I promised that there are no bio preregs, so I'll quickly review some of the main concepts we'll need for course.

(focus will be on trey #'s that you may not have seen before in your bio course in high school)

Organisms: (modil?)

Im I man & kopm & spin & frid fly

human cell yeast backen

(E.cdi)

An instructions to make turn or encoded in a single love molecule of DNA TITUTE "nucleotides" (nitogenes bases in "base pas" polymor)

Note: we take this for granted rates now, but this is pretty carry from a physicists perspective!

(E. Schroedinger, "What is life")

the entire DNA molecule is known as genone	
lengths of general vary underly across organisms.	
human: ~ 10 bp yeast ~ 10 bp viruses 10-10 bp. find fly: ~ 10 bp bechain ~ 10 bp (16b, 1Mb, 1kb 00) 10 bp	
information after encoded in genes (make proteins)	
RNA polymense RNA polymense MRNA Ribosom & 20 Alfsee. Includy this. Pamino acids (~20) Famino acids (~20)	
how does Ribosom do it? ATTO = codon + lamino and solution codons -> 20 amino acid + "start" codon + degeroney (will revisit)	

* real life is of cause a lith we couplied.

* typical proteins are a 300 M long (1000 bp	of DNA) (3)
# of genes also very across arganisms, to	
humans: ~ 70,000 geres. Yeast 6000 geres, Ecoli ~ ~ 4000 gres Virists ~ 10 geres.	
1000 x bigger genome, but only Sx as many genus. The staff genome is noncoding (regulation / junk?)	End of Ledvel
11 Pel & all this down stull is that arganism	ribosaus! eu)
2 reeds to capy its DN,	4.
* Viruses are tricky: Huy have to his-ch whost cell's machinery! Aubling time voies across arganisms: human ~ 2043. Opposition E. colin 20 human cells ~ Iday Prochlemous (occan back)	mins-lhr

when genome gets copied, there's a chance for	
when genome gets copied, there's a chance for introducing an error (since It's a single ndecule),	
"mutation" ATGCCA	
ATOTE A	1.
Simplest kirds of mulations are single nucleated mulations	(point muda "substitution
7	
bul can also have bigger things; insurbions ATGTTTT	CA T
delations: ATGTX(1 (slipping of DND pol.)	
rearrangements deplications -	- FOOT
profly complicated!) offen via special goes -	
cells have sophisticated machinery for detecting a fixing (point) mutation rates very widely	rg 67013.
= matter (point) mutation rates very modely	across
arsanisms.	
eg. Humans: $\mu \sim 10^{10}$ be/gen Ecoli - $\mu \sim 10^{-10}$ /be/dinson.	
humancells: N-1010/bp/divens VINSES ~ N-10/bp/division	"\

U

worth pausing a thinking about these #s a bit:
Humans: genome is 3410 bp loy -> so 30 mutations per general introduced every generation.
humans on earth, so evay sight by mutation is present in ~ 160 individuals. The or alm today. I all dust mutations or rol (10"×10"×10") - [sequence space 11 by!] E, coli: genera is 4×10 by lag, so 4×10 mutations per /ge >> 1060 replications before e.coli produces a single error!
in gut, eali an at 10 cells, so almost evry by motor the motor of every duy. × 109 billion guts -> almost all dable mutants around in worldwide pap. (but not triple)
what do mutations do? (gerotype => phenotype map) => in gerval, we don't know. (even for e.coli) => but can make some gresses based on what we know about "central dogma"

· e.g. if mutation occurs in middle of a geve, it will change (6
the coden: ATC > ATT	
(thefre, decent change protein) "synanymous" modation.	
2) might change Al to southing else "nonsyranymous"	
Ly other AA (small charge?)	
(2) might croys might charge?) A (small charge?) ("MISSENSE")	
Ly stop codon -> truncates gene (big charge) ("nonsense") "loss-of-function"	
these 3 classes of mutations on easiest to think about because we have some prior easiest expedicions.	
I title of mutations occur outside of goes as well.	
=> Some missense mulations will be not important than al	w

That's enough background for now. will introduce new stull as needed.