Biophysics in Physics Department at Rutgers

Gyan Bhanot

Physics and MBB

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Biology vs Physics

- Why is Biology different from Physics?
  - No conservation laws, open system, few equations/laws
  - Huge Complexity
- What should physicists do to be relevant in biology?
  - Do something biologists cannot do.

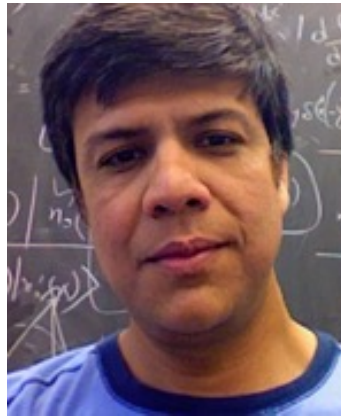
Center for Quantitative Biology (cqb.rutgers.edu)

- CQB seminar series
- Summer student support
- Travel support
- Organizing meetings at Rutgers

Biophysics Research at Rutgers

Alexandre Morozov

Anirvan Sengupta



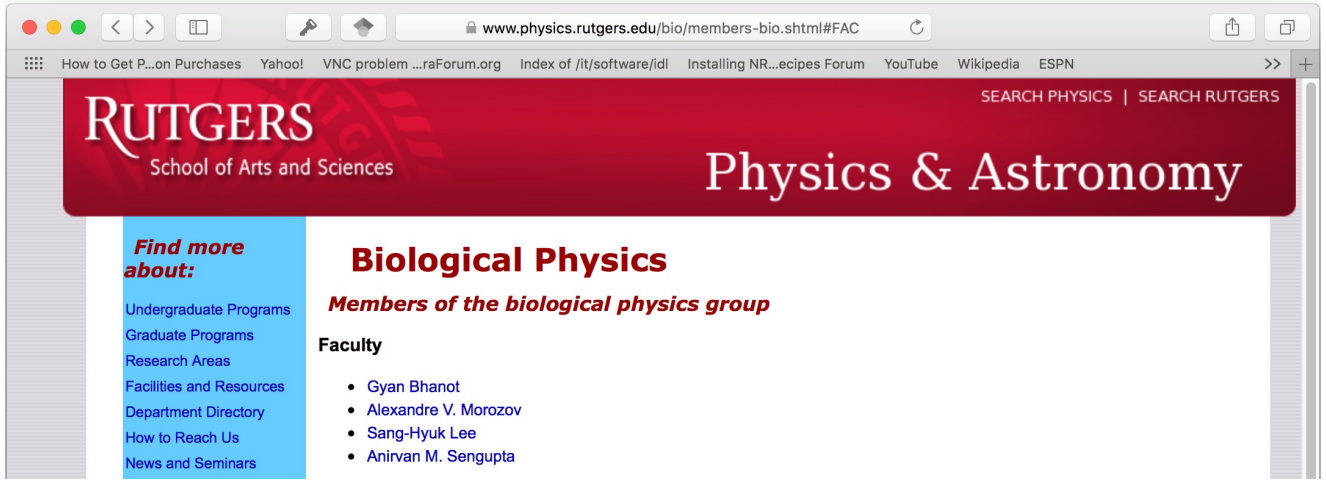
Wilma Olson

Gyan Bhanot

Sang-Hyuk Lee

Theory

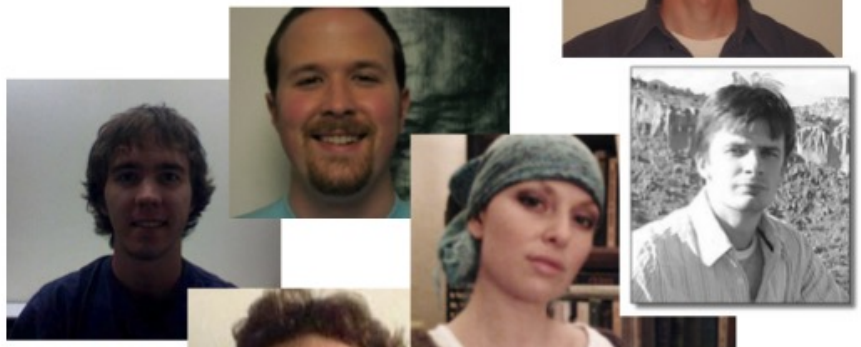
Experiment



Morozov Lab

Former and current lab members:

- Allan Haldane (Temple)
- George Locke (Biogen)
- Michael Manhart (ETH Zurich)
- Dr. Denis Tolkunov (Roche)
- Razvan Chereji (NIH/NICHD)
- Julia Tsitron (NYC Parks & Recreation)
- Ted Malliaris
- Willow Kion-Crosby
- Pavel Khromov
- Aditya Ballal
- Unab Javed
- Jesus Rives



Funding:

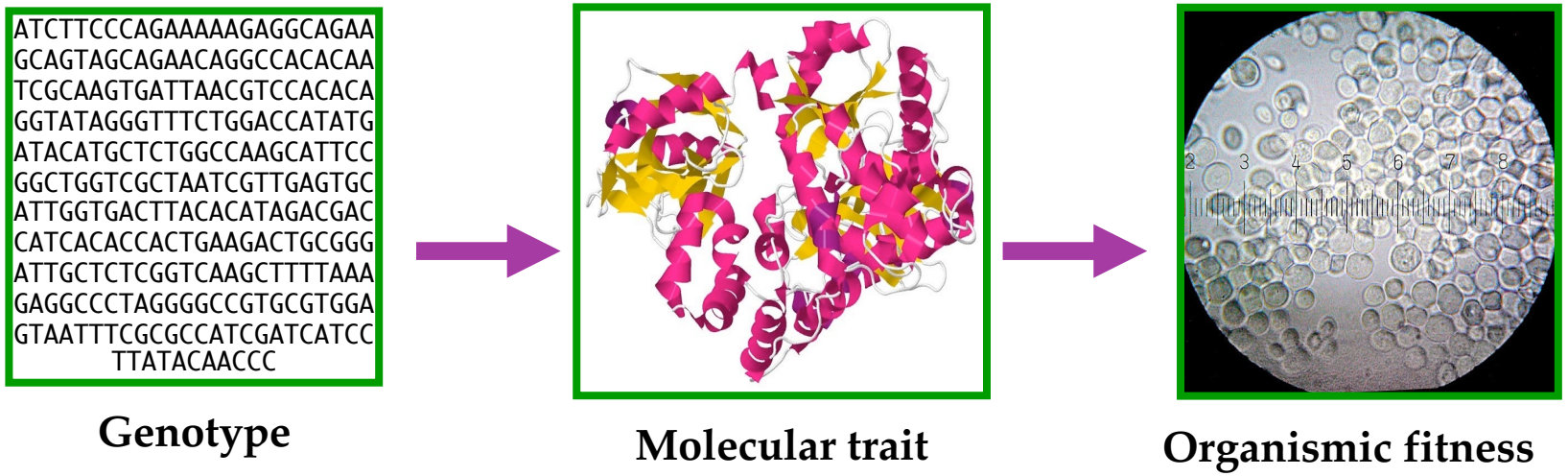
NATIONAL INSTITUTES OF HEALTH

BioMaPS

ALFRED P. SLOAN FOUNDATION

Los Alamos NATIONAL LABORATORY EST. 1943

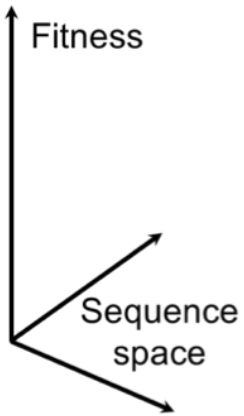
Theme 1: Understanding molecular evolution

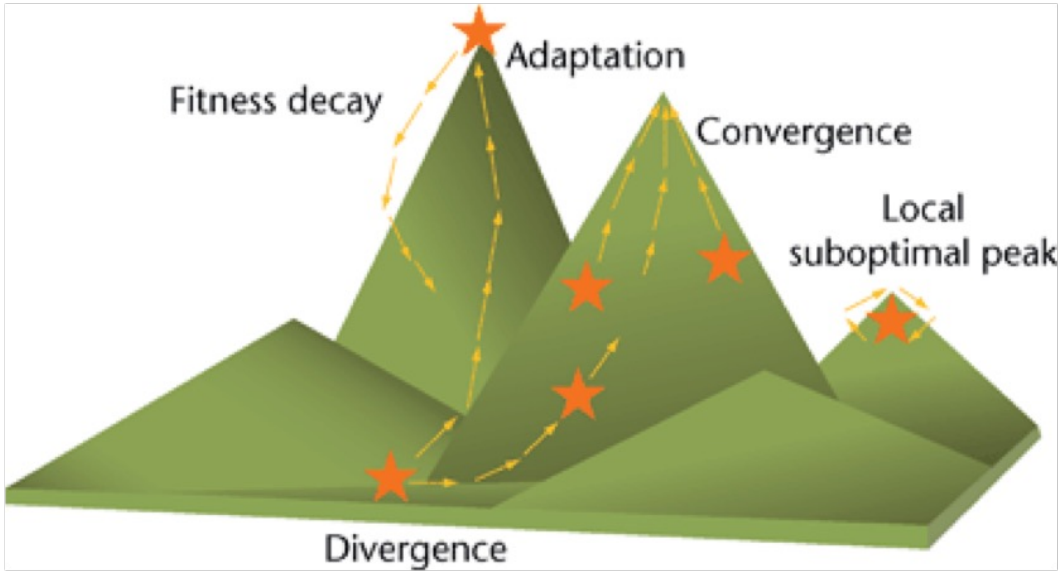


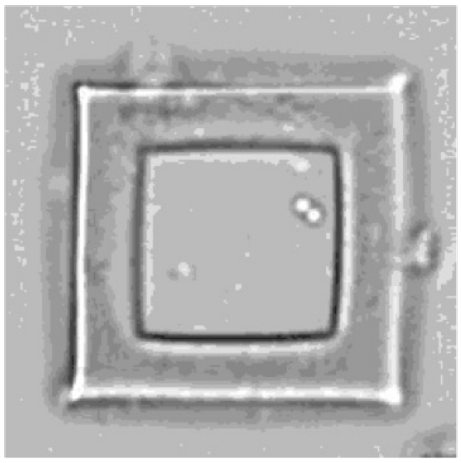
We use tools from non-equilibrium statistical physics and population genetics to build models of molecular evolution

Our approach provides mechanistic understanding of evolutionary dynamics based on underlying biophysics

Evolution as random walks on fitness landscapes

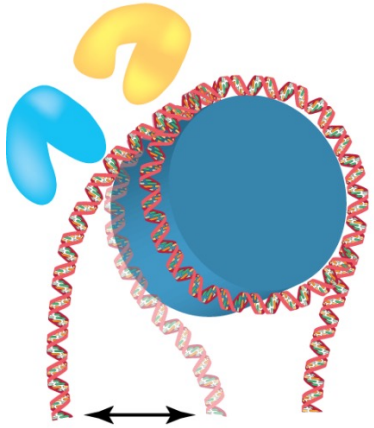


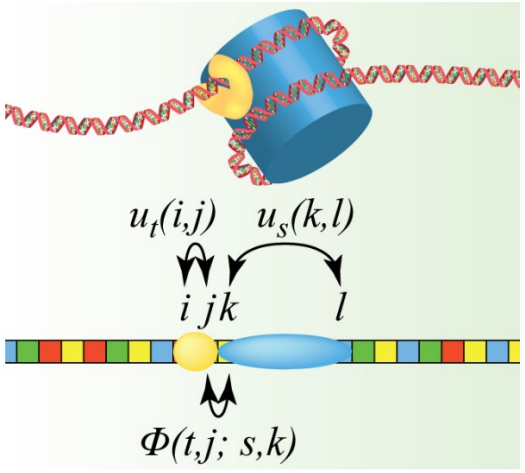


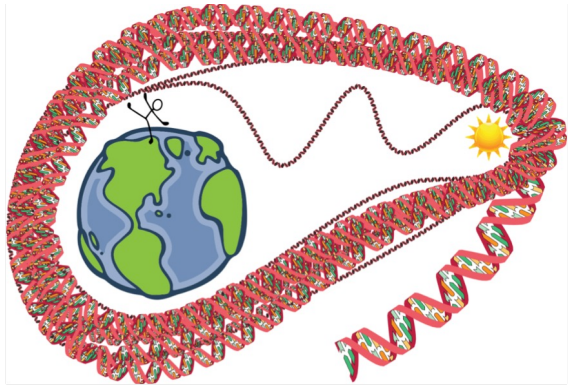


Theme 2: Statistical mechanics of protein-DNA interactions

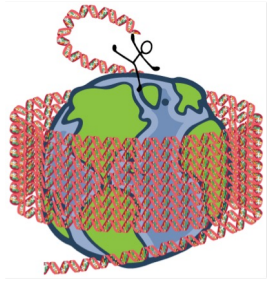
Total length of DNA in one human body ~ 43x distance from earth to sun







More than 300 turns!



More than 2.5 million turns!

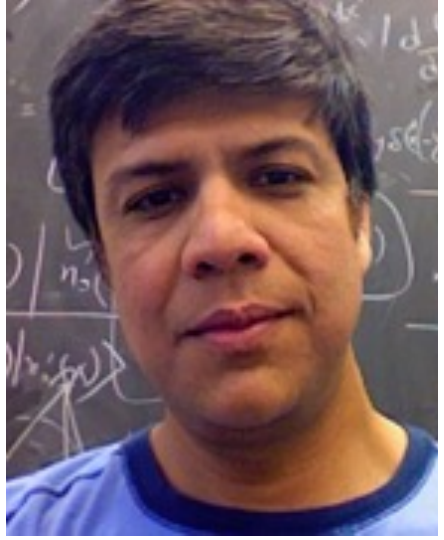
We are developing statistical mechanics models of chromatin with the following ingredients:

- nucleosome unwrapping,
- multiple species of DNA-binding proteins,
- sequence-dependent binding energies,
- sequence-independent potential barriers and wells,
- effective two-body interactions.

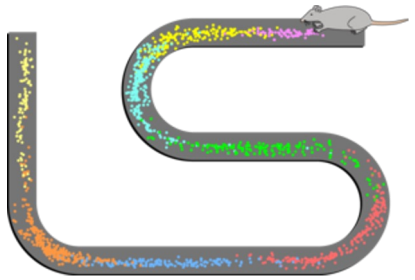
Theme 3: Machine learning in physics and biology, artificial intelligence

We are also developing machine learning tools for the physics community:

- **Global optimization techniques**
- **Data-driven inference of physical laws, e.g. empirical equations of motion**
- **Network analysis, clustering of network nodes into communities**
- **Computational analysis of cell motion**



Sengupta Lab :
Learning of Place Cell Receptive Fields (RFs)



[Source: Wikipedia]

Hippocampus forms spatial maps by having a set of neurons that fire up in overlapping patches. We study a network that can adaptively learn such maps.

[Sengupta et al., NeuriPS 2019]

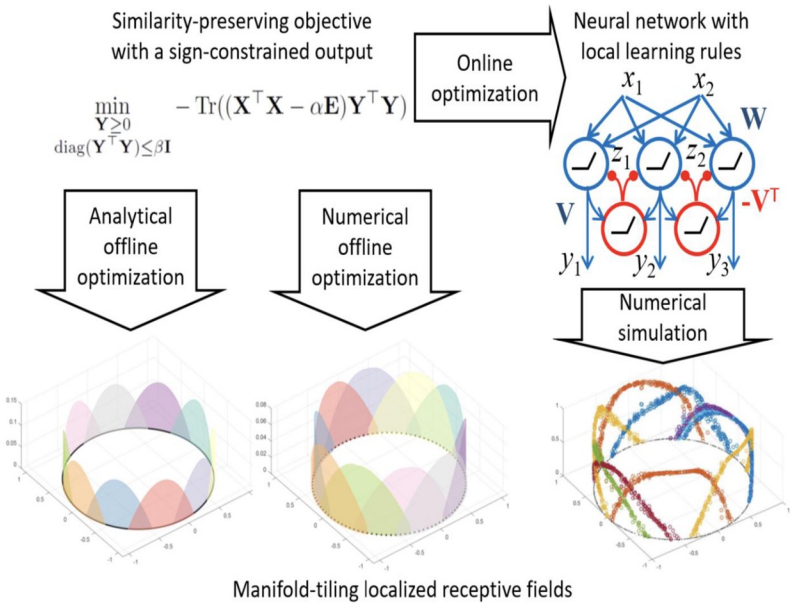


Figure 1: A schematic illustration of our normative approach.

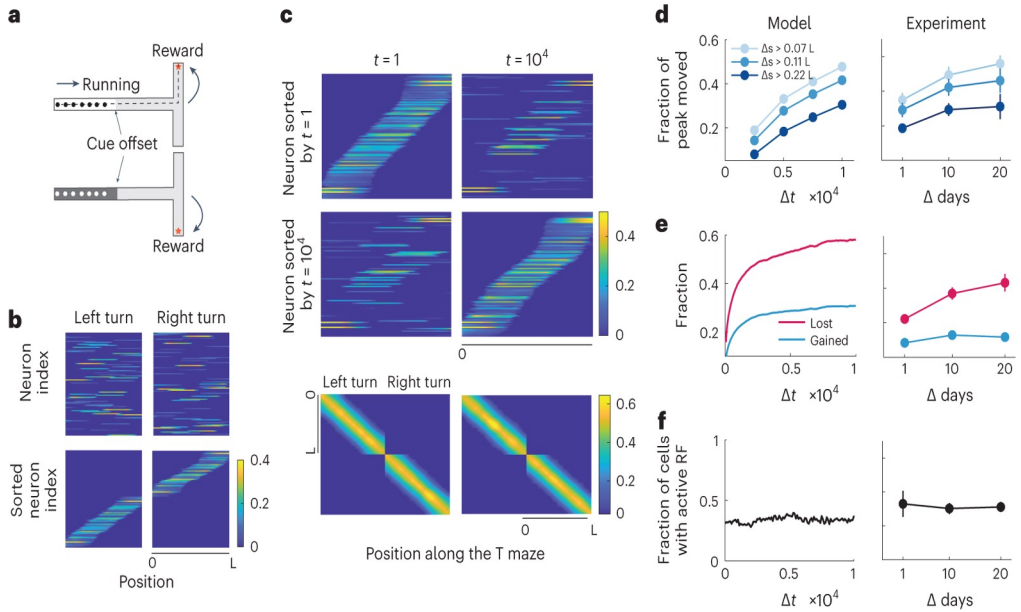
Analysis of the Drift of the RFs and their Fidelity

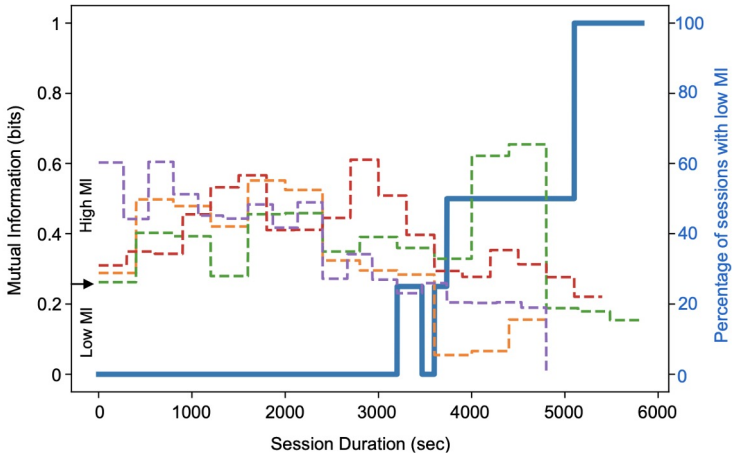
Manifold representation learned this way can lead to coordinated drift of receptive fields. This is predicted and compared with experiments.

[Qin et al., Nature Neuroscience 2023]

Using information theory for analyzing real data, we found the fidelity of the representations depends on behavioral engagement.

[Sridharan and Sengupta, NeurIPS InfoCog Workshop 2022]





Optimal Feedback Control with Local Neural Learning

Motor control requires learning tasks in a particular environment and operates under noisy sensory inputs.

We create a model of learning with local update rules that could do the task and achieve optimal feedback control, based on the reward signal. [Friedrich et al., NeurIPS 2021]

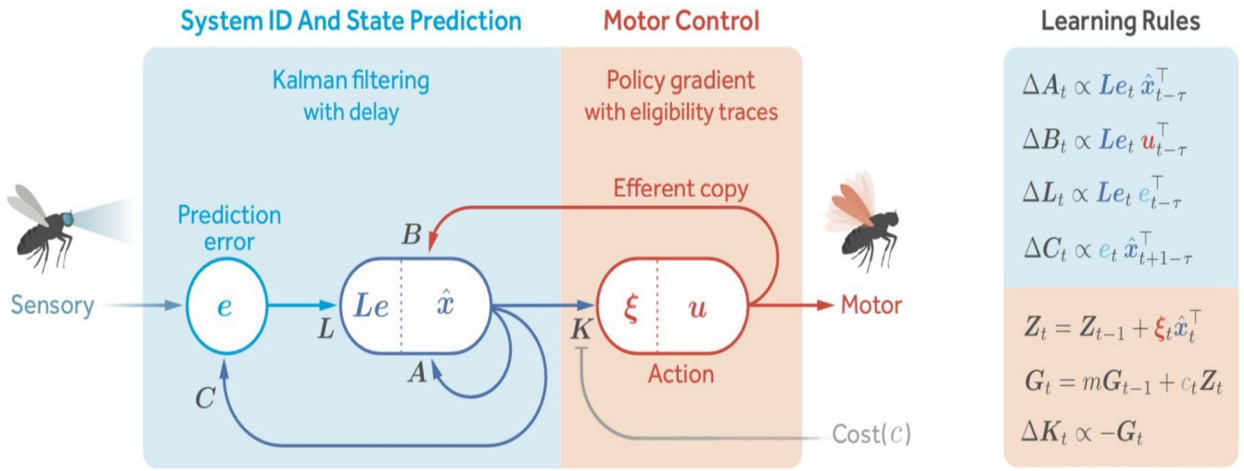


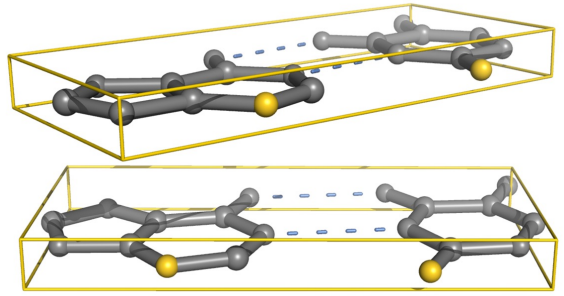
Figure 1: **The circuit and learning rules of the Bio-OFC algorithm.** Our circuit is comprised of two main parts. First (in blue), the circuit performs Kalman filtering. Then (in red), the circuit performs control using policy gradients with eligibility traces. Triangular arrowheads denote synaptic connections and the flat arrowhead denotes the modulatory effect of the cost signal.

Wilma Olson

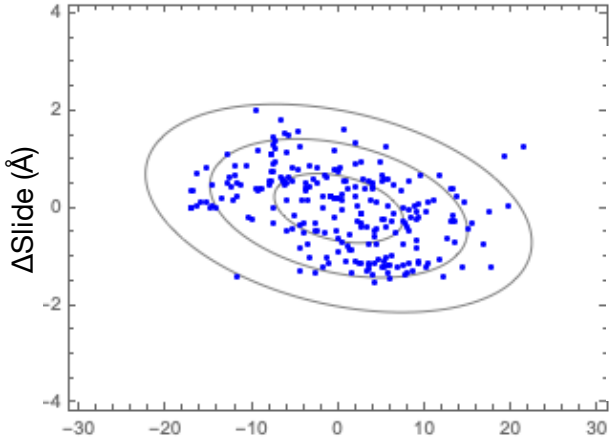
Olson Lab

Insights into DNA and chromatin properties based on statistical mechanical treatments of sequence-dependent chain architecture, deformability, and protein uptake.

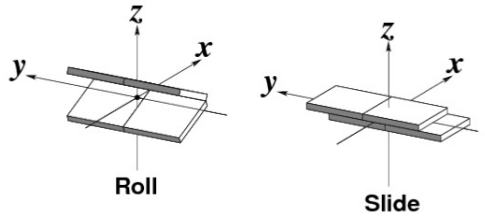
Recent undergraduate projects in the Olson lab have included:

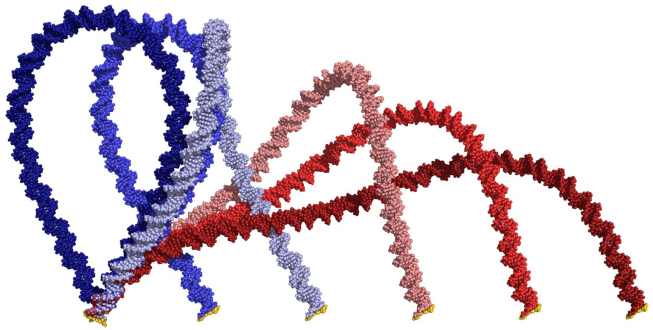


Quantitative characterization of base pair architecture in DNA structures



Development of knowledge-based potentials based on the observed 3D states





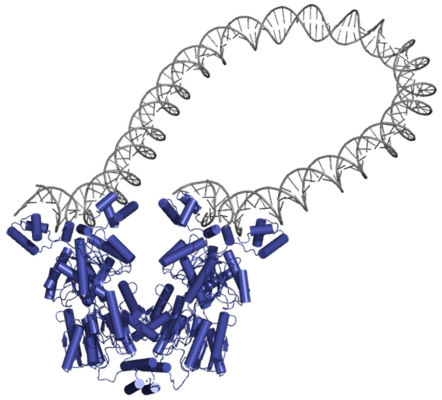
Simulation of DNA polymers, incorporating these potentials (here single-molecule pulling)

Wilma Olson

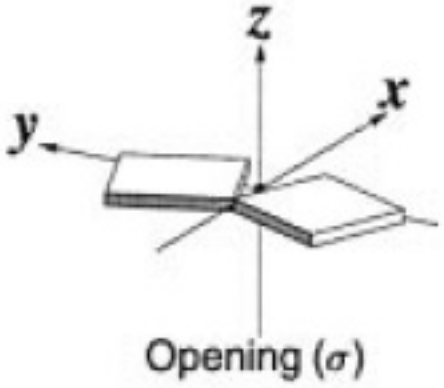
Olson Lab

Insights into DNA and chromatin properties based on statistical mechanical treatments of sequence-dependent chain architecture, deformability, and protein uptake.

New undergraduate projects involve:



Effects of sequence on protein-mediated DNA loops involved in gene processing



Higher-order potentials incorporating motions within base pairs

Protein-bound minicircles (here ~2500 base pairs wrapped around 12 virtual proteins)

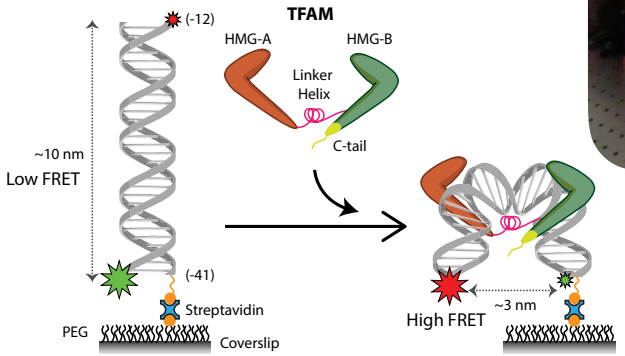
Lee Lab: Bio-optics & Single-molecule Biophysics (Research Overview and Past Work)

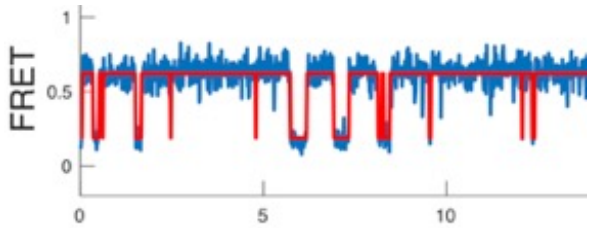
Develop Revolutionary Optical Microscopy/Spectroscopy

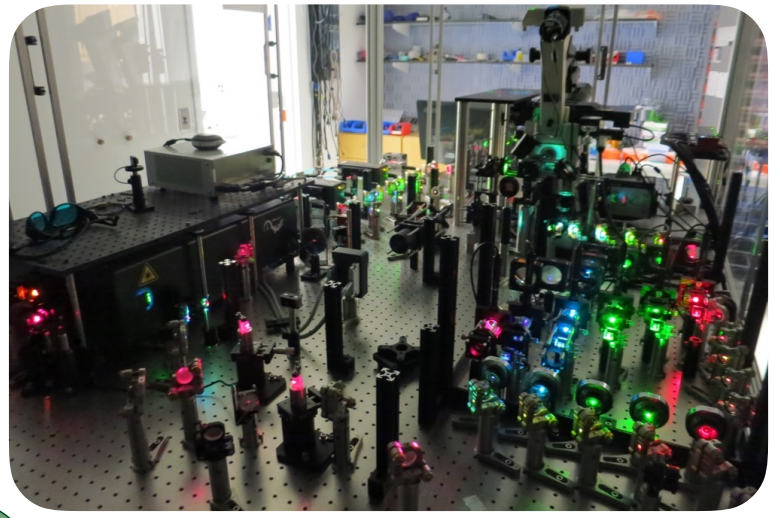
- **Break the diffraction-limited optical resolution**
- **Track and manipulate biomolecules with single-molecule precision**
- **Understand (undiscovered) rules of life phenomena from simply watching the processes as they happen**

In vitro Single-molecule Study

- Study interaction and dynamics of biomolecules one molecule at a time using fluorescence or optical tweezers (e.g., DNA-bending by TFAM protein)

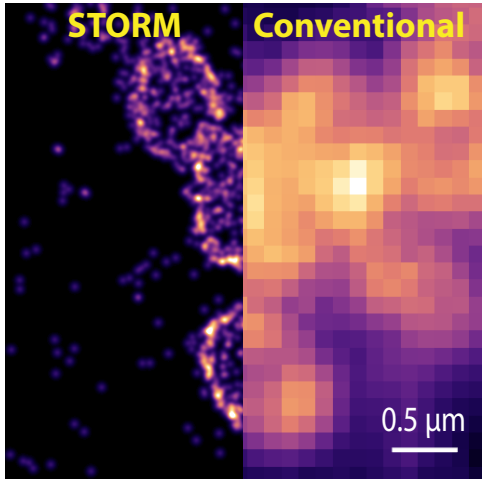




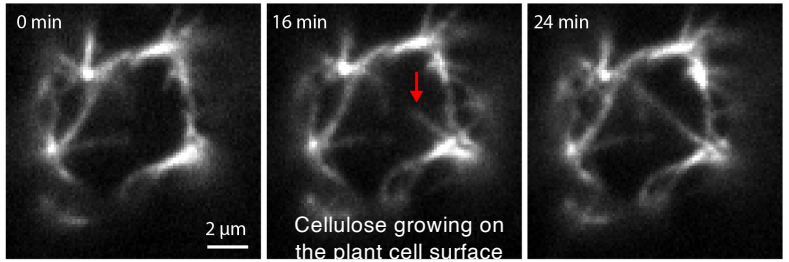


High Resolution Fluorescence Imaging of Cells/Organisms

- Resolve intracellular structures and functions at super-resolution (e.g., pathogenic bacteria)



Live Cell Imaging of Plant Cell Wall Synthesis



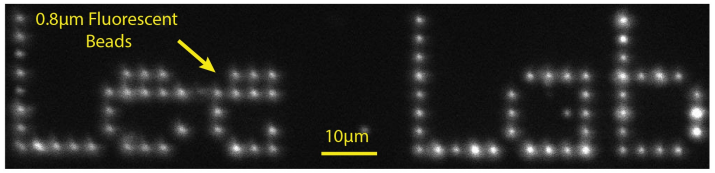
Other Ongoing Research

1. Multimodal Microscopy Instrument Development

- Integration of holographic optical tweezers fluorescence microscopy (completed)

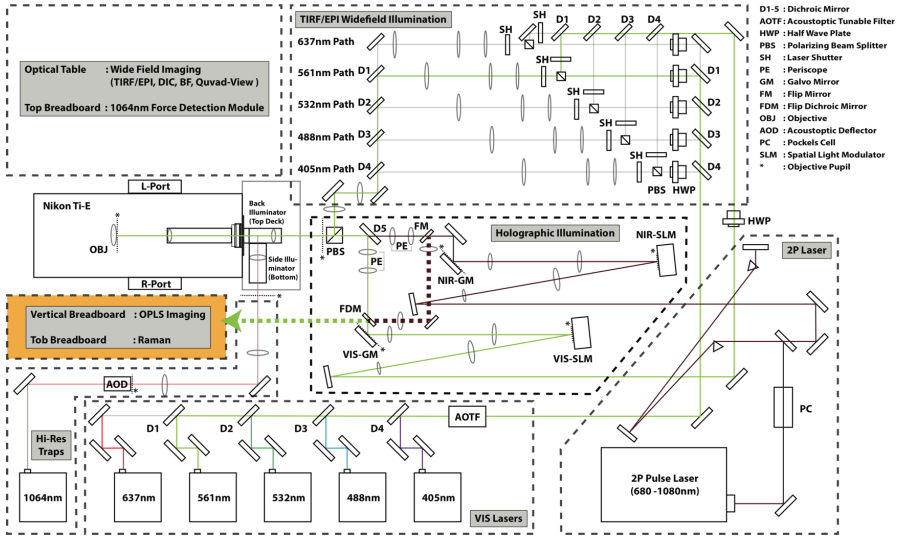
- Ultra-high resolution optical tweezers for measuring bio-molecular force and motion (under construction with 1064nm laser)
- Ultra-fast (~1000 frame per sec) 3D fluorescence and Raman microscopy for real-time cell/tissue imaging (under development)

Optical Trapping & Fluorescence Microscopy



Trapping Laser: 561nm / Excitation Laser: 405nm

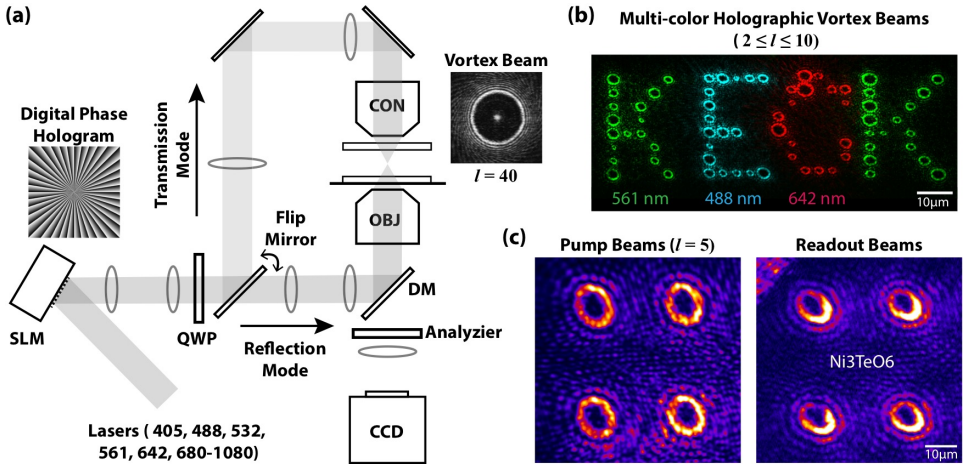
Ultimate Dream Instrument Under Development



2. Interaction of Quantum Magnetism with Vortex Beams (with Sang-Wook Cheong, Valery Kiryukhin, Andrei Sirenko)

- Light can carry orbital angular momentum (topological phase pattern) in addition to spin angular momentum (circular polarization)
- We will study how the light with orbital angular momentum is coupled with topological quantum magnetism

Laser Vortex Beam Microscopy on Quantum Magnetism

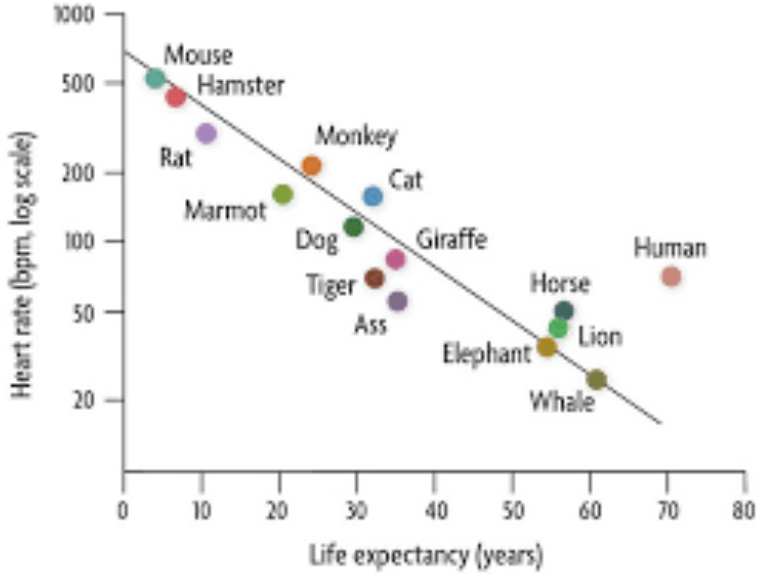


My Background

- PhD 1979 – Theoretical Physics, Cornell
- Post-Doc (‘79-’85): BNL, IAS, CERN, ITP
- Faculty: FSU (‘85-’89): Physics
- Thinking Machines Corporation (‘89-’94) (Computer Science – CM2, CM5)
- IBM Research (’94-’06)
  - Physics/Computer-Science ‘94-00, Blue Gene
  - Comp Bio (‘00-’06)
- Rutgers (‘06-present) – Joint Appointment Physics and Molecular Biology

Possible projects

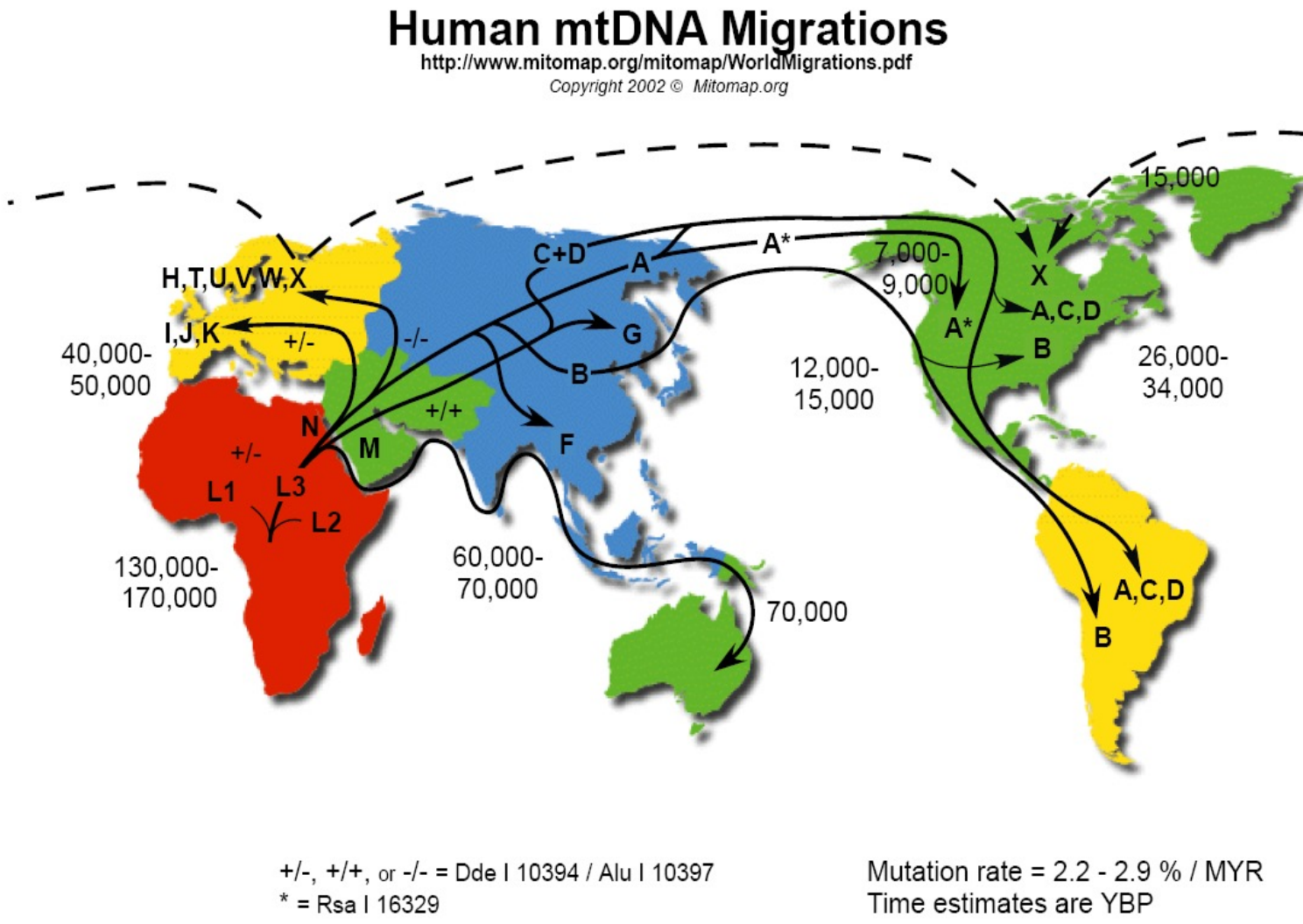
- Epidemiology:
  - Is the Covid-19 virus evolving to lower virulence and higher infectivity (as all viruses do)?
  - Using sequencing data and statistical mechanics ideas, is it possible to predict emerging strains?
  - Can the novel method based on peak widths be applied to the FLU virus?
- New methods to analyze long-read sequencing data from tumors
- Life span and heart rate [within species]



How I got into Biology

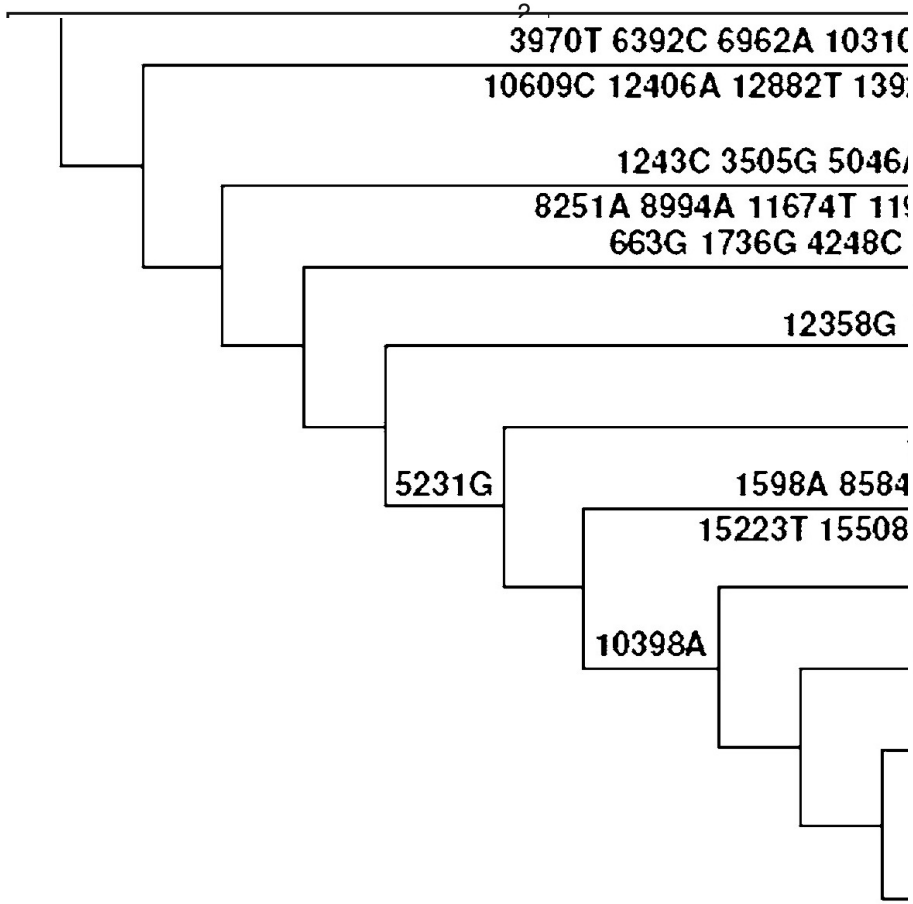
- IBM Project with National Geographic
- Human Migrations/Origins
- Study mutations on mtDNA and Y-chr
- To understand migrations since the "Out of Africa" event 200,000 years ago.

Meave Leakey



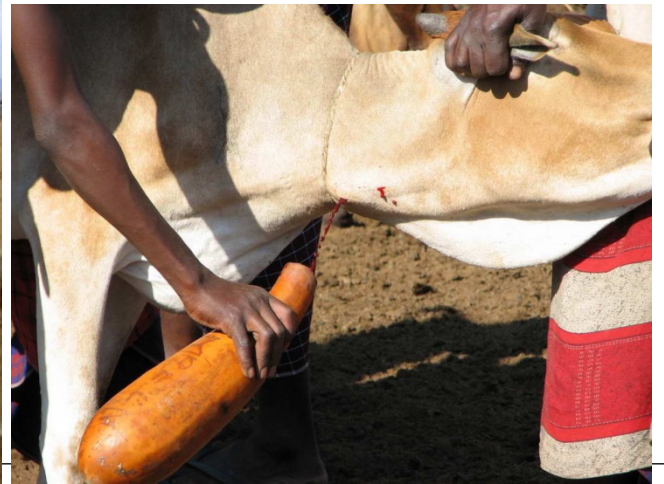
Recursive PCA Reveals Alternate Phylogeny of Humans

J Mol Evol (2008) 67:465–487



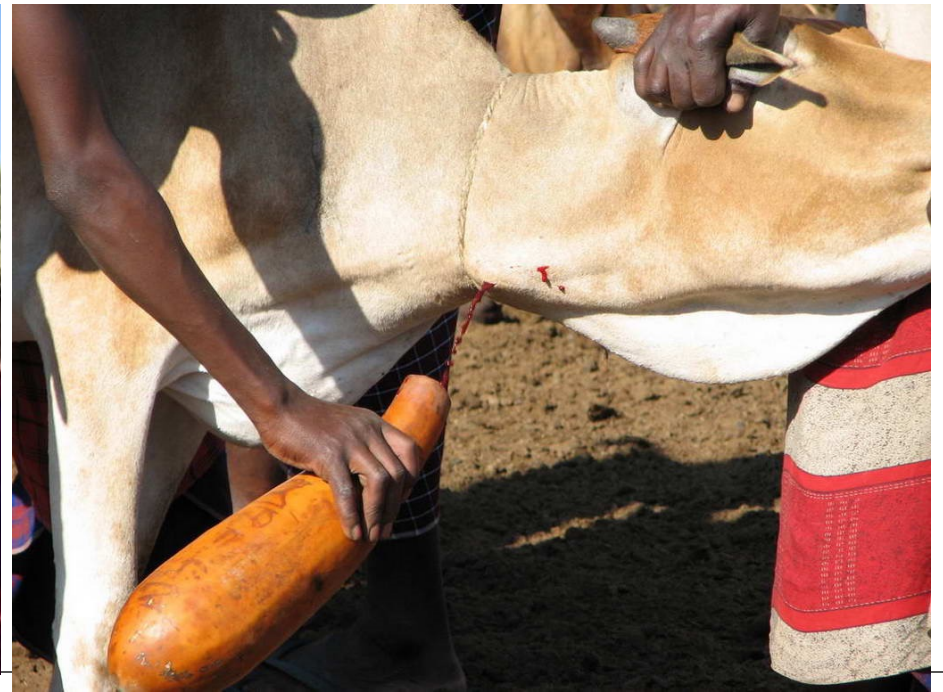
There are many other homoplasy mutations (like 12705) in the data. For instance, there is a mutation at locus 5417 which appears in both N9a and N9b but is not present in any other N haplogroups (Tanaka et al. 2004; Kong et al. 2006). Parsimony methods identify this mutation as a founder mutation and, consequently, place N9a and N9b on adjacent leaves of the N-clade subtree (Bandelt et al. 2006). Indeed the names of these groups are themselves derived from such a placement. However, from a study of the Jomon and Yayoi people in Japan (Shinoda 2005), the N9a haplogroup is believed to have entered Japan from South China through Korea along an eastern route, while the N9b haplogroup came into Japan via a northern route. According to this analysis, these two

Dietary Pressure and Genetic Adaptation in the Maasai



The Maasai are a rural, pastoral people in Kenya/Tanzania. Their traditional diet consists of milk, blood and occasionally, meat.

Motivation: Taylor, B.C., K.J. Ho, Studies on the Masai. Amer. J. of Clin. Nutr., 1971. 24: 1291-1293.



Cholesterol levels of Maasai versus US Males and Females

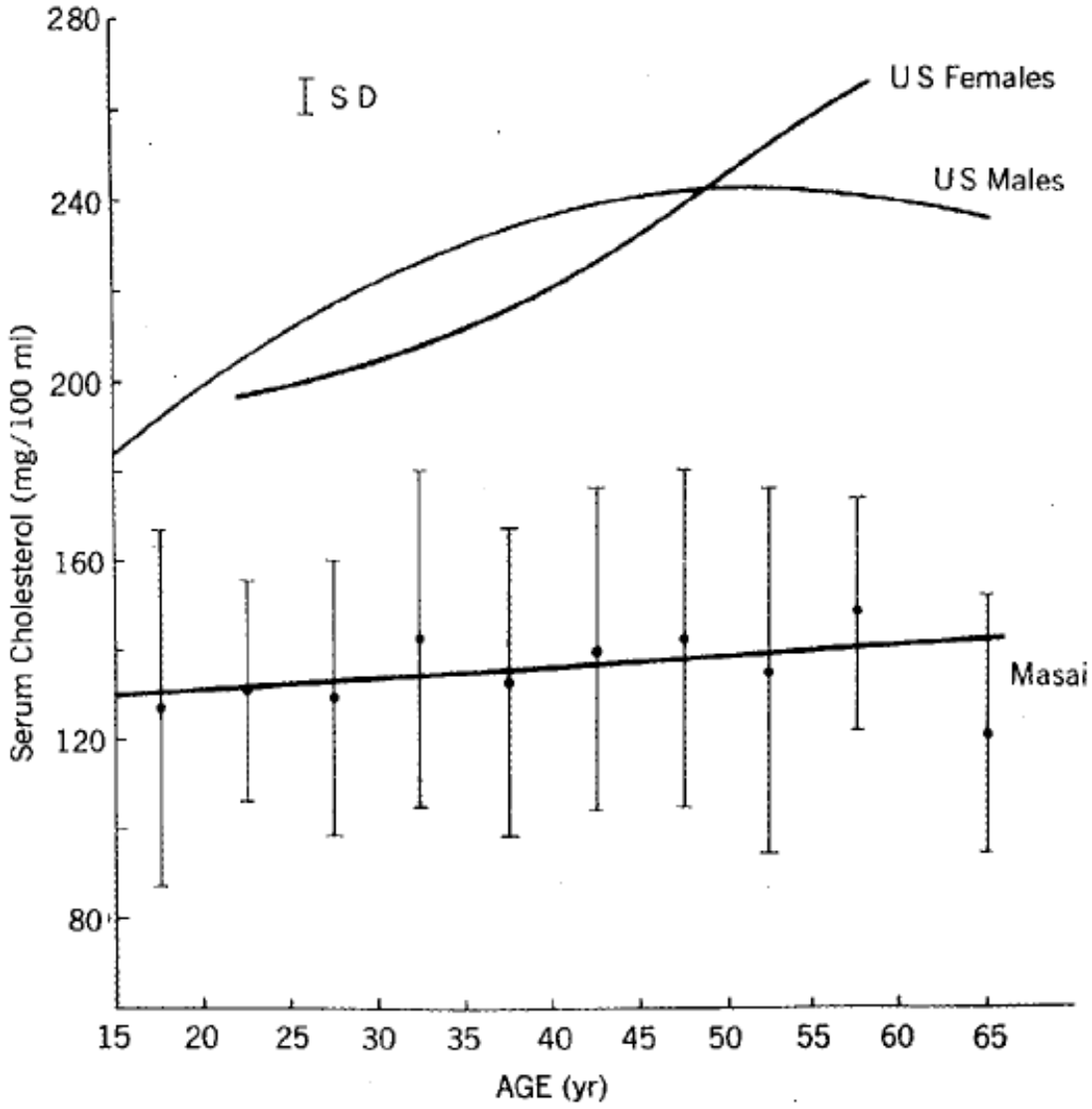


Fig 1.—Comparison of the serum cholesterol levels of the Masai and US populations at various ages.

ATHEROSCLEROTIC INDEX

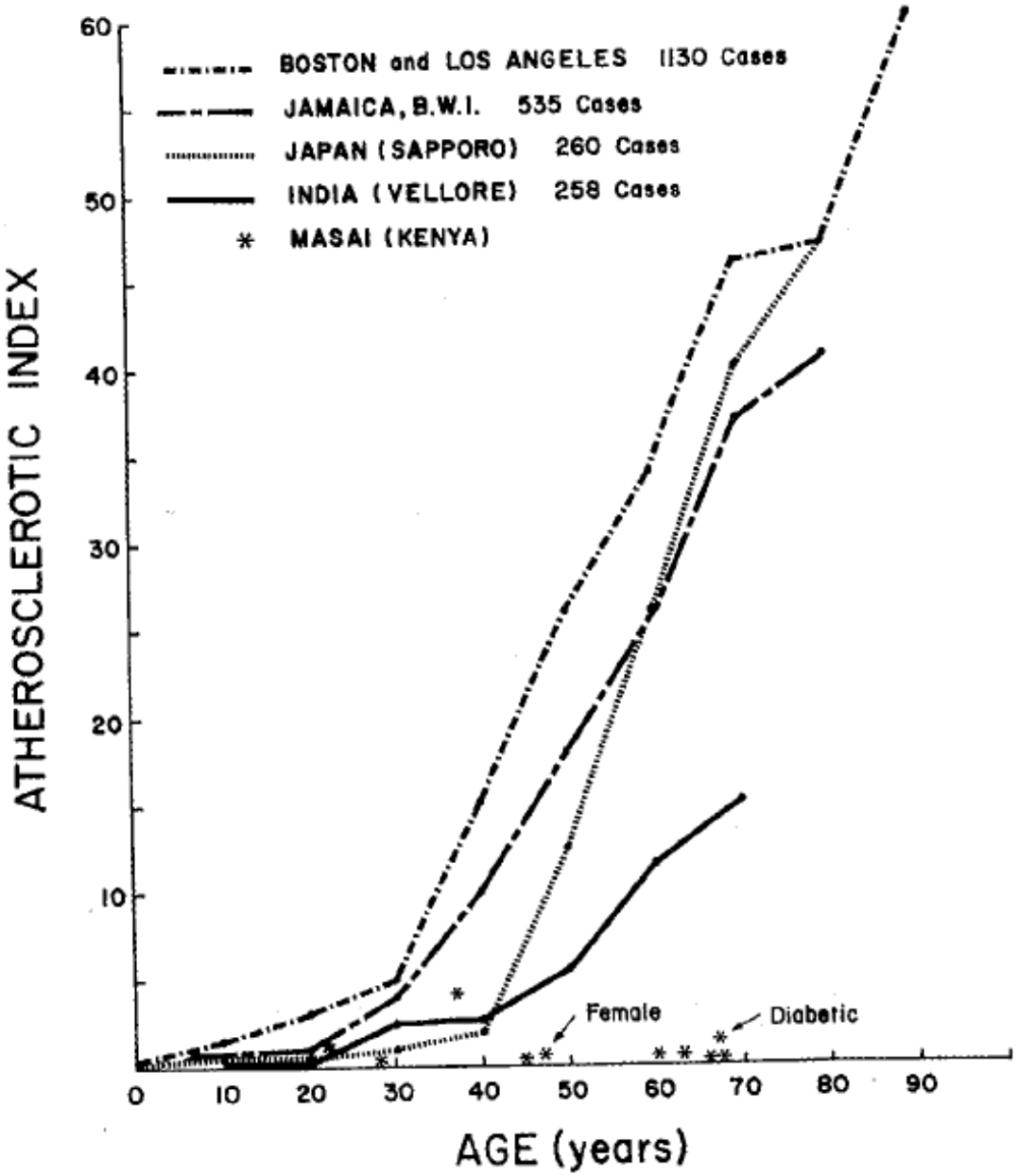
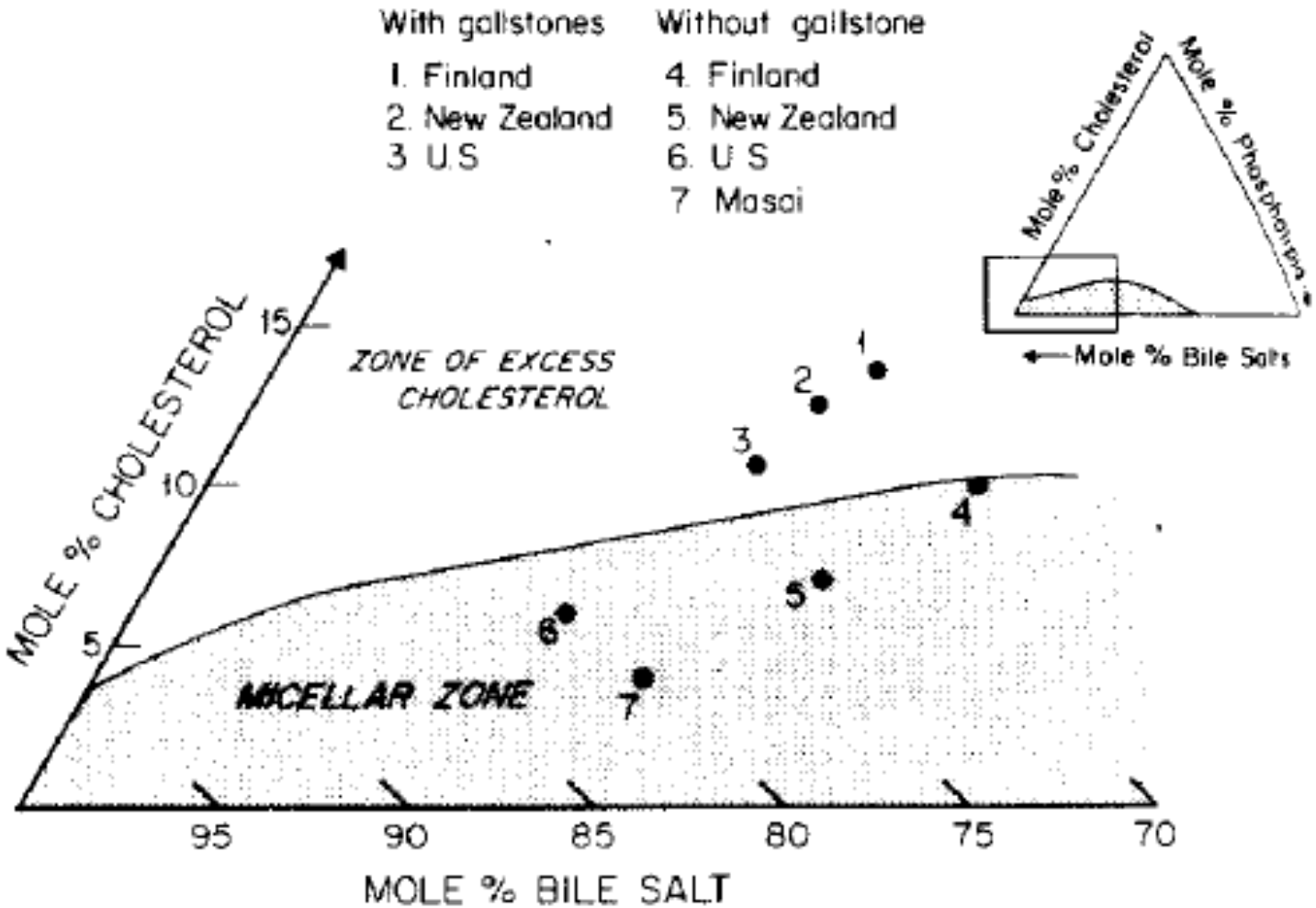


Fig 3.—Comparison of atherosclerotic indices of ten Masai aortas with studies by Gore and Tejada[10] on aortas from Boston and Los Angeles areas and on aortas from Jamaicans, Japanese, and Asian Indians.

Absence of Cholesterol Gallstones

Figure 2. Triangular Co-ordinate Plotting of Three Majo Gallbladder-Bile Components among Different Ethni Groups.



12 Control and 11 Case. 8 week + 6 month follow-up

Base diet = corn syrup solids, vegetable fat, corn, beans, sugar, Mazola

Experimental group fed 2 gm crystalline Cholesterol/day

Both groups fed 1 micro-Curie Cholesterol-4-^{14}C as a marker.

Blood serum and fecal sterols determined weekly for 8 weeks.

6 month follow up: rates of absorption, synthesis and turnover, size and turnover time of body cholesterol pool

Table 2. Various Aspects of Cholesterol Metabolism in the Control and Experimental Masai Groups.*

Group	No. of Subjects	Rate of Synthesis	Rate of Absorption	Turnover Rate	Turnover Time	Pool Size
		g/day	*g/day*	*g/day*	*days*	*g*
Control	12	1.37±0.15	–	1.37±0.15	60± 9	82.4±15
Experimental	11	0.65±0.18†	0.65±0.12†	1.30±0.19	63±12	81.8±19

*Mean ±SD.

†Significant difference from control

Study Conclusion in 1980

Taylor, B.C., K.J. Ho, Studies on the Masai. Amer. J. of Clin. Nutr., 1971. 24: 1291-1293.

This leads us to believe, but without direct proof, that the Masai have some basically different genetic traits that result in their having superior biologic mechanisms for protection from hypercholesteremia and from many pathogenic organisms.

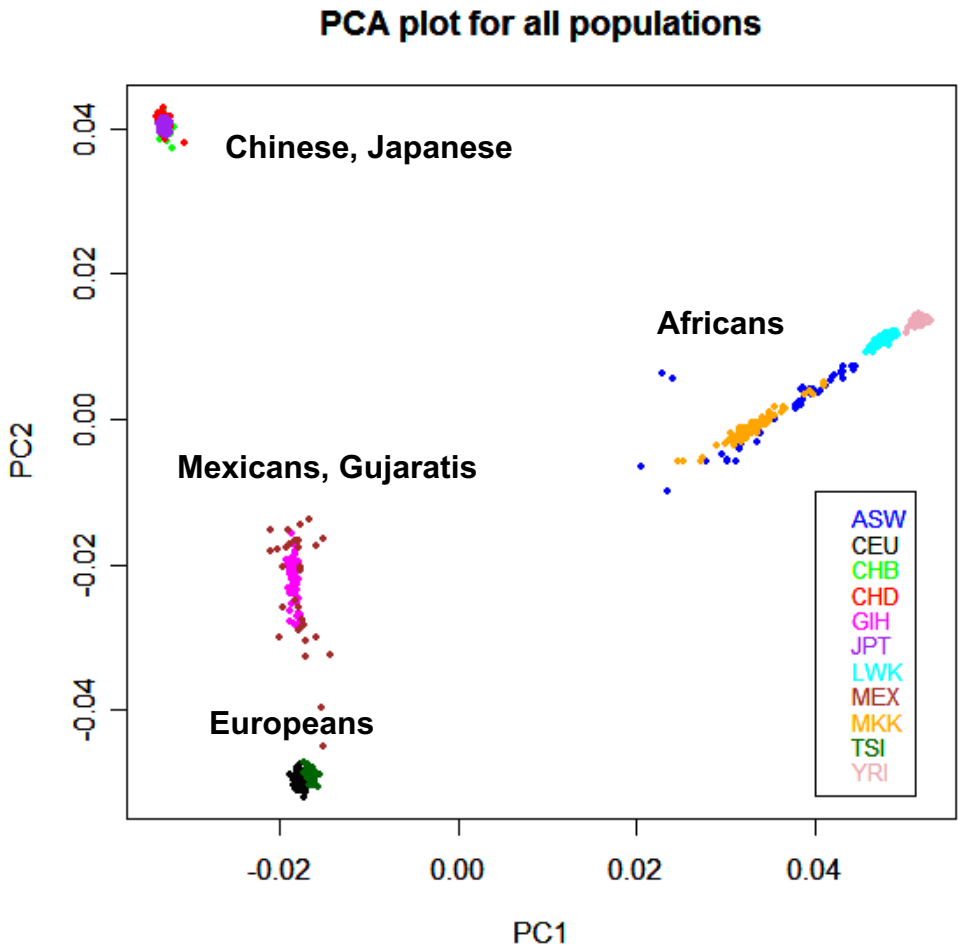
Possible Explanations

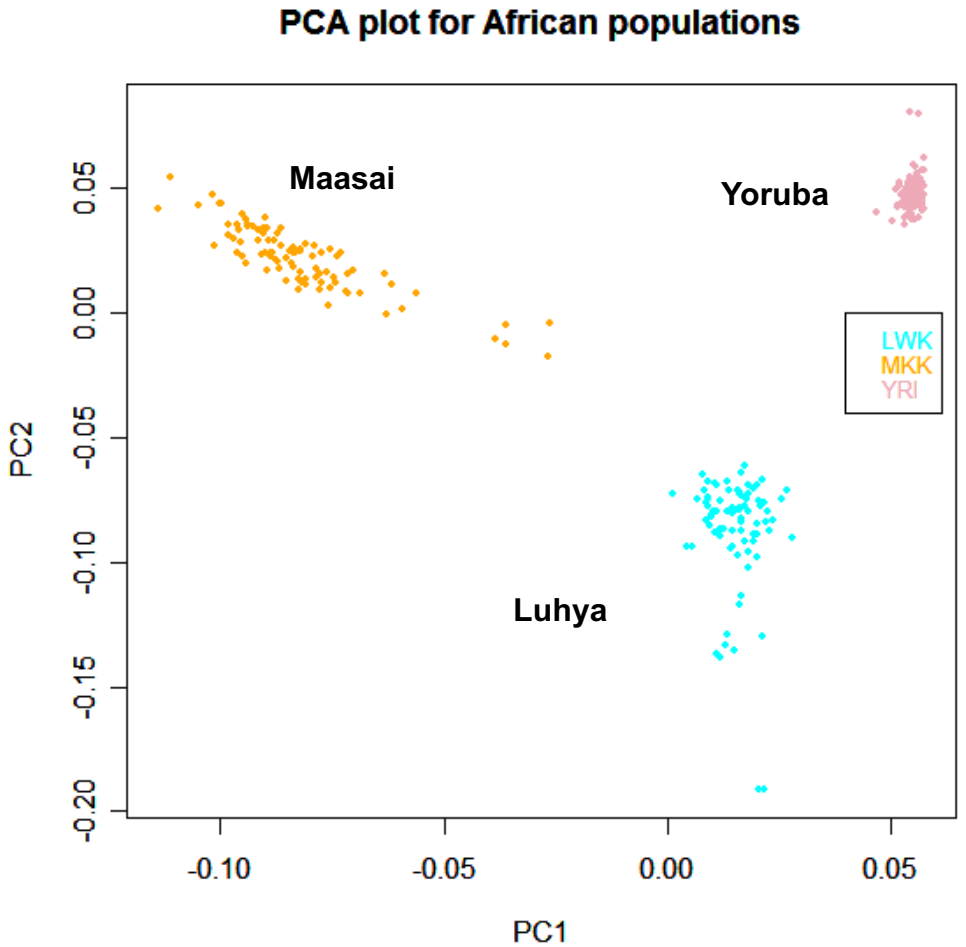
- **Hypo-Cholesterolemic factor in Milk**
- **Physical fitness and freedom from emotional stress**
- **Saponins in bitter plants/herbs (eaten in soups).**
- **Altered Genetics from Diet Induced Selection**
- **Unusual Social Customs**

HapMaP3 Project

- **CEU – Utah Residents (N or W Europe)**
- **TSI – Italians from Tuscany**
- **CHB – Han Chinese from Beijing**
- **CHD – Chinese in Metropolitan Denver**
- **JPT – Japanese from Tokyo**
- **GIH – Asian Indian Gujaratis from Houston**
- **MEX – Mexicans from Los Angeles**
- **ASW – African Americans from SW USA**
- **LWK – Luhya Tribe from Kenya**
- **YRI – Yoruba from Nigeria**
- **MKK – Maasai from Kenya**

Population Structure of HapMap Data

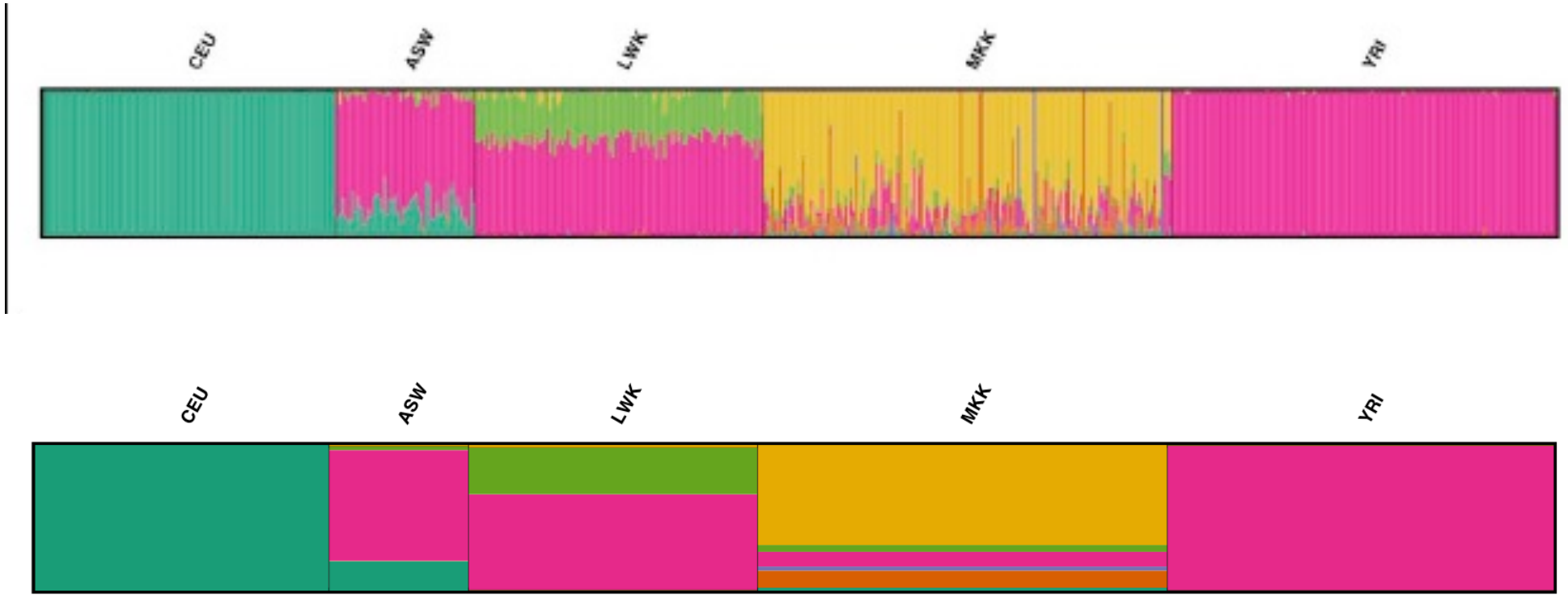




The Maasai (MKK) are as different from Luhya (LWK) as from Yoruba (YRI) even though they live in the same region as LWK and are separated from the YRI by the African Continent.

Population Admixture
Results from STRUCTURE

- http://pritch.bsd.uchicago.edu/structure.html
- Max. Likelihood assignment of pop. structure/admixture



We used three strategies to detect natural selection in genomes

- Allele Frequency Spectrum (AFS): Compare frequency of alleles in MKK vs reference population (LWK). Use distribution of neutral SNPs as control.

- Fst: Compares genotype heterozygocities in MKK vs LWK. Exact permutation test + neutral loci to get p-values

- EHH/iHS and XP-EHH: Identifies reduced haplotype diversity around selected loci (within a population and relative to a reference population)

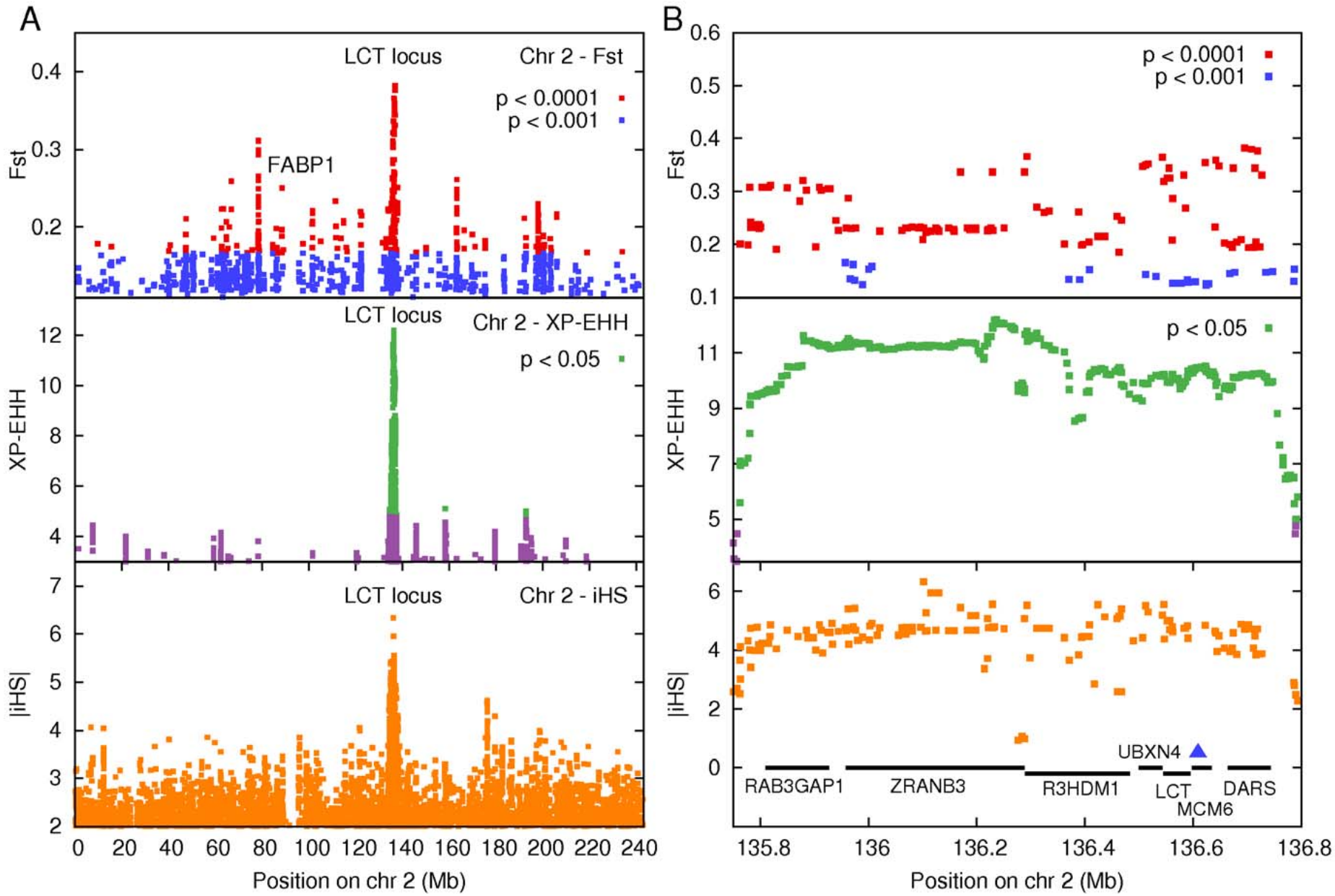

A
LCT locus
Chr 2 - Fst
p < 0.0001
p < 0.001
FABP1
Fst
LCT locus
Chr 2 - XP-EHH
p < 0.05
XP-EHH
LCT locus
Chr 2 - iHS
|iHS|
Position on chr 2 (Mb)
B
p < 0.0001
p < 0.001
Fst
p < 0.05
XP-EHH
|iHS|
UBXN4
RAB3GAP1
ZRANB3
R3HDM1
LCT
MCM6
DARS
Position on chr 2 (Mb)

Table 5. Concordant genomic regions identified by at least two of three metrics as candidates for selection in MKK.

Chr	Genomic Extent	Significant by (Method)	Genes in Region	Number of SNPs identified by each Method
2	135058615–136726567	Fst, iHS, XP-EHH	MGAT5, TMEM163, ACMSD, CCNT2, YSK4, RAB3GAP1, ZRANB3, R3HDM1, UBXN4, LCT, MCM6, DARS	Fst: 123, iHS: 545, XP-EHH: 572
3	191943578–191989642	Fst, XP-EHH	FGF12	Fst:13, XP-EHH: 10
5	14747247–14750823	Fst, iHS, XP-EHH	ANKH	Fst: 4, iHS: 23, XP-EHH: 25
5	115885574–115885672	Fst,XP-EHH	SEMA6A	Fst: 2, XP-EHH: 21
7	99053816–99314986	Fst, iHS	ZNF789, CPSF4, ATP5J2, FAM200A, ZNF655, ZNF498, CYP3A7, ZKSCAN5, CYP3A5	Fst: 17, iHS: 24
17	75427551–75428021	Fst, XP-EHH	SEPT9	Fst: 3, XP-EHH: 2
18	66714832–66724690	Fst, iHS, XP-EHH	CCDC102B	Fst: 4, iHS: 33, XP-EHH: 12

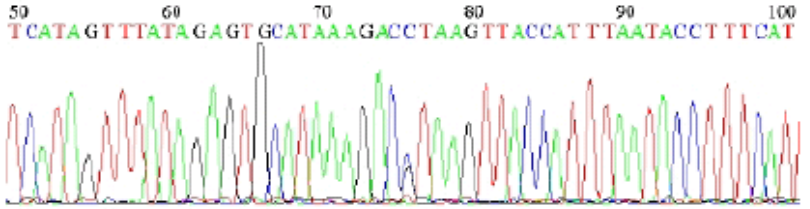
Genomic regions identified as genome-wide significant by at least two of the three methods - Fst, iHS and XP-EHH.
doi:10.1371/journal.pone.0044751.t005

Most significant Non-Syn SNP in MKK

- Chr 2: Threonine>Alanine substitution at rs2241883 in exon 3 of FABP1: a fatty acid binding protein expressed in liver.
- Protective allele frequency: 0.45 in MKK, 0.095 in LWK
- GWAS results on FABP1 SNP:
  - 826 Northern Germans: Associated with lower levels of plasma triglycerides and LDL
  - 623 French Canadians: Protective against high ApoB levels with high fat and saturated fat diets

Sanger Sequencing of LCT locus

6 MKK DNA samples from Coriell Inc.



SNPs
rs4988233
rs41525747
rs4988235
rs41380347
rs182549

	rs4988233 G/C - 14010	rs41380347 T/G – 13915	rs4988235 C/T - 13910	rs41525747 C/G - 13907	rs182549 G/A - 22018
NA21367	C	T	C	C	G
NA21379	C/G	T	C	C	G
NA21454	C/G	T	C	C	G
NA21519	C	T	C	C	G
NA21522	G	T	C	C	G
NA21650	C/G	T	C	C	G

rs4988233 segregating in Maasai at a frequency of 0.58+/- 0.14

Ketogenic Diets and Hyperlipidemia

- Ketogenic diets, rich in saturated fats and cholesterol are used to control epileptic seizures in children < age 12-15
- Complications: hypertriglyceridemia, hypercholesterolemia, low HDL levels, osteopenia, renal stones, and cardiomyopathy
- Without protection, a high fat high cholesterol diet induces strong negative selection in naïve populations

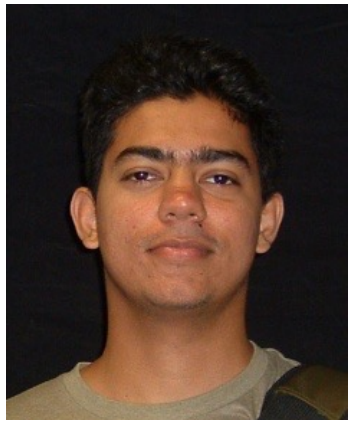
Maasai Social Customs

- Maasai practice open marriage
- Older men often marry nulliparous women
- Gerontocratic polygyny leads to many widows
- Widows rarely remarry - choose their own sex partners without social stigma
- These customs may select for protection against diseases of the elderly by allowing older men to contribute to the gene pool

Wagh K, Bhatia A, *Lactase persistence and lipid pathway selection in the Maasai*, PLoS ONE 2012, 7(9): e44751.

Collaborators

Kshitij Wagh



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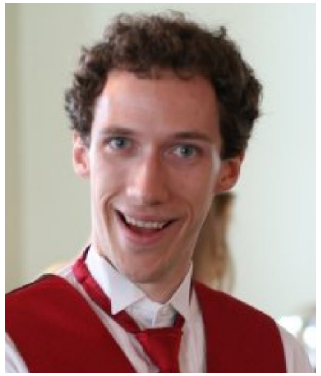

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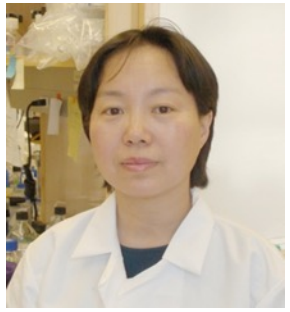
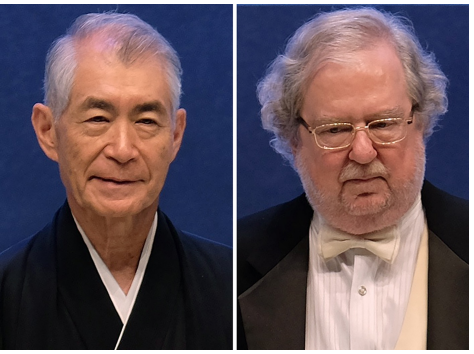


Ming Yao

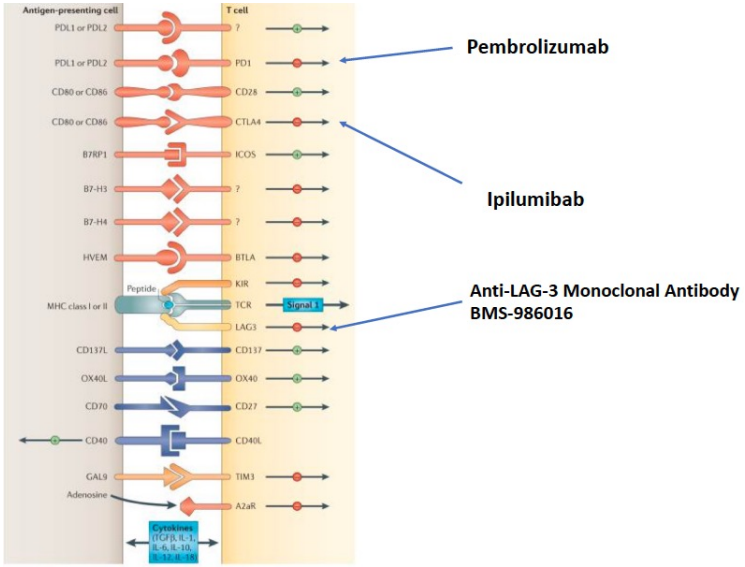
2018 Medicine Nobel Prize: T. Honjo and J. P. Allison for discovery of drugs targeting immune checkpoint pathways.

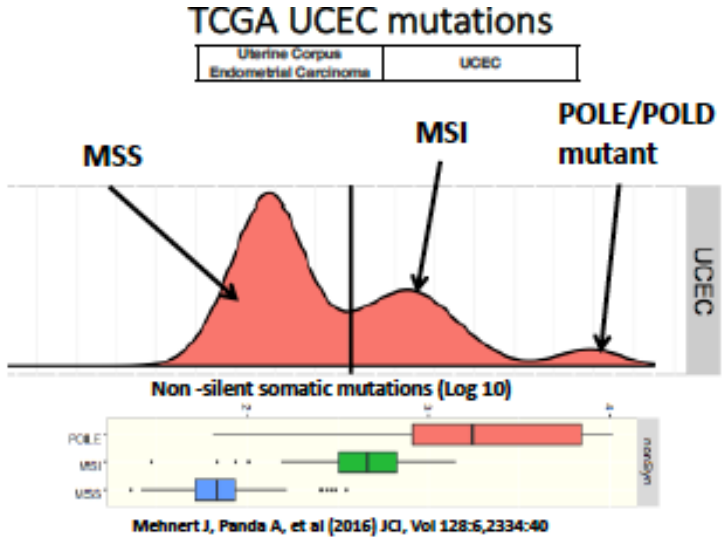


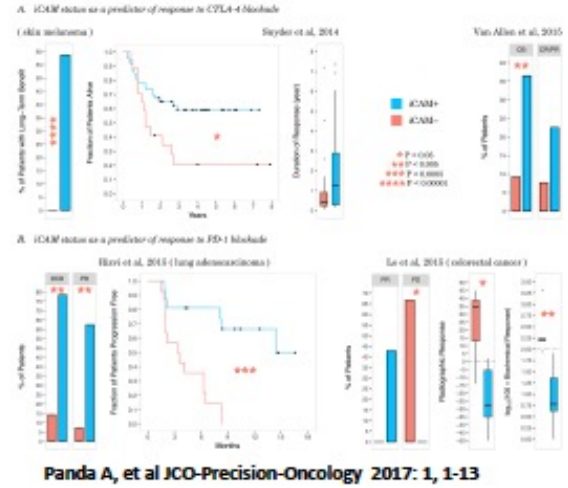
Immune Checkpoint Therapy

Found many other biomarkers in other cancers
Clinically useful to stratify patients into response classes
Our work is used in the clinic to stratify patients
It has initiated several clinical trials.

Anshuman Panda







Panda A, et al JCO-Precision-Oncology 2017: 1, 1-13

- JCI Insight. 2018 23;3(16); JCI Insight. 2020 5(11):e137569; Oncoimmunology, 2020, 9:1, 1756116;
- JCO-PO 2017: 1, 1-13; J Natl. Cancer Inst. 2018, 1;110(3):316; J. Clin. Invest. 2016;126(6):2334.

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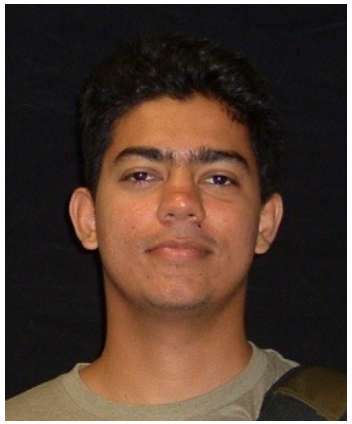
Anil Betigeri, MD
Strand Genomics

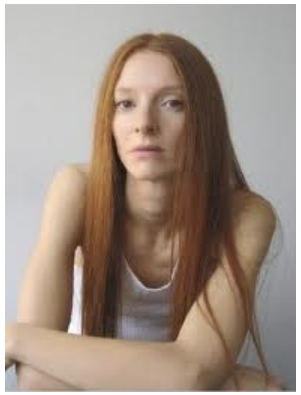
Kshitij Wagh



Aatish Bhatia

Erhan Bilal

Anupama Yadav



Sunniva Bjorklund

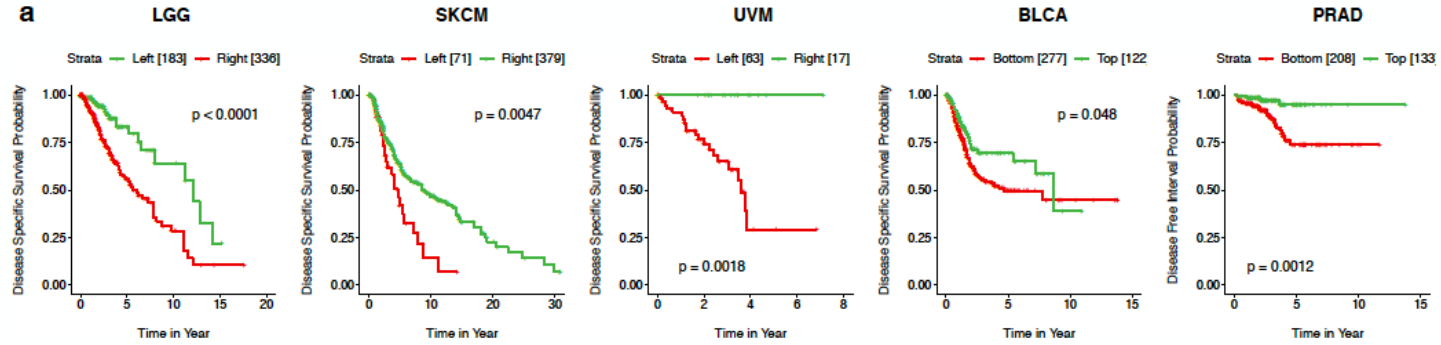
Gabriela Alexe

Michael Seiler

Anupama Reddy

Anshuman Panda

Aguirre A. de Cubas Vanderbilt, VICC

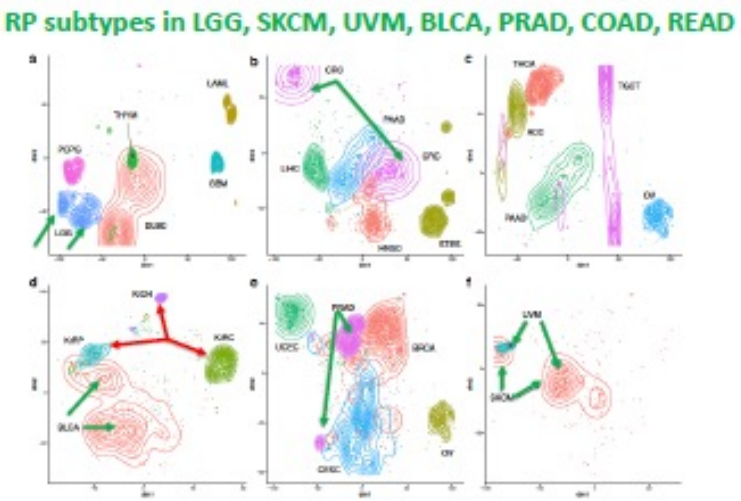


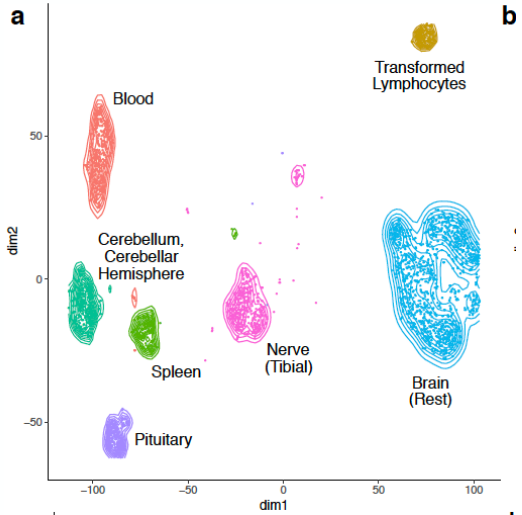
The 2009 Chemistry Nobel Prize awarded for the Structure of the Ribosome. WE SHOWED THAT IN FACT:

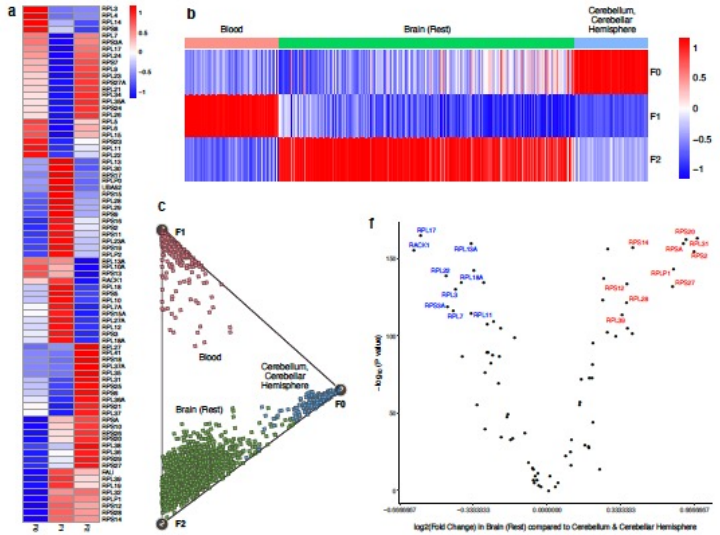
- Ribosome Protein (RP) composition is tissue and development stage specific.
- CRISPR knockout of RP genes does not affect cell division or cell growth..
- Many RP genes are deleted in cancers with distinct rates of survival and recurrence.
- Our results suggest novel treatments of cancer targeting ribosomes, similar to antibiotics.

Ribosome Biology: Anshuman Panda and Anupama Yadav (Harvard)

Panda A, Yadav A, et al, NAR (2020), 48:13, 7079–98







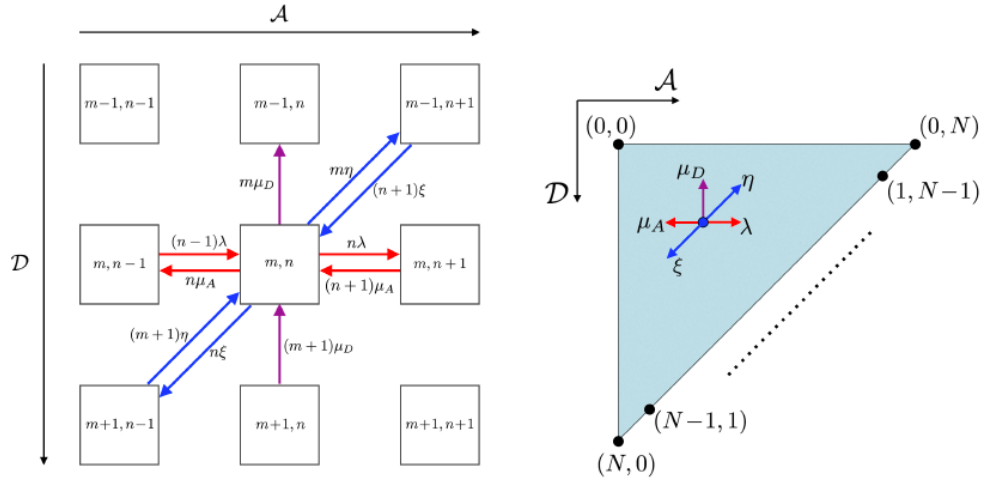
Optimizing chemotherapy duration/dosage

- Improving Chemotherapy Regimens
  - Santana L et al, J. of Theor. Biology 480 (2019) 175.

$$\mathcal{L}_b\left[p_{rec}(\infty)\,T^{(1)}_{rec}(\vec{z}_0)\right] = -p_{rec}(\infty)$$

$$\mathcal{L}_b = -\left[\eta z_0 - \xi(w_0 - z_0)\right]\frac{\partial}{\partial z_0} + (\lambda - \mu_A)(w_0 - z_0)\frac{\partial}{\partial w_0} + \\ + \frac{1}{2N}\left[\eta z_0 + \xi(w_0 - z_0)\right]\frac{\partial^2}{\partial z_0^2} + \frac{1}{2N}(\lambda + \mu_A)(w_0 - z_0)\frac{\partial^2}{\partial w_0^2}$$

$$p_{rec}(\infty) = \frac{1 - e^{-2RN_0}}{1 - e^{-2RN}}, \qquad R \equiv \frac{1 - \mu_A/\lambda}{1 + \mu_A/\lambda}.$$



(a) Possible transitions on the lattice of states (m,n), where m is the number of dormant ($\mathcal{D}$) tumor foci and n is the number of active ($\mathcal{A}$) foci.

(b) Boundaries of the state space $\mathcal{D}\otimes\mathcal{A}$. The boundary conditions are absorbing at the cure state $(0,0)$ and also at the recurrence line $m+n=N$.

Figure 1: Structure of the Fock-like state space of the QBD model for tumor recurrence.

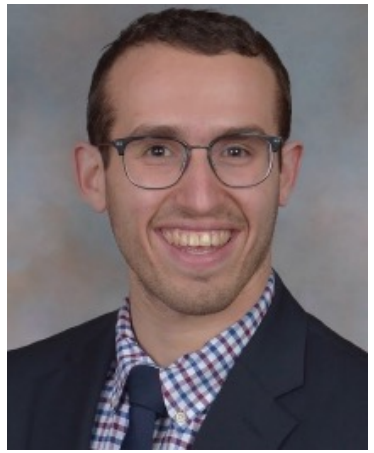
Leonardo Santana
Rutgers, Physics

We have developed a detailed mathematical model to study cancer recurrence, including the effects of cell cycle dynamics and chemotherapy. The model is exactly solved in the limit of large tumor size to predict the probability of recurrence p_{rec}. Using recurrence data for ovarian cancer, we use the model to identify optimum chemotherapy duration and dosage levels for adjuvant (post surgery and radiation) treatment.

Covid Epidemiology

Raines KS, Doniach S, Bhanot G. The transmission of SARS-CoV-2 is likely comodulated by temperature and by relative humidity. PLoS One. 2021 Jul 29;16(7)

Schulman A, Bhanot G, Using Postal Change-of-Address Data to Predict Second Waves in Infections near Pandemic Epicenters (2022) Epidemiology and Infection, 1-23.



Universal Scaling Law for Pandemics: Predictions for Covid-19

Mingyang Ma (Physics)

Mary Zsolway (Math)

Ayush Tarafder (MBB)

Professor D. Foerster, University of Bordeaux

Dr. Sayali Bhatkar (Post-doc TIFR India)


Once upon a time we worried about
Chickens and FLU

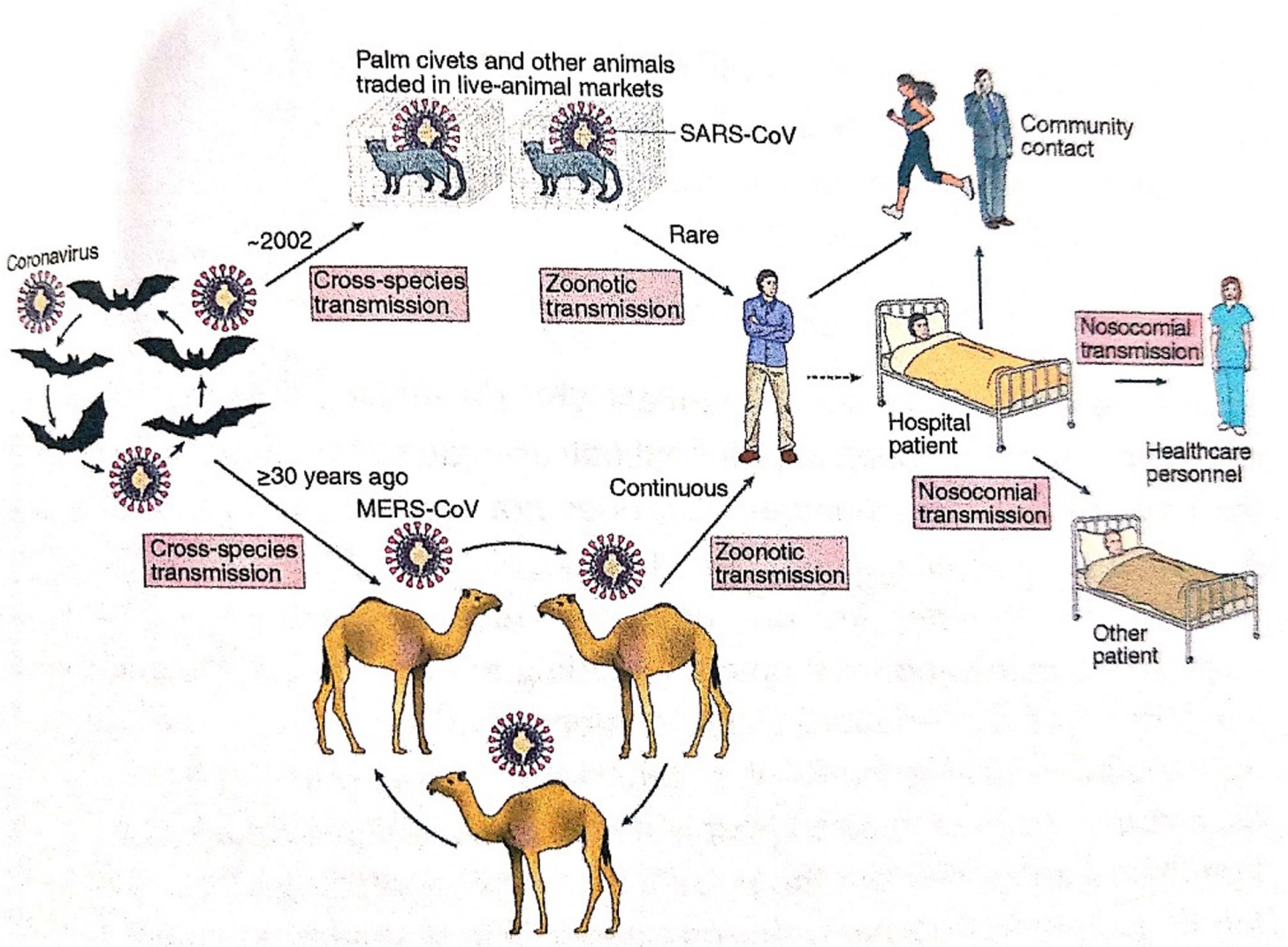
The looming threat was the H5N1 Flu Virus

←RESERVOIR

Mallards, Pintails

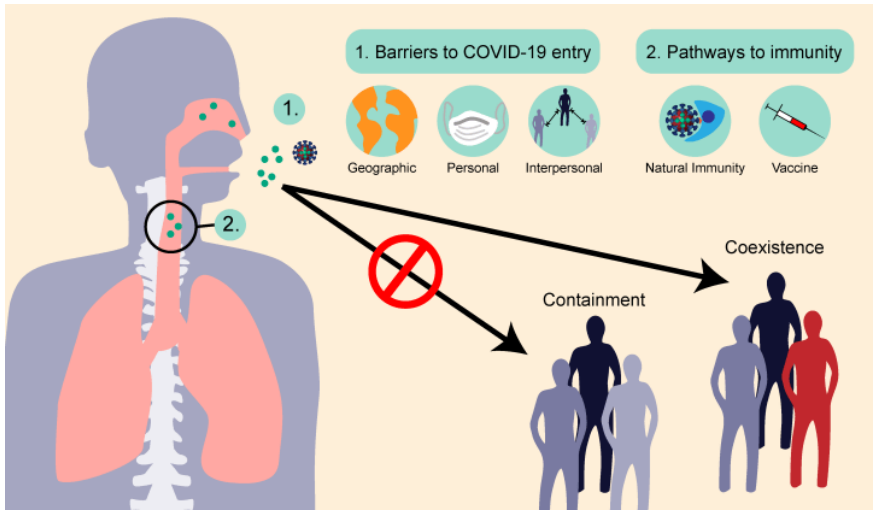
VECTORS: Poultry, Swans, Geese

But there was another looming threat- SARS-CoV



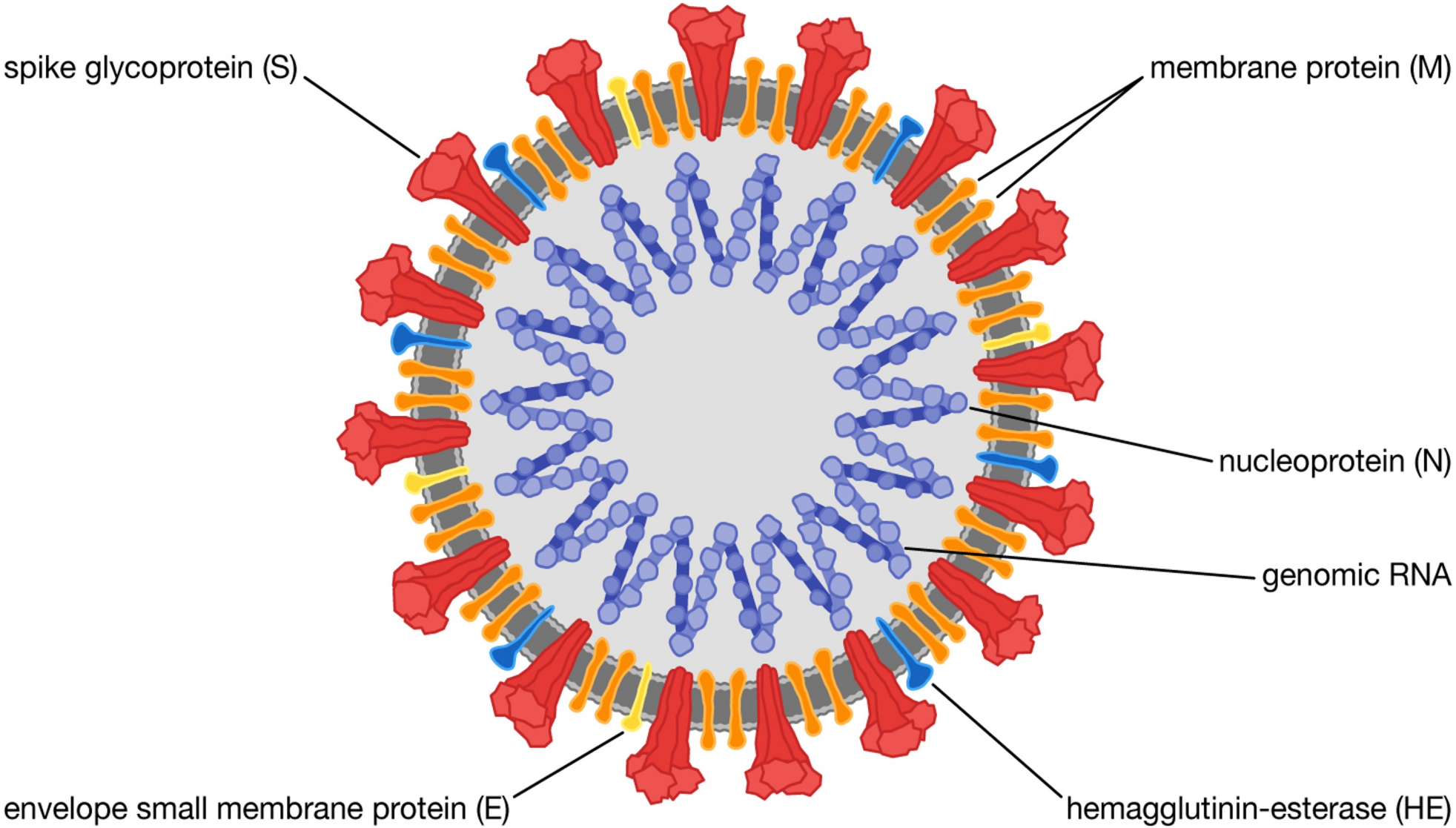
- SARS-CoV: Bats → Palm civets → Humans
- MERS-CoV: Bats → Dromedaries → Humans
- Bat → Human (no intermediate species) possible
- SARS-CoV started in 2003 in Guangdong province, China,

Sars-Cov evolved to Sars-Cov-2 in 2019

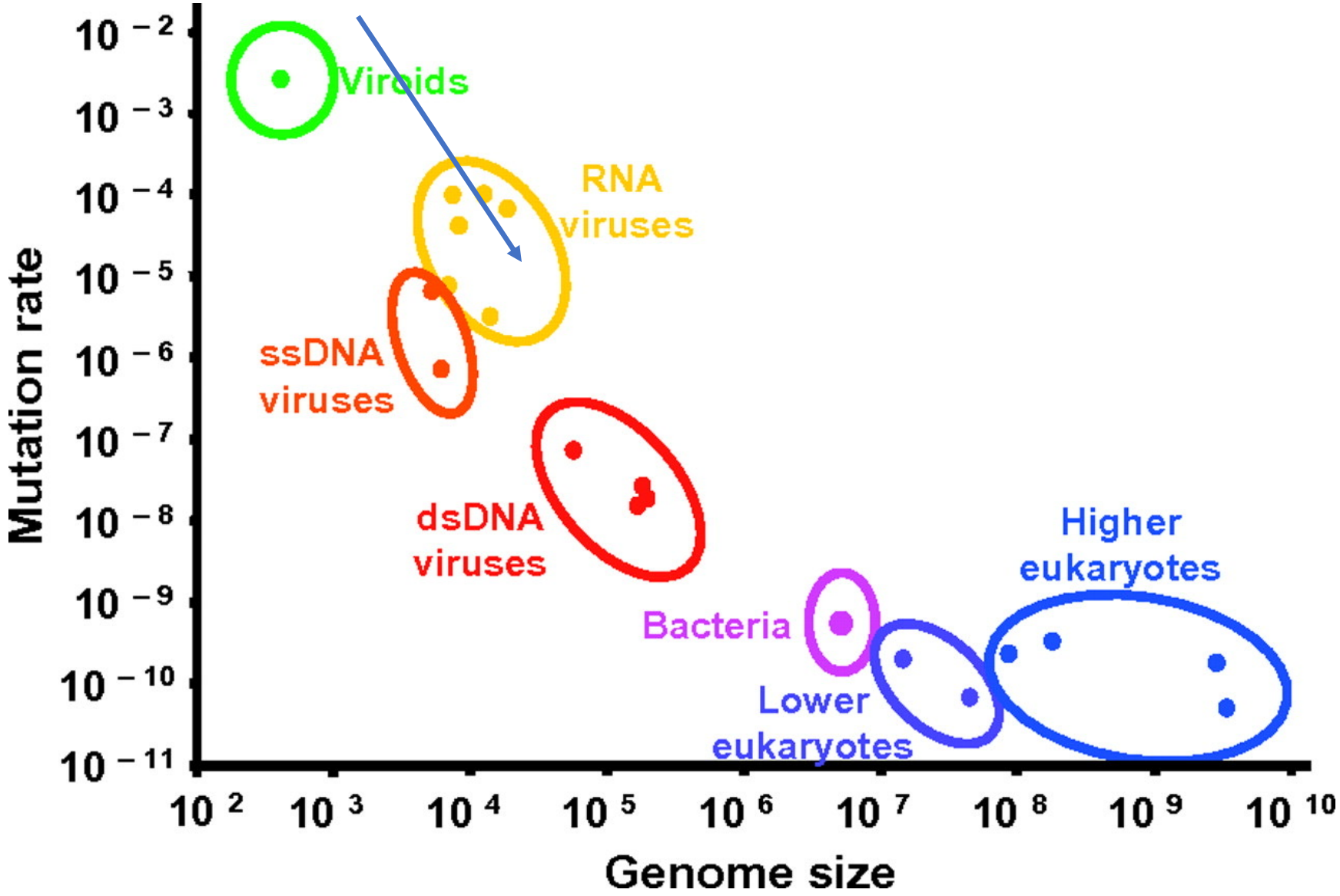


- Initial cases from Hunan Seafood Market in Wuhan, China
- 96% of SARS-CoV-2 genome identical to a virus RaTG13 in horseshoe bat:
- 80% of SARS-CoV-2 genome identical to SARS-CoV
- Spike protein similarity of SARS-CoV and SARS-CoV-2 suggested a recombination event, allowing SARS-CoV-2 to infect humans

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)



SARS-COV-2 is a positive-sense single-stranded RNA virus
~30 Kilobases, 80% of mutations in Spike Protein



The SARS-Cov2/Covid-19 pandemic begins

- Cases detected in China, lockdown in Wuhan in late 2019
- US personnel evacuated and the virus reaches California, New York and Washington States in Jan-March 2020.
- Cases worldwide, virus spreads – death rate ~ 3-20%
- US reacts badly – political shenanigans, scientists ignored
- Some states impose lockdowns/quarantines, mask mandates
- RNA Vaccine Research starts – Moderna and Pfizer/BioNTech in front
- Lots of data collected, testing ramping up, best data from Europe

Standard SIR Model for Pandemics

- $S(t), I(t), R(t) =$ Number Susceptible, Infected, Removed at time t.
- $S(t) + I(t) + R(t) = \aleph$ = total size of pool
- $\frac{dS}{dt} = -(\frac{\alpha}{\aleph})SI$
- $\frac{dI}{dt} = (\frac{\alpha}{\aleph})SI - \gamma I$
- $\propto =$ infection rate per unit time if S meets I
- $\gamma = \frac{1}{L_0} =$ Rate of “removal” (cured or dead)
- $L_0 =$ time when I can infect S

Extended SIR (includes unidentified infectives)

$$\frac{dS}{dt} = -\left(\frac{\alpha}{N}\right)SI$$

$$\frac{dI}{dt} = \frac{dI_1}{dt} + \frac{dI_0}{dt} = \left(\frac{\alpha}{N}\right)SI - \gamma_{eff}I = \left(\frac{\alpha}{N}\right)SI - (\omega\gamma_1 + (1-\omega)\gamma_0)\, I$$

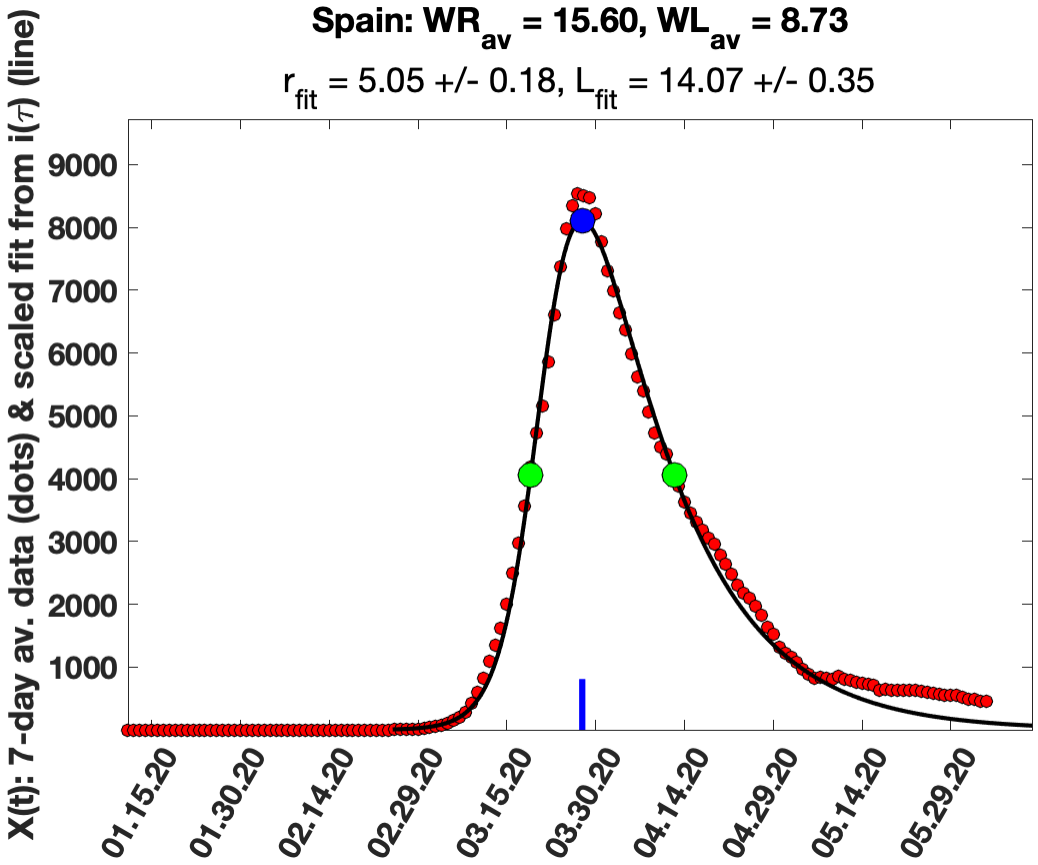
$$\frac{dR}{dt} = \frac{dR_1}{dt} + \frac{dR_0}{dt} = (\omega\gamma_1 + (1-\omega)\gamma_0)\, I = \gamma_{eff}I$$

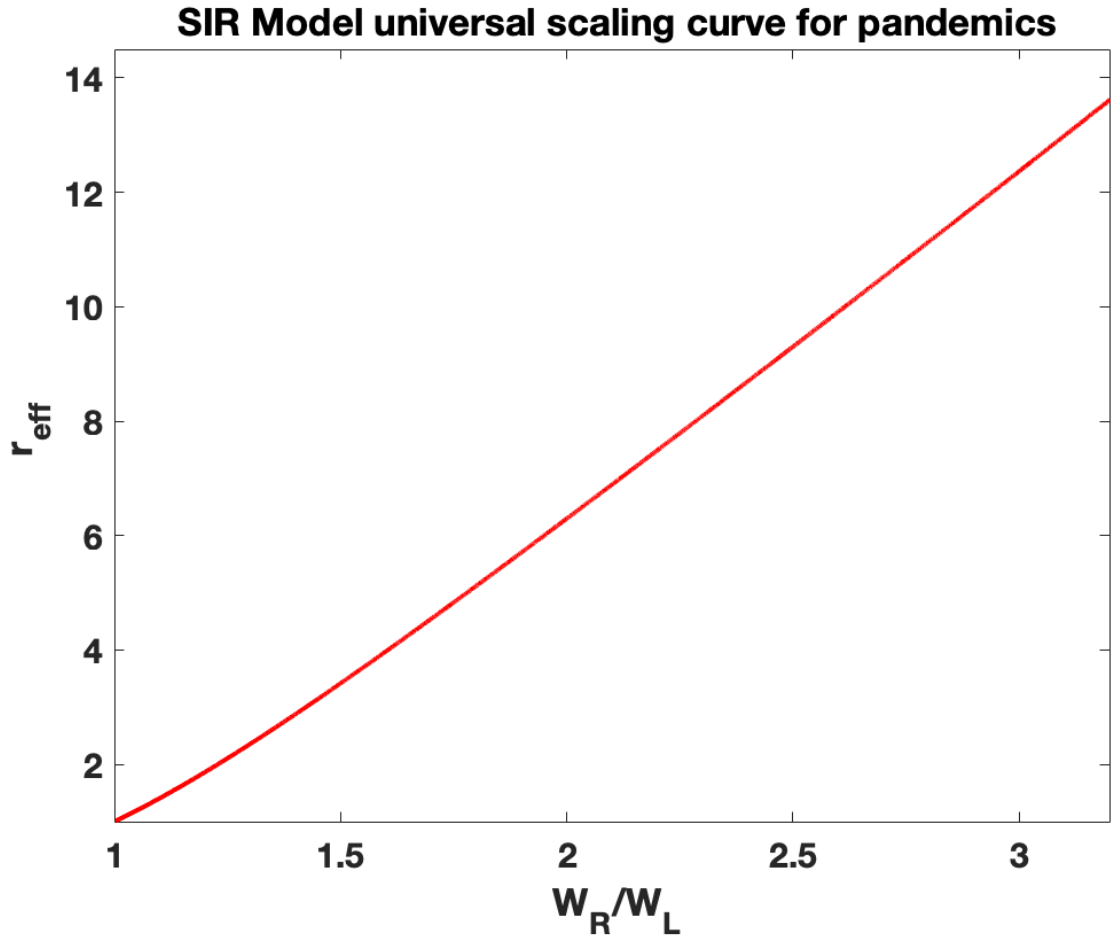
X(t) = daily recorded cases

$X(t) = dR_1/dt = \omega\gamma_1 I(t)$

So X(t) and I(t) have the same peak location and peak halfwidth

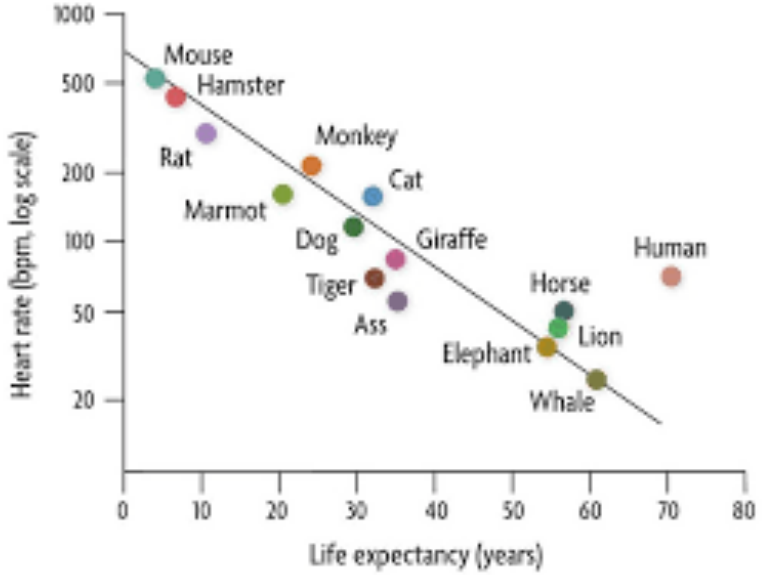
r_{eff} = Pandemic R-parameter. Must be > 1 to have a pandemic
It controls the total fraction of people infected





Possible projects

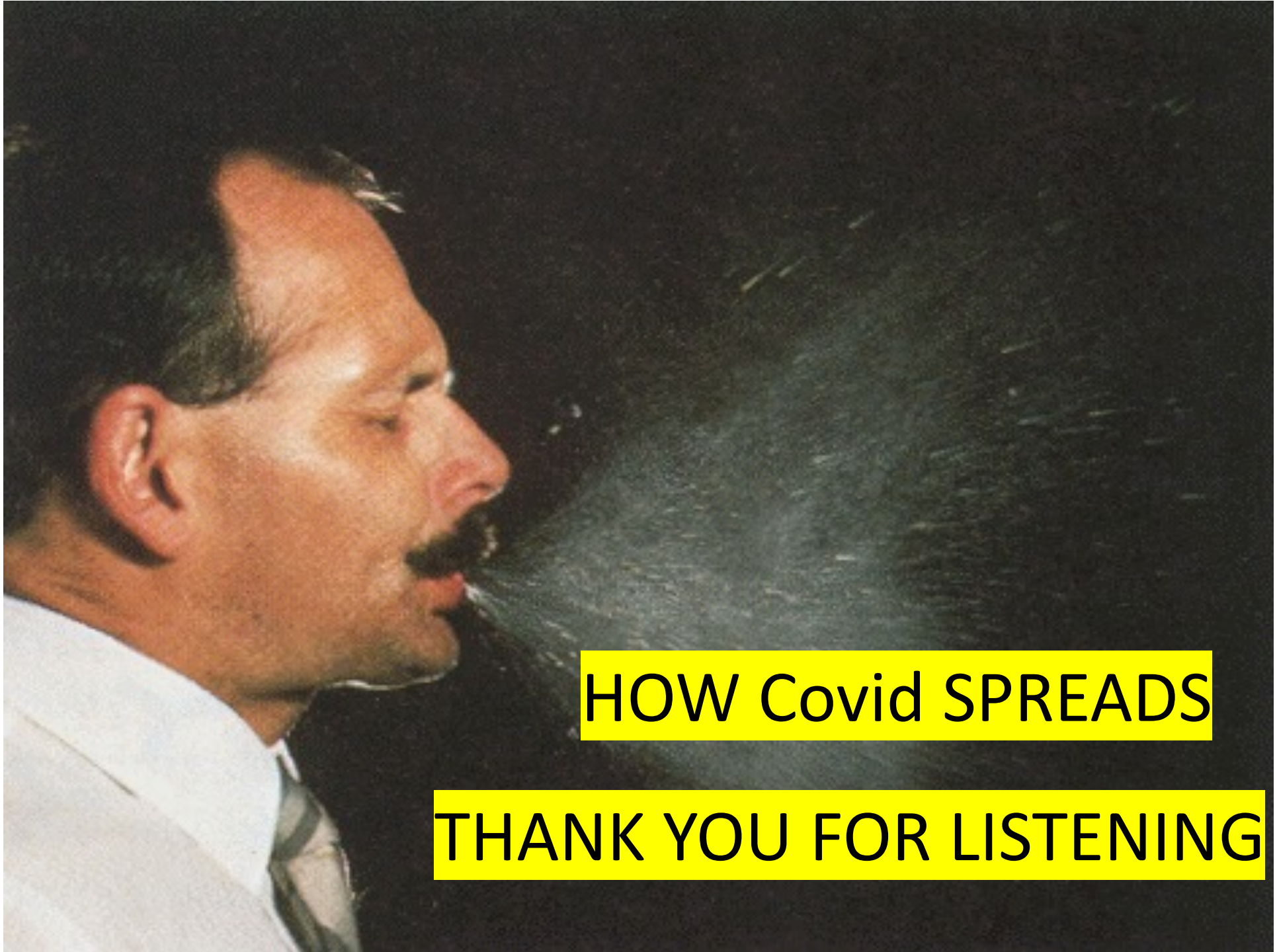
- Epidemiology:
  - Is the Covid-19 virus evolving to lower virulence and higher infectivity (as all viruses do)?
  - Using sequencing data and statistical mechanics ideas, is it possible to predict emerging strains?
  - Can the novel method based on peak widths be applied to the FLU virus?
- New methods to analyze long-read sequencing data from tumors
- Life span and heart rate [within species]



Live bird market – Giza, Pyramids Road


Market is ready
for customers


Fresh poultry must be kept fresh


HOW Covid SPREADS
THANK YOU FOR LISTENING