Poisson and Geometric Distributions

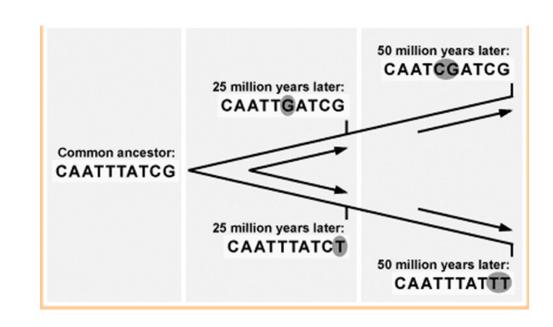
Molecular clock hypothesis

 Conjectured by Émile Zuckerkandl and Linus Pauling in 1962



 Justified by the neutral theory of molecular evolution developed by Motoo Kimura in 1968





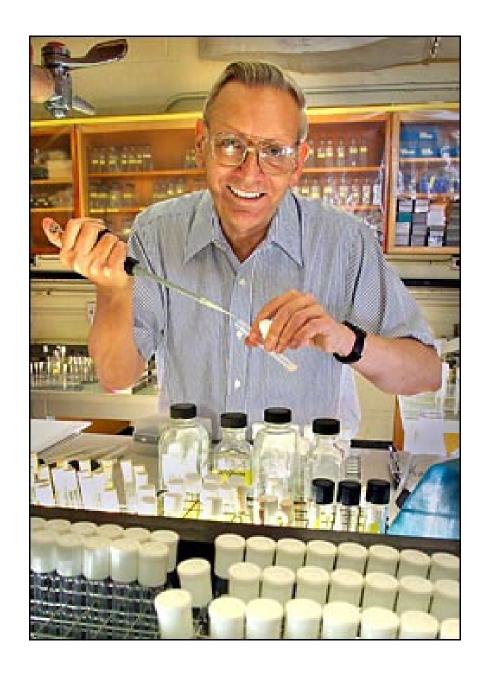
ho - density of differences between two sequences

$$\rho = 2 \mu T$$

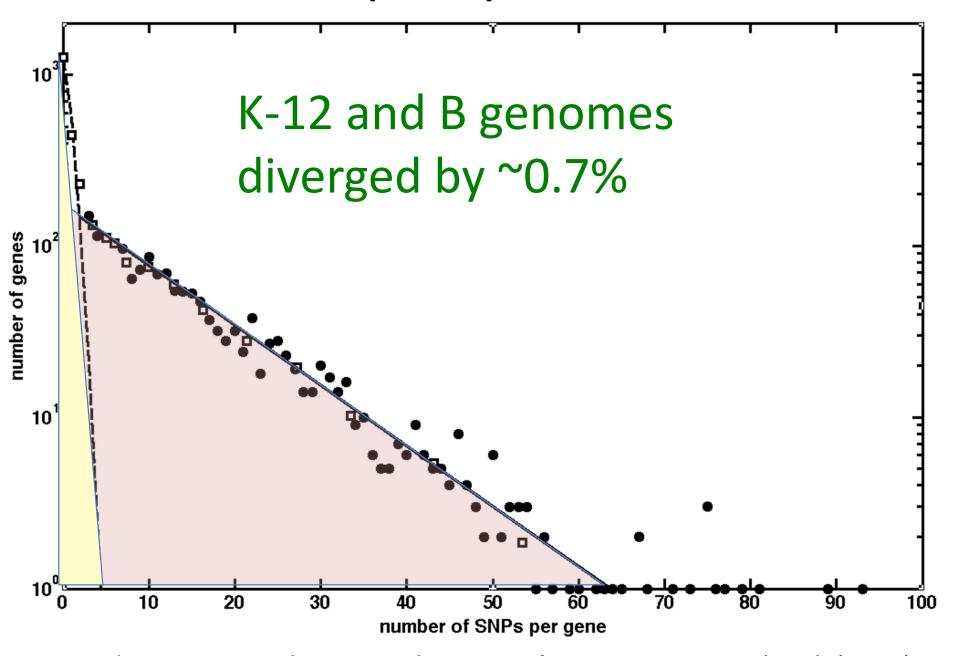
Where μ is the mutation rate per base pair per generation and T is the number of generations since last common ancestor

F. William Studier

- Worked at Brookhaven National Laboratory, Long Island, NY since 1964
- Inventor of slab gel electrophoresis in 1970 (not patented- back then no incentive to patent work if you are supported by the US givernment)
- Inventor of T7 phage expression system for fast production of proteins.
 Licensed by over 900 companies, generated over \$55 million for the lab https://en.wikipedia.org/wiki/T7 expression system

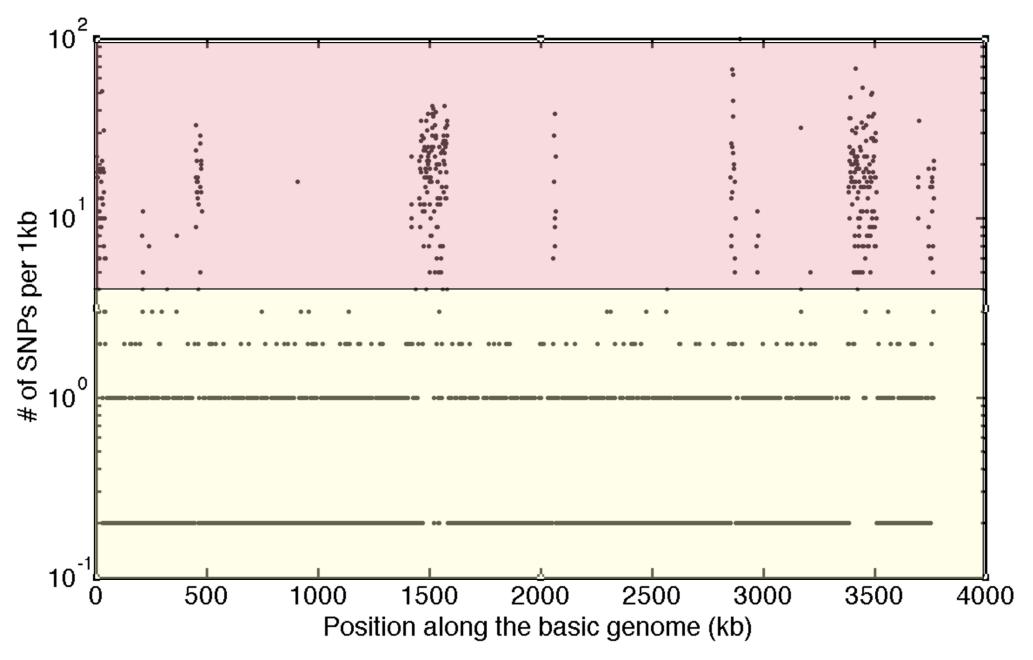


K-12 vs BL21(DE3) strains of E. coli



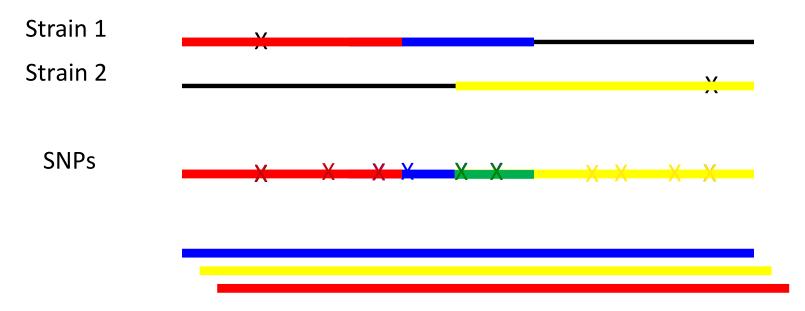
Studier FW, Daegelen P, Lenski RE, Maslov S, Kim JF, J. Mol Biol. (2009)

Highly variable segments are clustered



K-12 vs UMNF18 diverged by ~0.18%

Model of bacterial evolution by mutations and homologous recombination



- Mutation rate μ (bp/generation)
- Recombination rate ρ (bp/generation)
- I_R- average length of recombined segments
- $\theta = 2\mu N_e$ depending on N_e (effective) population size
- δ_{TE} transfer efficiency: Prob(successful transfer + recombination): $\sim \exp(-\delta/\delta_{TE})$

Why exponential tail?

- Empirical data for E. coli: Prob(δ)=exp(- δ /0.01) Similar slopes in other species as distant as B. subtilis
- Theory 1: <u>PopGen 101 coalescence time distribution</u>:
 - Prob(T) ~ exp(-T/N_e) → Prob(δ) ~ exp(- δ/ 2μN_e) = $\frac{\exp(-\delta/\theta)}{\theta}$ $\theta = 2\mu N_e \sim 0.01$, $\mu \sim 10^{-10} \rightarrow N_e \sim 10^8$
- Theory 2: <u>biophysics of homologous recombination</u>:
 - − Requires perfect matches of L=30bp on each side → Prob(δ)=(1- δ)^{2L}=exp(-60•δ)=exp(-δ/0.016)=exp(-δ/ δ _{TE})
- Both mechanisms likely to work together:
 <u>biophysics of recombination affects the</u>
 effective population size

Negative Binomial Definition

 In a series of independent trials with constant probability of success, p, let the random variable X denote the number of trials until r successes occur. Then X is a negative binomial random variable with parameters:

$$0 and $r = 1, 2, 3,$$$

The probability mass function is:

$$f(x) = C_{r-1}^{x-1} p^r (1-p)^{x-r}$$
 for $x = r, r+1, r+2...$ (3-11)

Compare it to binomial

$$f(x) = C_x^n p^x (1-p)^{n-x}$$
 for $x = 1, 2, ... n$

NOTE OF CAUTION: Matlab, Mathematica, and many other sources use x to denote the number of failures until one gets r successes. We stick with Montgomery-Runger.

Negative Binomial Mean & Variance

 If X is a negative binomial random variable with parameters p and r,

$$\mu = E(X) = \frac{r}{p}$$
 and $\sigma^2 = V(X) = \frac{r(1-p)}{p^2}$ (3-12)

Compare to geometric distribution:

$$\mu = E(X) = \frac{1}{p}$$
 and $\sigma^2 = V(X) = \frac{(1-p)}{p^2}$ (3-10)

Matlab exercise

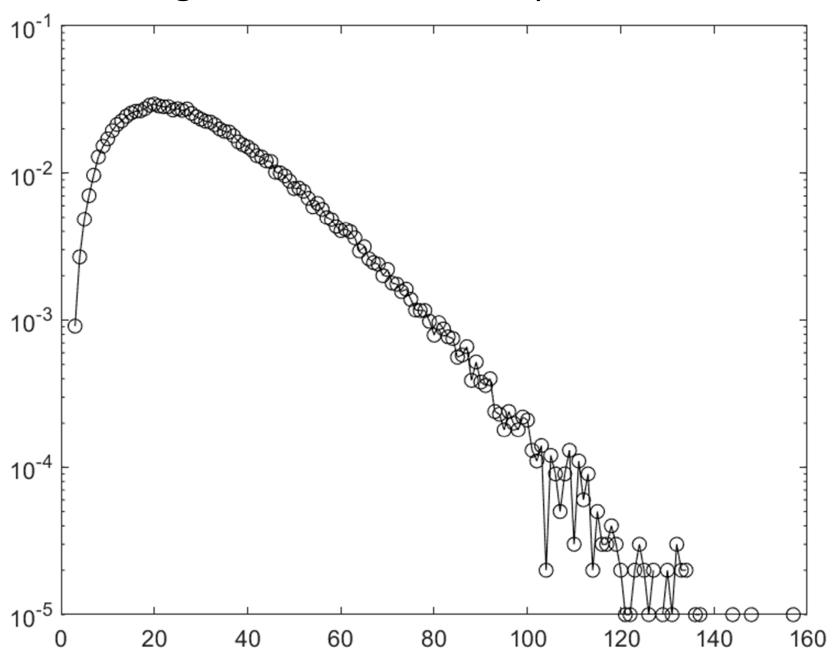
 Estimate mean, variance, and PMF based on 100,000 random variables drawn from a negative binomial distribution with p=0.1, r=3

 Repeat with negative binomial distribution with p=0.1, r=100

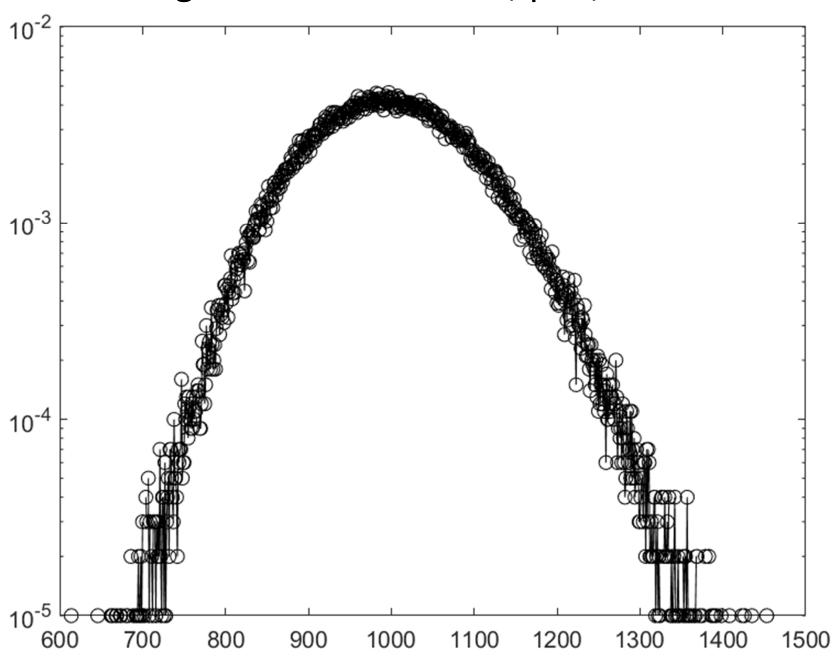
Matlab: Negative binomial distribution

```
Stats=100000;
r=3; p=0.1;
r2=zeros(Stats,1);
for k=1:Stats
  n_trials=0;
  n successes=0;
  while n_successes<r
    if rand<p
       n successes=n successes+1;
    end;
    n_trials=n_trials+1;
  end;
  r2(k)=n_trials;
end:
disp('Observed average value'); disp(sum(r2)./Stats);
disp('Expected average value'); disp(r./p);
disp('Observed variance'); disp(sum(r2.^2)./Stats-(sum(r2)./Stats).^2);
disp('Expected variance'); disp(r.*(1-p)./p^2);
[a,b]=hist(r2, 1:max(r2));
p_nb=a./sum(a);
figure; semilogy(b,p_nb,'ko-');
```

Negative binomial PMF, p=0,1 r=3



Negative binomial PMF, p=0,1 r=100



Cancer is scary!

 Approximately 40% of men and women will be diagnosed with cancer at some point during their lifetimes (source: NCI website)

TABLE 21.2 Leading causes of death in United States in 2010. Cause of death is based on the International Classification of Diseases, Tenth Revision, 1992.

Rank	Cause of death	Number	Percent of all deaths
_	All causes	2,468,435	100.0
1	Diseases of heart	597,689	24.2
2	Malignant neoplasms	574,743	23.3
3	Chronic lower respiratory diseases	138,080	5.6
4	Cerebrovascular diseases	129,476	5.2
5	Accidents (unintentional injuries)	120,859	4.9
6	Alzheimer's disease	83,494	3.4
7	Diabetes mellitus	69,071	2.8
8	Nephritis, nephrotic syndrome, and nephrosis	50,476	2.0
9	Influenza and pneumonia	50,097	2.0
10	Intentional self-harm (suicide)	38,364	1.6

Table from J. Pevsner 3rd edition

Source: National Vital Statistics Reports, 62(6) (http://www.cdc.gov/nchs/data/nvsr/nvsr62/nvsr62_06.pdf)

"War on Cancer" – president Nixon 1971.
 "Moonshot to Cure Cancer" – vice-president Joe Biden 2016

"War on Cancer" progress report

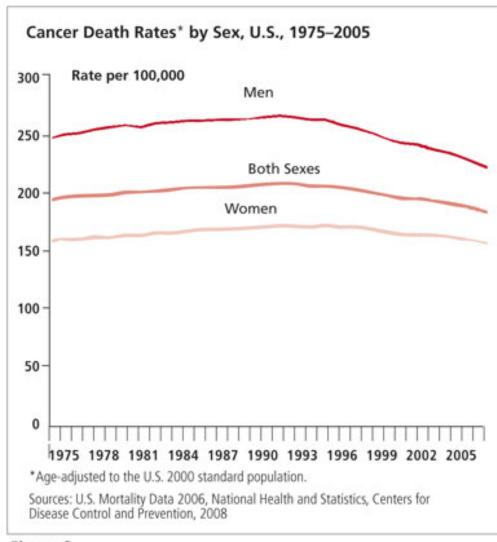


Figure 2

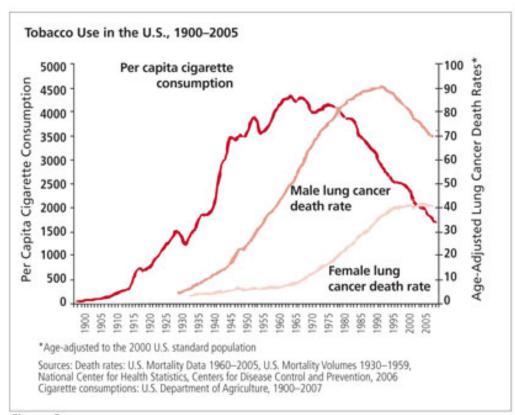


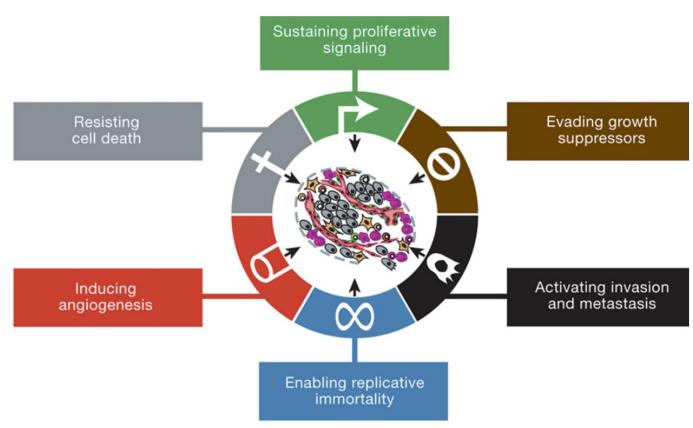
Figure 3

Probability theory and statistics is a powerful tool to learn new cancer biology

"Driver genes" theory

- Progression of cancer is caused by accumulation of mutations in a handful of "driver" genes
- Mutations in driver genes boost the growth of a tumor
- Oncogenes: expression needs to be elevated for cancer
- Tumor suppressors (e.g. p53) need to be turned off in cancer

Douglas Hanahan and Robert A. Weinberg <u>Hallmarks of Cancer</u>: The Next Generation Cell 144, 2011



Statistics of cancer incidence vs age

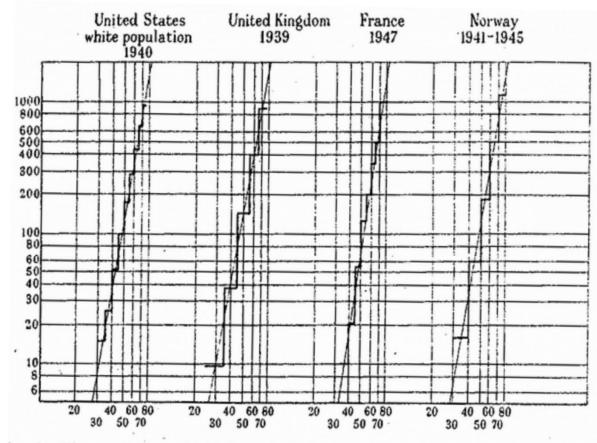


Fig. 1.—Diagram drawn to double logarithmic (log/log) scale showing the cancer death-rate (in the case of the United Kingdom, the carcinoma death-rate) in males at different ages. Deaths per 100,000 males are shown on the vertical scale, age figures on the horizontal scale.

Multi-mutation theory of cancer: Carl O. Nordling (British J. of Cancer, March 1953):

Cancer death rate

~ (patient age)⁶

It suggests the existence of k=7 driver genes

$$P(T_{cancer} \leq t) \sim (u_1 t)(u_2 t)...(u_k t) \sim u_1 u_2 ... u_k t^k$$

$$P(T_{cancer} = t) \sim \frac{d}{dt} (u_1 t) (u_2 t) ... (u_k t) \sim k u_1 u_2 ... u_k t^{k-1}$$

How many driver gene mutations for different types of cancer?

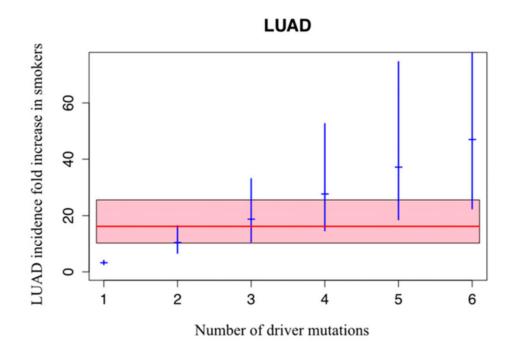
Only three driver gene mutations are required for the development of lung and colorectal cancers

Cristian Tomasetti^{a,b,1}, Luigi Marchionni^c, Martin A. Nowak^d, Giovanni Parmigiani^e, and Bert Vogelstein^{f,g,1}

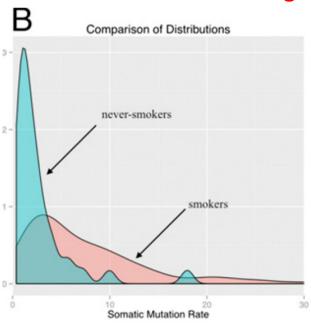
^aDivision of Biostatistics and Bioinformatics, Department of Oncology, Sidney Kimmel Cancer Center, Johns Hopkins University School of Medicine, and ^bDepartment of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD 21205; ^cCancer Biology Program, Sidney Kimmel Cancer Center, Johns Hopkins University School of Medicine, Baltimore, MD 21205; ^dProgram for Evolutionary Dynamics, Department of Mathematics, Harvard University, Cambridge, MA 02138; ^eDepartment of Biostatistics and Computational Biology, Dana-Farber Cancer Institute and Harvard School of Public Health, Boston, MA 02215; and ^fLudwig Center for Cancer Genetics and Therapeutics and ^gHoward Hughes Medical Institute, Sidney Kimmel Cancer Center, Johns Hopkins University School of Medicine, Baltimore, MD 21205

Contributed by Bert Vogelstein, November 21, 2014 (sent for review July 31, 2014; reviewed by Zvia Agur)

Smokers have 3.23 times more mutations in lungs



SANG



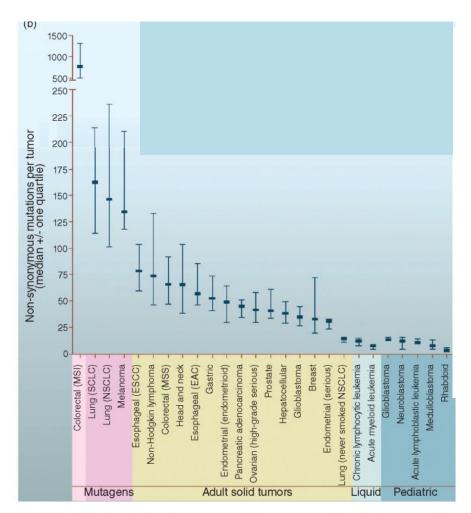
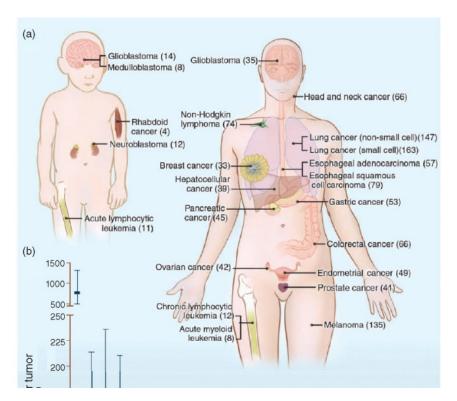


FIGURE 21.10 Somatic mutations in representative human cancers, based on genome-wide sequencing studies. (a) The genomes of adult (right) and pediatric (left) cancers are represented. Numbers in parentheses are the median number of nonsynonymous mutations per tumor. Redrawn from Vogelstein et al. (2013). Reproduced with permission from AAAS. (b) Median number of nonsynonymous substitutions per tumor. Horizonal bars indicate the 25% and 75% quartiles. MSI: microsatellite instability; SCLC: small cell lung cancers; NSCLC: non-small cell lung cancers; ESCC: esophageal squamous cell carcinomas; MSS: microsatellite stable; EAC: esophageal adenocarcinomas.

Bioinformatics and Functional Genomics, Third Edition, Jonathan Pevsner.

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Companion Website: www.wiley.com/go/pevsnerbioinformatics



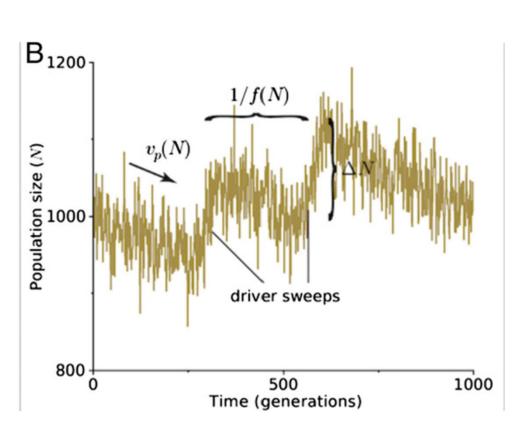
- Cancer cells carry both "Driver" and "Passengers" mutations
 - Passenger mutations cause little to no harm (see later for how even little harm matters)
- Both are common as cancers elevate mutation rate

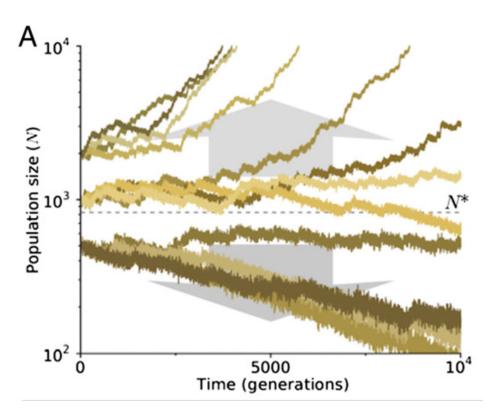
Number of passenger+driver mutations follows negative binomial distribution

- What is the probability to have n_p passenger mutations or (n_p+k) total mutations by the time you are diagnosed with cancer requiring k driver mutations?
- Let p is the probability that a mutation is a driver (p= Genome_target_of_driv/
 (Genome_target_of_driv+Genome_target_of_pass)
 (1-p) it is a passenger mutation

$$P(n_p + k \mid p, k) = \binom{n_p + k - 1}{n_p} (1 - p)^{n_p} p^k$$

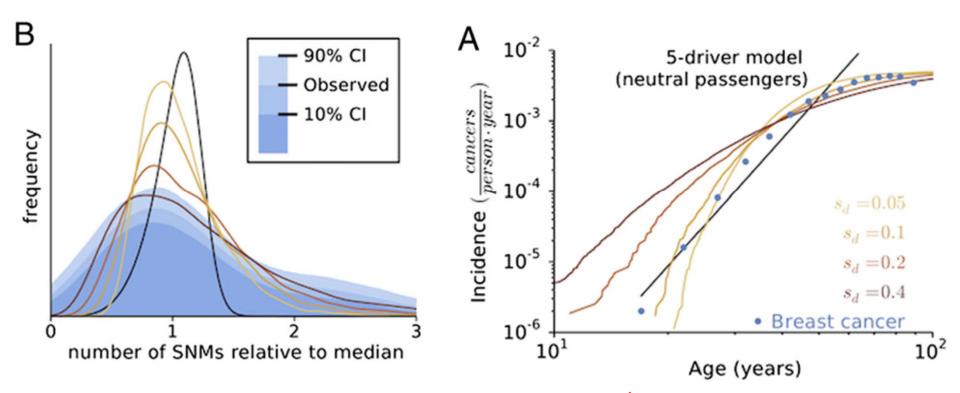
What if passenger mutations slow down the growth of cancer tumors?





McFarland CD, Mirny L, Korolev KS, PNAS 2014

Can we prove/quantify it using statistics?



Assume: growth rate of cancer= $(1+s_d)^{Nd}/(1+s_p)^{Np}$

 μ =10⁻⁸, Target_d=1,400, Target_p=10⁷, s_d=0.05 to 0.4, s_p=0.001 s_p/s_d for breast: 0.0060±0.0010;

melanoma: 0.016±0.003; lung: 0.0094±0.0093;

Blue - data on breast cancer: incidence; non-synonymous mutations

