
each other..

was to stay up all night and pipette with both hands and run hundreds of gels.



And in this way they generated so much data that they lost track, and they didn’t know what to do about it.

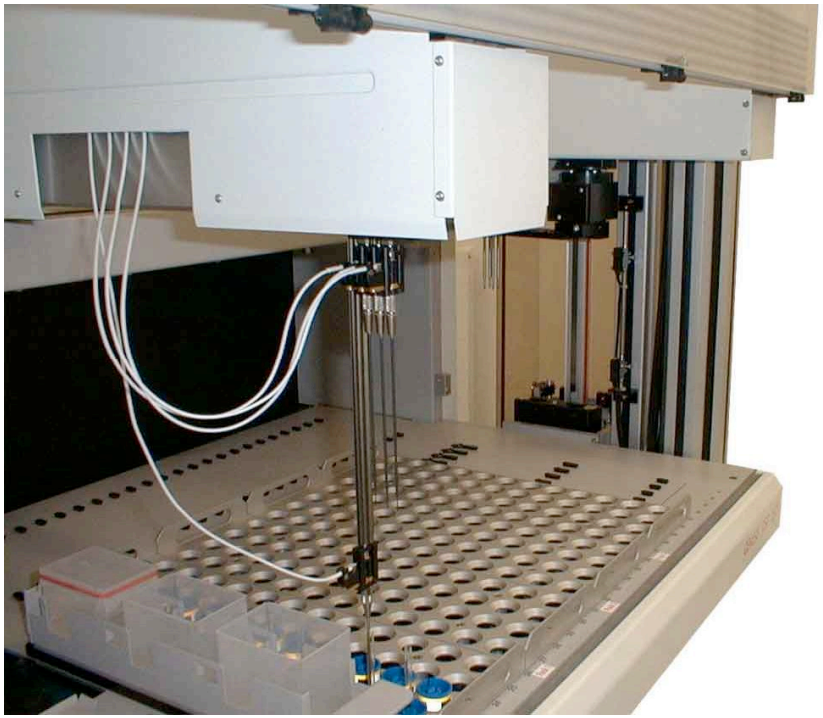
And when people don't know what to do about something, the time is ripe for the engineers!



So the engineers came into the labs..

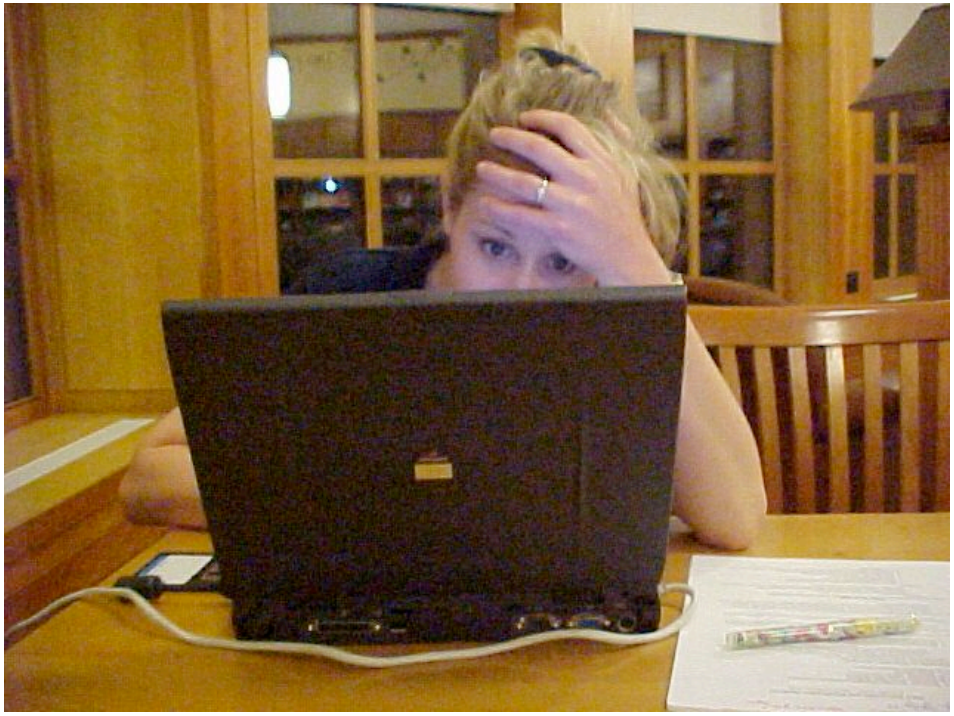
and they replaced the Eppendorf tubes with disposable multi-well plates..

and they built
machines that could
pipette and run gels..

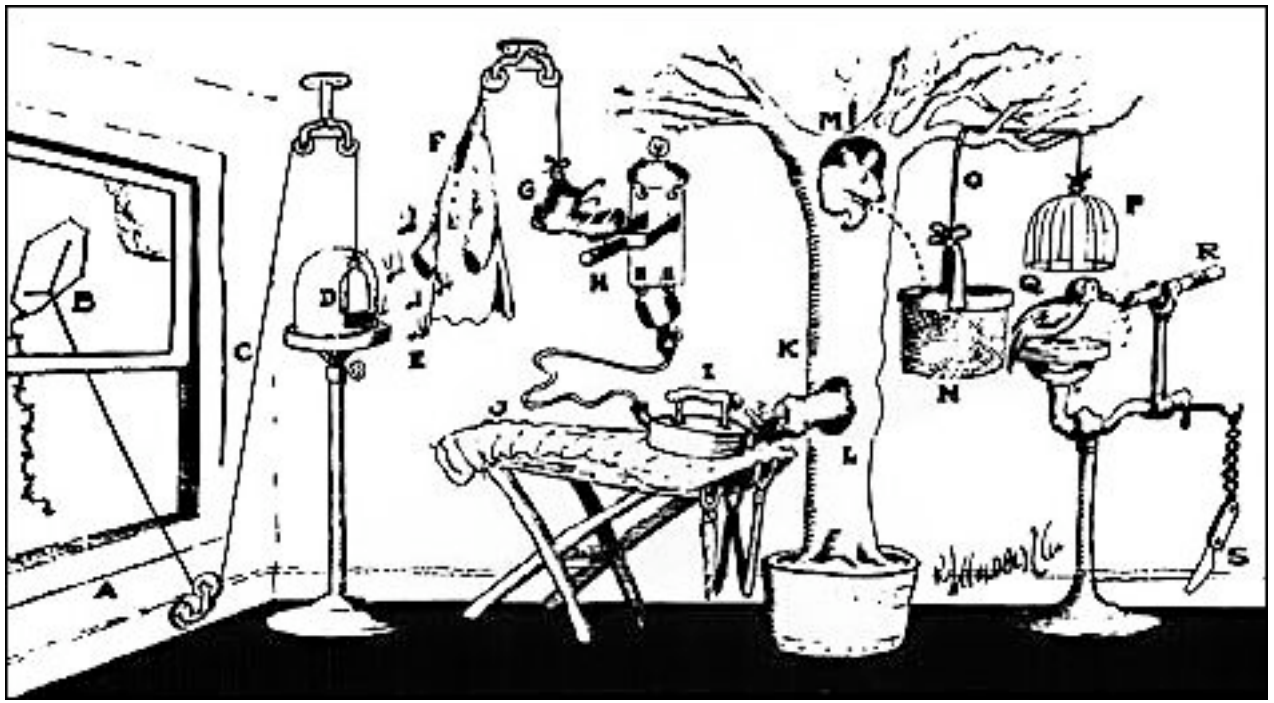


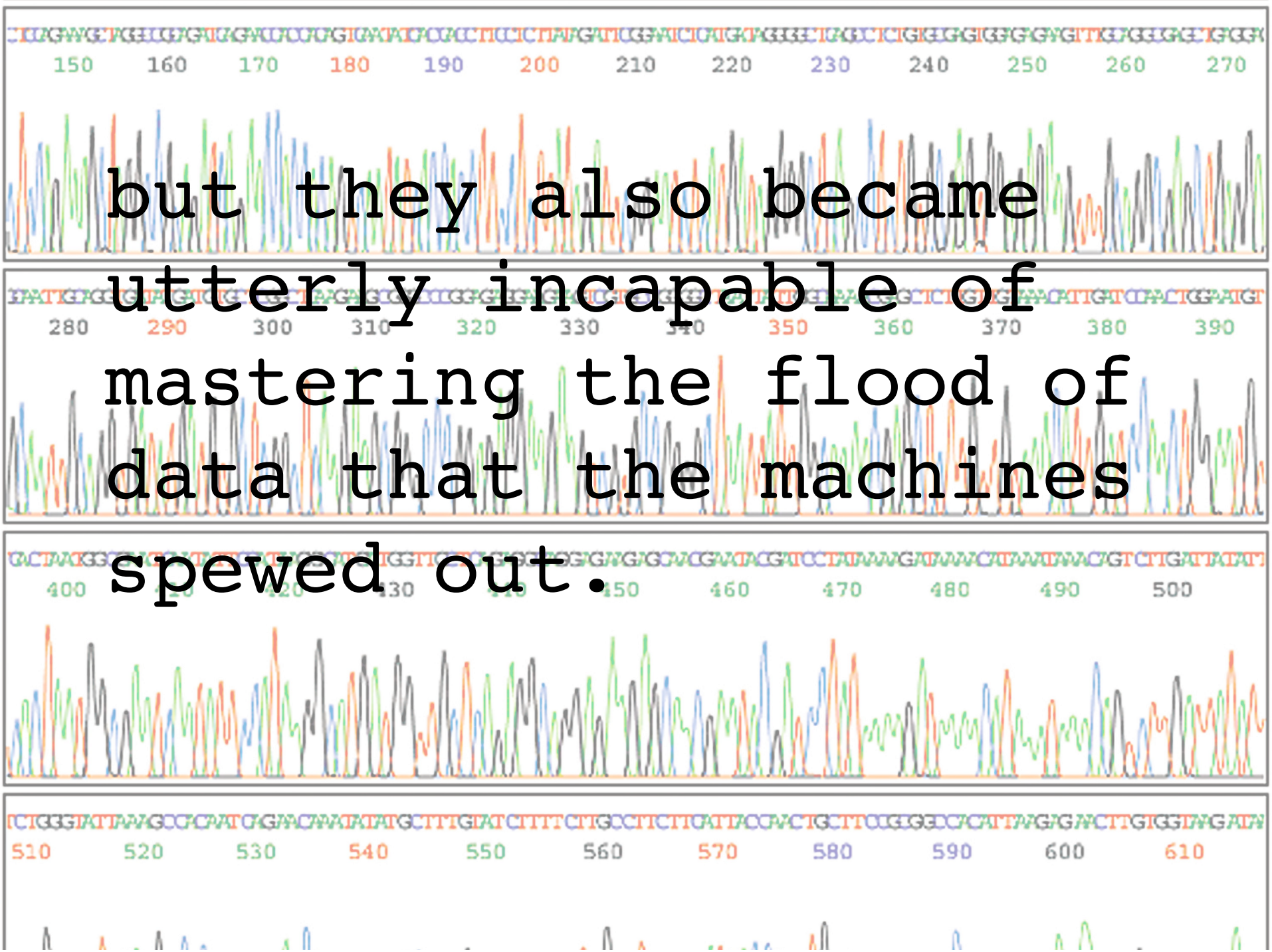
And they put computers and strange cabinets everywhere.

Of course, this only made matters worse for the molecular biologists..



because not only could they not run the fancy new machines..





but they also became utterly incapable of mastering the flood of data that the machines spewed out.

So they hired computer kids which, for some obscure reason, they called bioinformaticians,

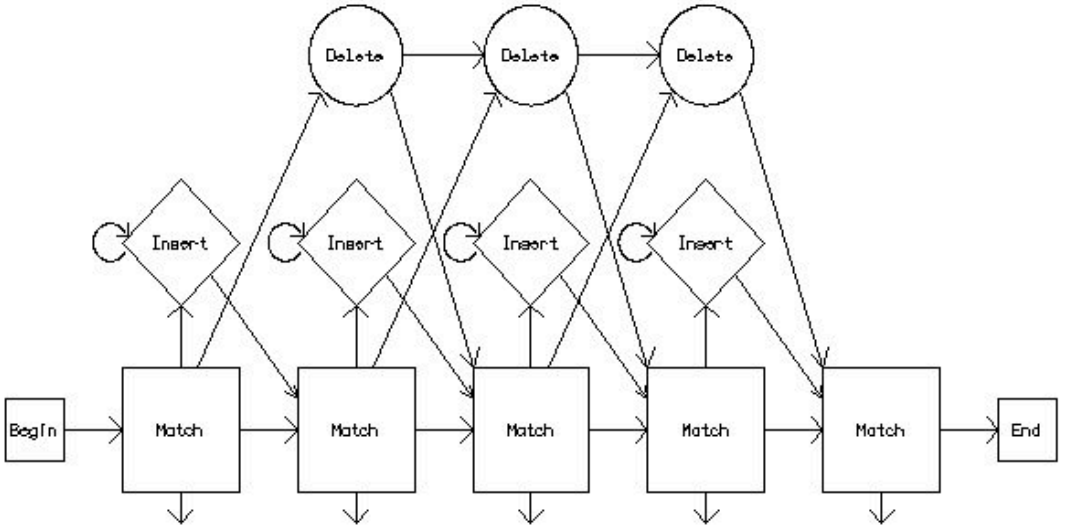
National Center for Biotechnology Information
National Library of Medicine National Institutes of Health

hoping that they would help them make sense out of all this data.

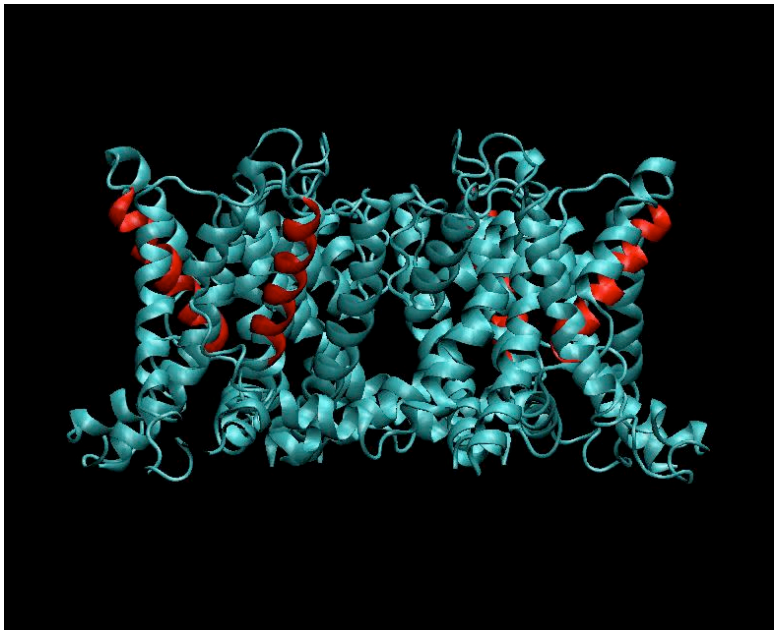
And the computer guys came in, and they were even cooler than the molecular biologists because..

not only did they dress like complete junkies, but they spent their days drinking Coke and playing rock music in their headphones.

And you know how it is with computer nerds: you give them a finger and they turn it into a hidden Markov model.



so they turned all the neat reaction schemes and beautiful protein structures produced by the molecular biologists..



into droves of computer code and Oracle tables..

```
//This method defines the ComplexMethod class
public class ComplexMethod extends MILOSObject {
        ListOfProcesses subprocesses=null;
    //defined static strings that represent different event listeners
    private static final String
            SUBPROCESSADDED="subprocessAddedEventListener";
    private static final String
            SUBPROCESSREMOVED="subprocessRemovedEventListener";
    private static final String
            MAPPINGADDED="mappingAddedEventListener";
    private static final String
            MAPPINGREMOVED="mappingRemovedEventListener";


                                    lefine subprocesses created by applying this ComplexMehtod.
                                    MILOSProcess

                                    ss(MILOS.ProcessModelMILOS.MILOSProcess aSubProcess)
                                    Exception,MethodInListException, IsSuperProcessException{
                                    rocess().isSuperProcess(aSubProcess)){
                                    ss as the subprocess of another process
                                    s.add(aSubProcess);

                                    ess.addParentMethod(this )
                                    Exception e){}
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                                    ddedEvent mEvent=new SubprocessAddedEvent(this);
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                                    UBPROCESSADDED,mEvent);
                                    IsSuperProcessException();
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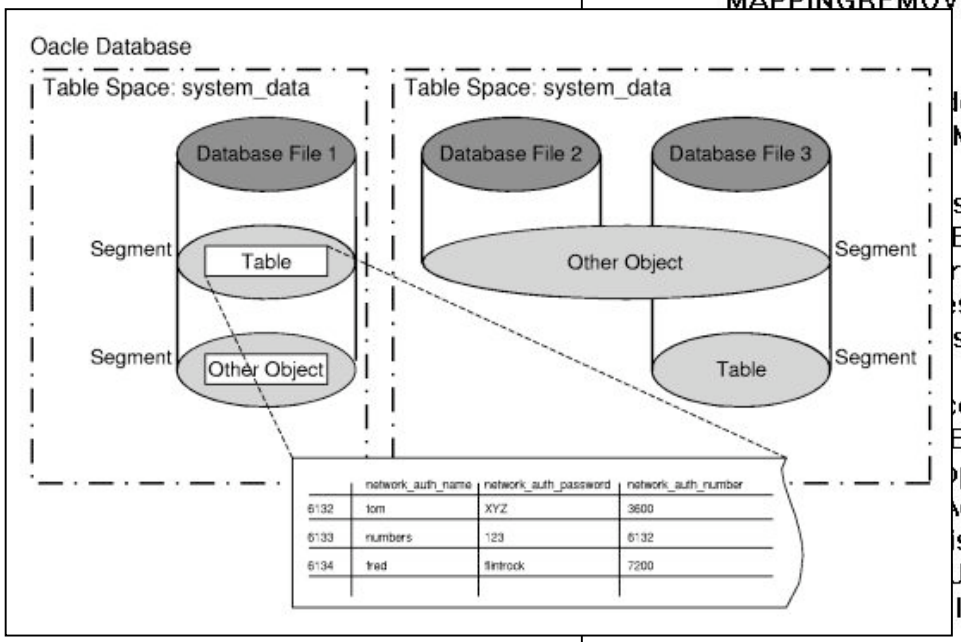
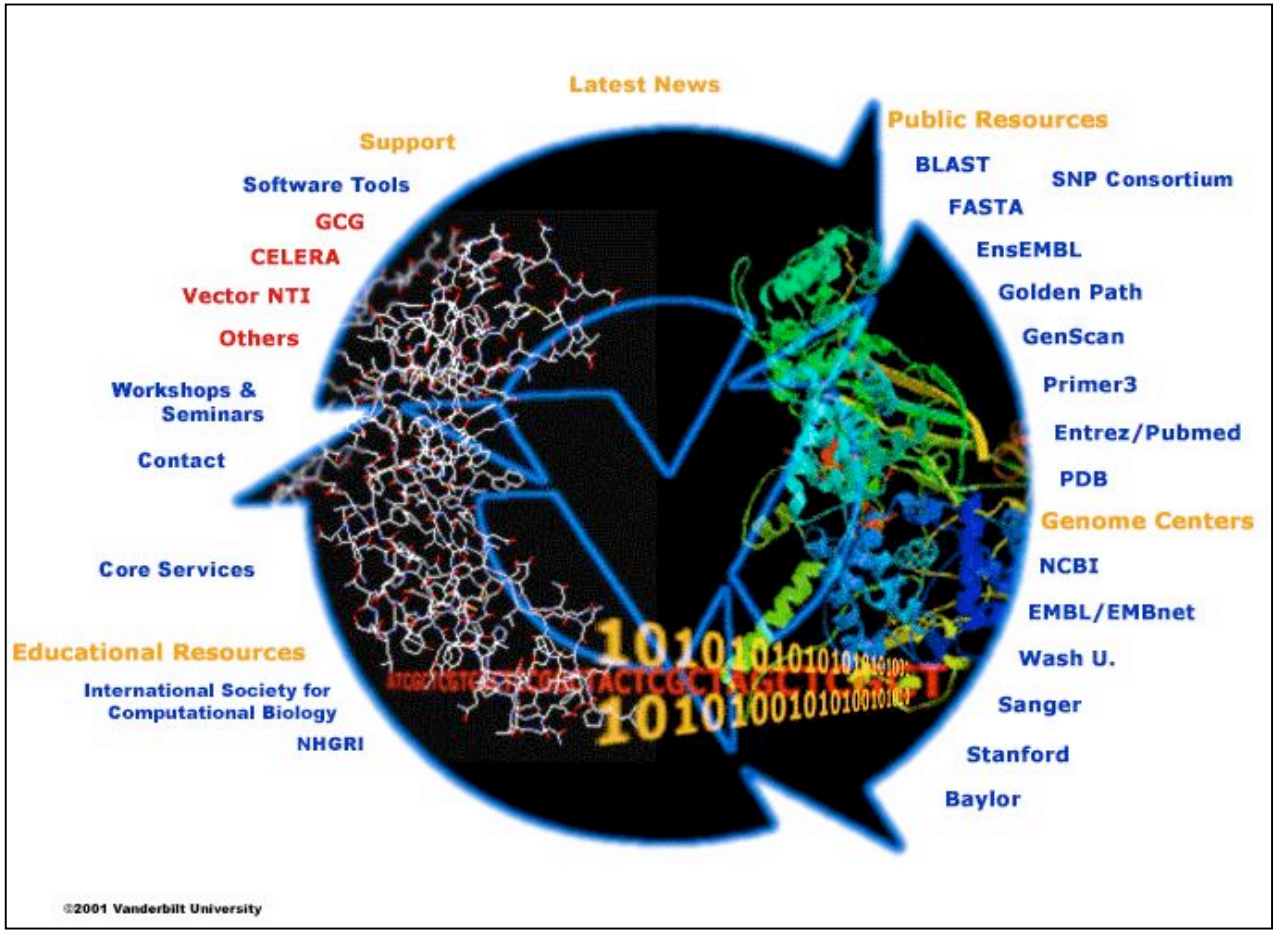
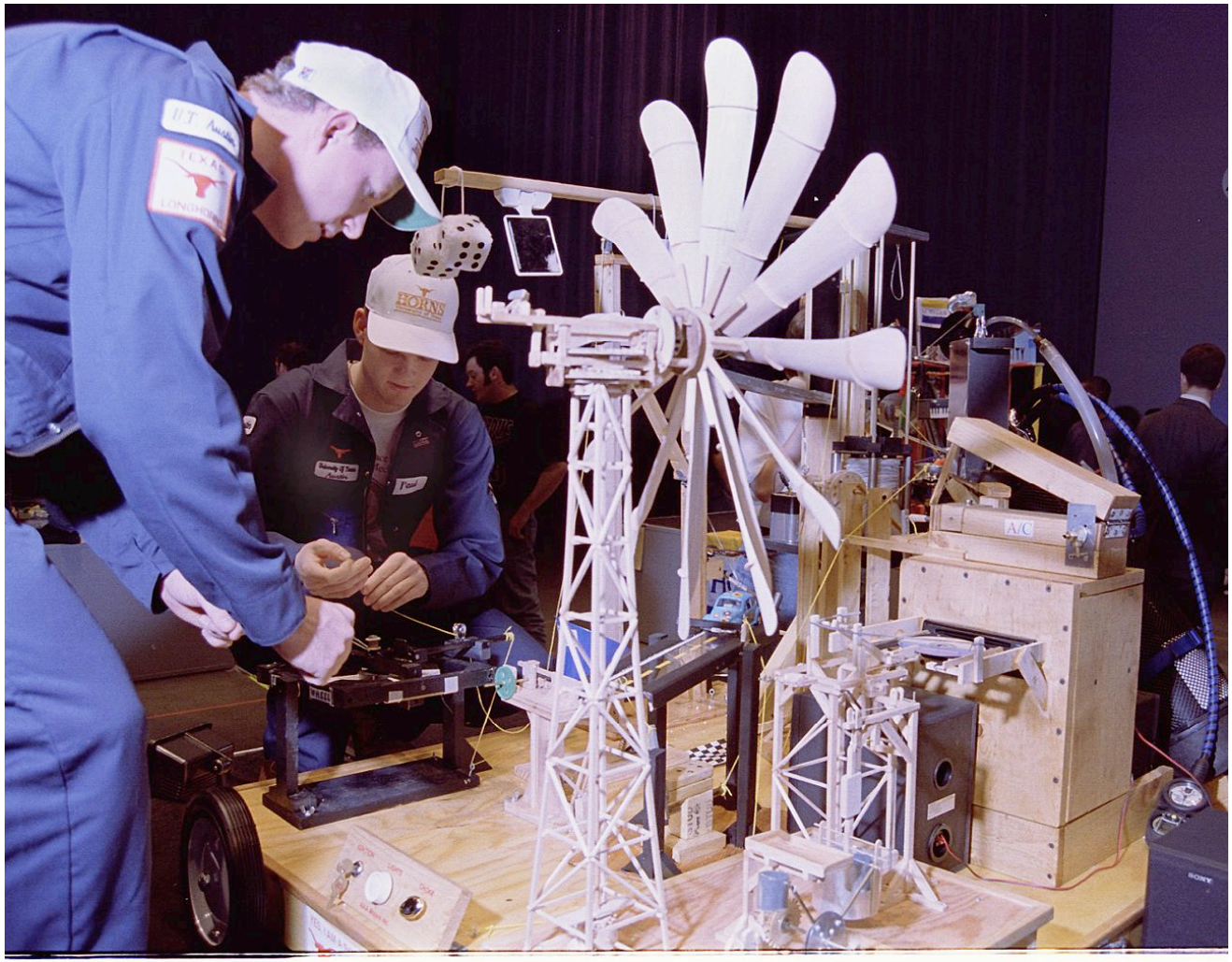


and dumped it all on the web.



So this is modern biology: the pipetters keep pipetting..

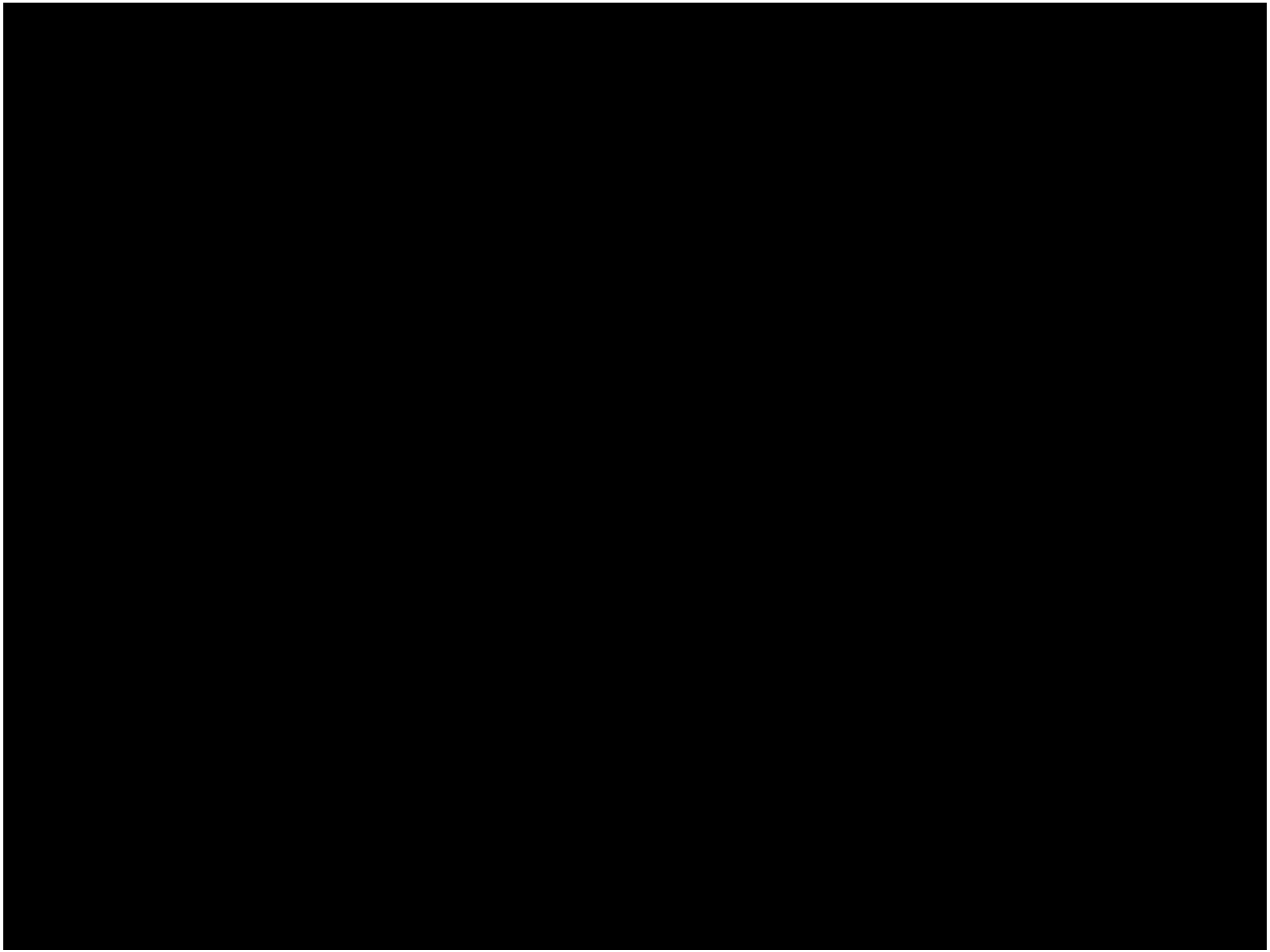
the engineers keep engineering..



and the bioinformatics people do the best they can to bring even the fastest supercomputer to its knees.

And, amazingly, great new science brews in this hotchpotch of lab rats, nerdy engineers, and computer geeks..

If only they can work together!




DNA (Friday)
PRINCETO

equipment, and to Dr. G. E. R. Deacon and the captain and officers of R.R.S. *Discovery II* for their part in making the observations.

[1] Young, F. B., Gerrard, E., and Jevons, W., *Phil. Mag.*, **40**, 149 (1920).
[2] Longuet-Higgins, M. S., *Mon. Not. Roy. Astro. Soc., Geophys. Supp.*, **5**, 285 (1949).
[3] Von Arx, W. S., Woods Hole Papers in Phys. Oceanog. Meteor., **11** (3) (1950).
[4] Ekman, V. W., *Arkiv. Mat. Astron. Fysik.* (Stockholm), **2** (11) (1906).

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A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biologseal interest.

A structure for nucleic acid has already been proposed by Pauling and Corey[1]. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.

This figure is purely diagrammatic. The two ribbons symbolize the two phosphate–sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate diester groups joining β-D-deoxyribofursanose residues with 3′,5′ linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's[2] model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being roughly perpendicular to the attached base. There is a residue o
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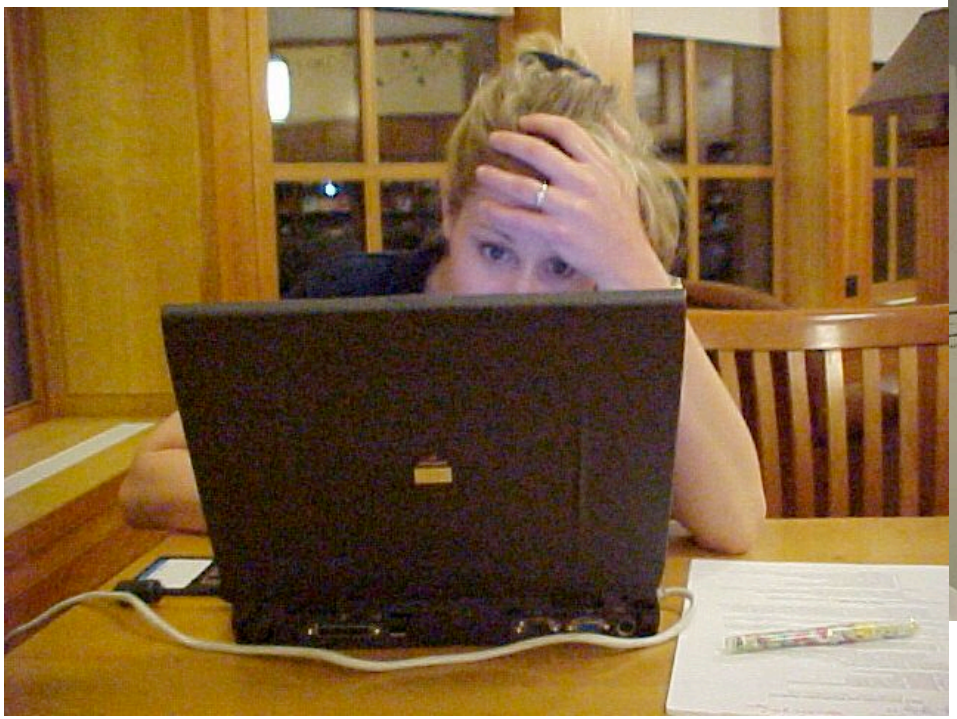
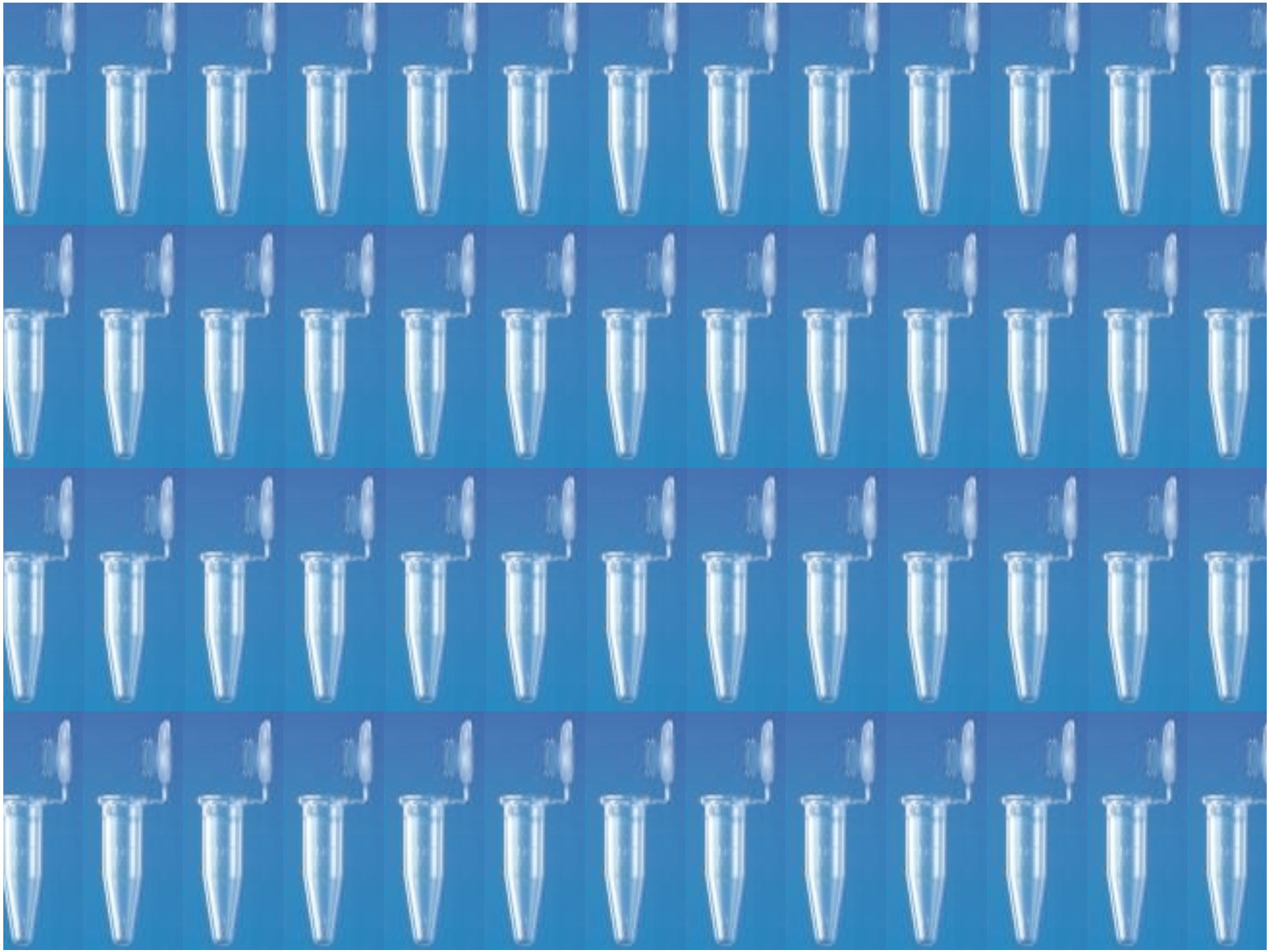
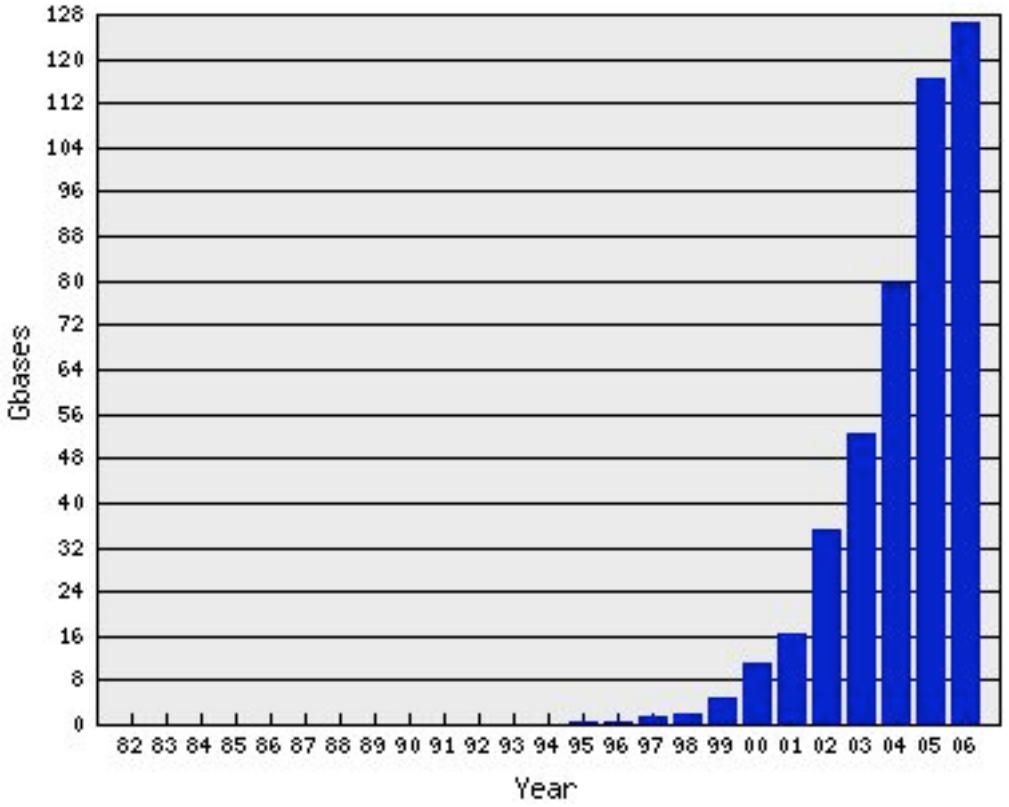





TIME
Shaping Life in the Lab
The Boom In Genetic Engineering
Genentech's Herbert Boyer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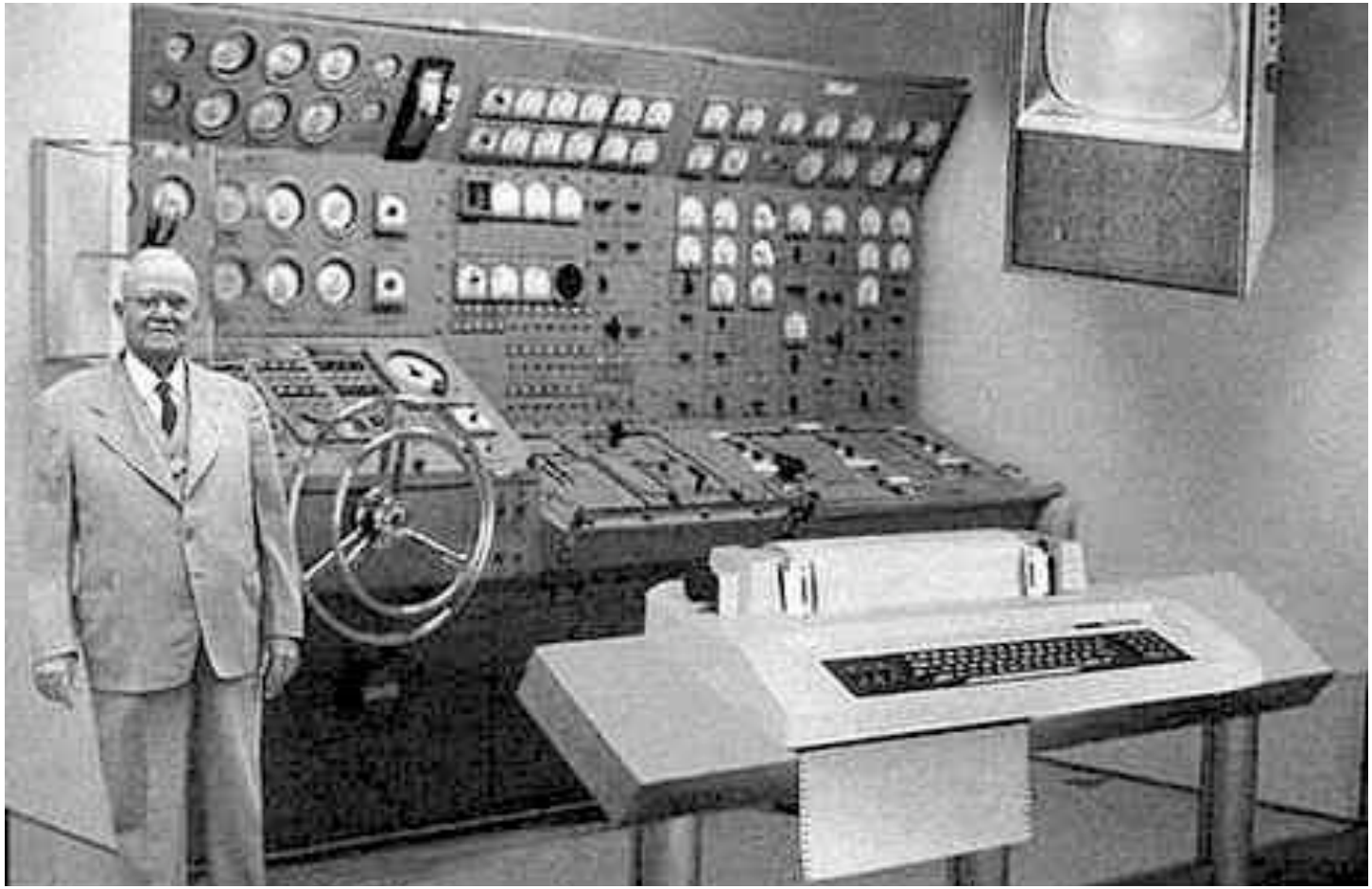

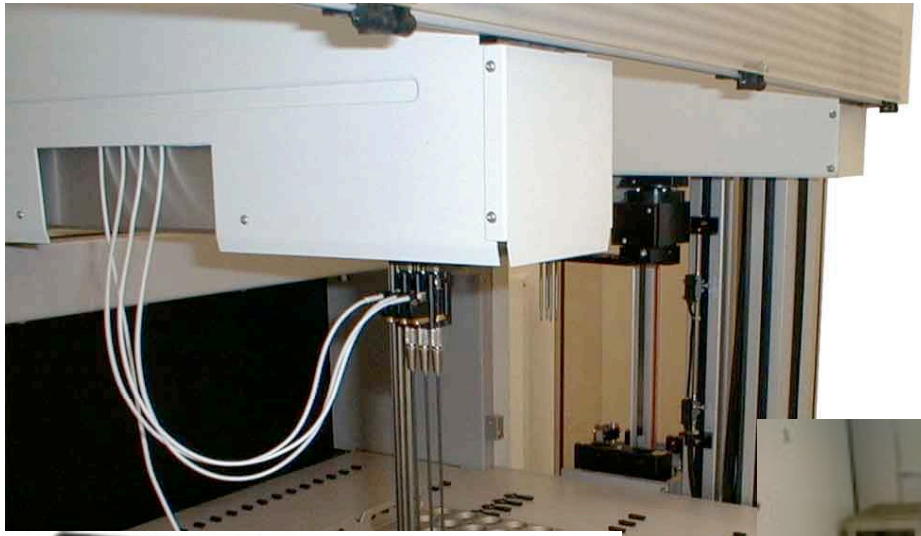


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