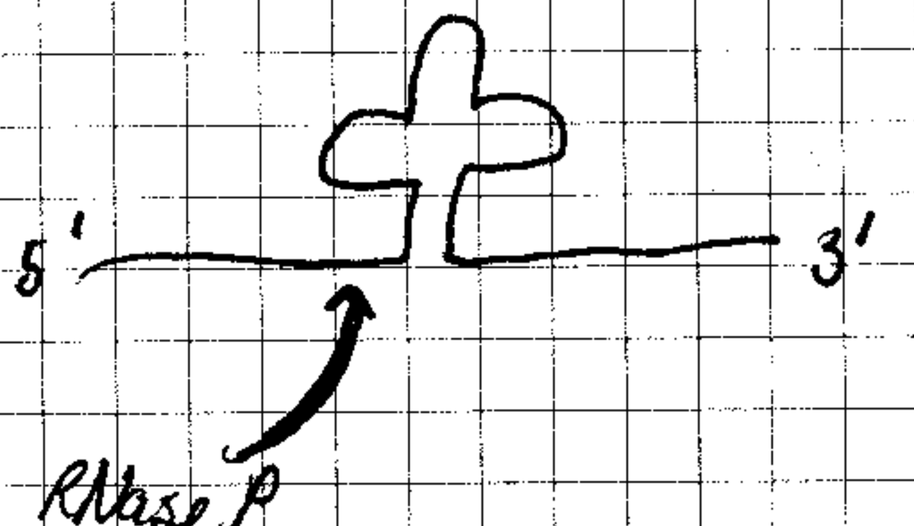
2/7/90

Norman Pace

Diversity can be invisible.

① align homologous sequences
② count differences in each pair of sequences
③ calculate the evolutionary distance between the sequences
④ define the tree that best fits ALL distances

Structural Analysis



- RNase P cuts 5' end of tRNA
  - v. similar in E. coli & B. subtilis
  - RNA and protein
    RNA is catalytic unit!!

- what is structure of RNA subunit of RNase P
  - 2°
  - 3°

- difficulties
  ① short binding regions (~5 BP) but only 4 diff. bases so very many poss. solutions
  ②

3 methods of working out 2° structure

①

② minimum energy

③ phylogeny

- compare E. coli & B. subtilis
since NOT v. similar can
pick a closer relative
(based on RNA phylogeny)

- see where similar complements
occur in closely related
organisms.

After get general 2° structure

④ deletion experiments

- moved "gaps" across molecule
and activity remained.

⑤ see what deletions
lead to damage

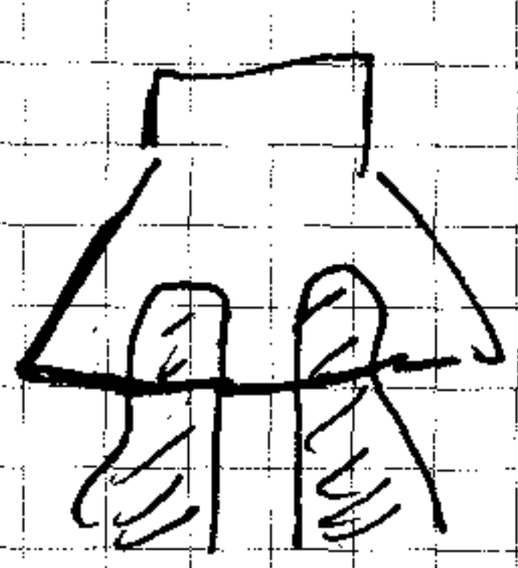
⑥ see what deletions
do nothing

w/ conserved structure that should be
the region of conserved function
so can remove other sequences

Upper Temperature limits of life

① put contact slides down

② vent caps



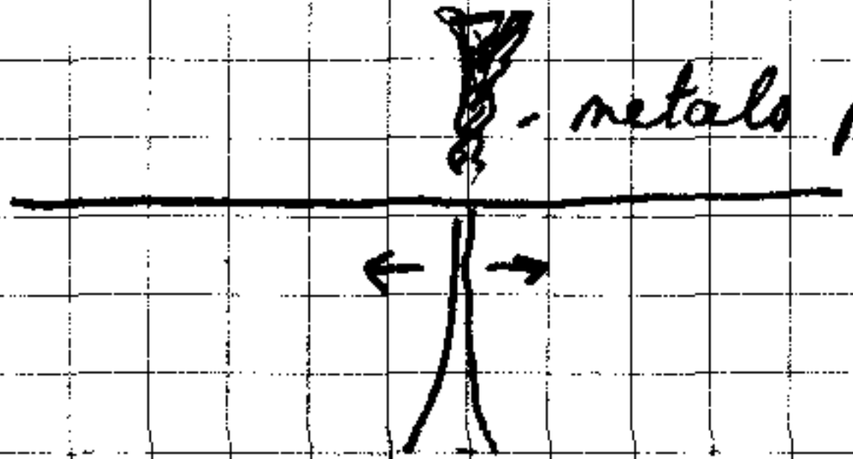
May be able to do phylogeny on
Single cells through oligonucleotide
probes.

① probes for def life

② kingdom level probes

③ species " "

(Growth rate determines # of ribosome
(or is it vice versa)



but

can't cultivate symbionts

- phylogeny may tell a great deal about general biochem of symbionts

Methods of Characterizing Microbial World

Problems

- Cultivation difficult

So what use --

- Phylogeny

- phylogeny can help guide future research (such as was used for RNAse P 2° structure)

(DNA)

↓

Library

↓

165 clones

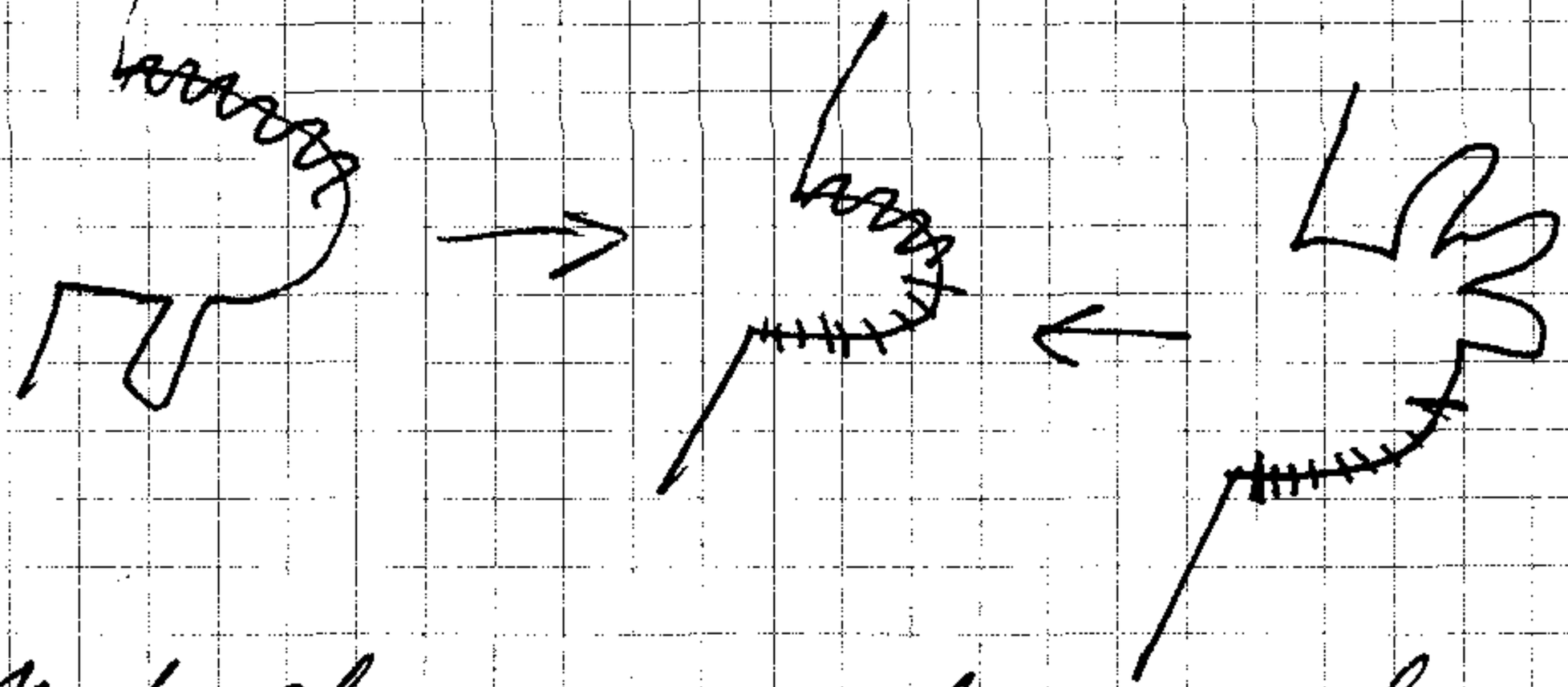
↓

Sequences

But there is a problem because you dont know what to learn

E. coli

B. subs



Make chimera - combine simpler regions of two molecules.