

Introduction to Bioengineering  
BIOE/ENGR.80  
Stanford University

Spring 2020 Class Slides

Day 6  
17 April 2020

These slides are made freely available to the fullest extent possible. Any copyrighted images used herein are used in good faith subject to the fair use exception for education. Please contact [undy@stanford.edu](mailto:undy@stanford.edu) directly re: any copyright concerns.

# *Political*

“... the set of activities that are associated with the governance of a country, state or area. It involves making decisions that apply to groups of members and achieving and exercising positions of governance—organized control over a human community.”

# *Health*

“a condition in which someone or something is thriving or doing well.”

*Bioengineers will...*

Cure diseases.

Save environments.

Understand & fix broken  
biological systems.

Design & build useful organisms.

Make doing the above easier.



Il retourne chez les Egaux.  
*Voyez la Note 13. p. 259.*

## DISCOURS

SUR L'ORIGINE ET LES FONDEMENS  
DE L'INÉGALITÉ PARMI LES HOMMES.

Par JEAN JAQUES ROUSSEAU  
CITOTEN DE GENÈVE.

Non in depravatis, sed in his quæ bene secundum  
naturam se habent, considerandum est quid sit na-  
turale. ARISTOT. Politic. L. 2.



A AMSTERDAM,  
Chez MARC MICHEL REY.

16° R M D C C L V.

6917

"The two fundamental principles of Rousseau's natural man are his natural, non-destructive love of self (amour de soi même), and pity/compassion for the suffering of others."

*Bioengineers will inevitably or accidentally...*

Create diseases.

Destroy environments.

Misunderstand & abuse natural  
biology & ecology.

Design & build harmful organisms.

Make doing the above easier.



“Hereby it is manifest that during the time men live without a common Power to keep them all in awe, they are in that condition which is called War; and such a war as is of every man against every man.

[...]

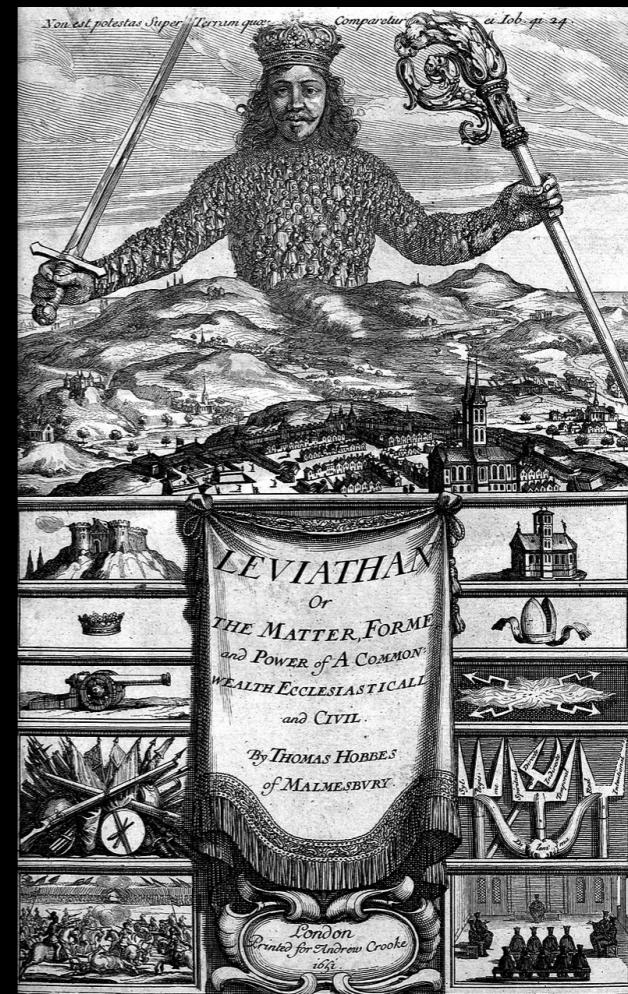
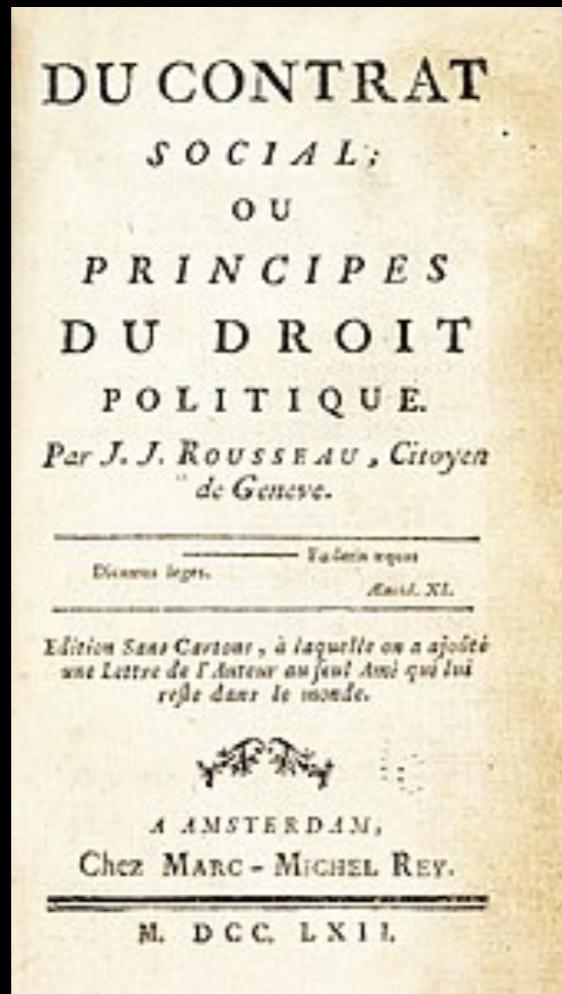
In such condition there is no place for Industry, because the fruit thereof is uncertain: and consequently no Culture of the Earth; no Navigation, nor use of the commodities that may be imported by Sea; no commodious Building; no Instruments of moving and removing such things as require much force; no Knowledge of the face of the Earth; no account of Time; no Arts; no Letters; no Society; and which is worst of all, continual Fear, and danger of violent death;

And the life of man solitary, poor, nasty, brutish, and short.”

— Hobbes, Leviathan

# Social Contract

“a theory or model that originated during the Age of Enlightenment and usually concerns the legitimacy of the authority of the state over the individual. Social contract arguments typically posit that individuals have consented, either explicitly or tacitly, to surrender some of their freedoms and submit to the authority (of the ruler, or to the decision of a majority) in exchange for protection of their remaining rights or maintenance of the social order.”



**“Third, the U.S needs Community & Citizenship. The U.S. must enable everyone to engage with this (biological) technology and its many uses to foster the best ideas and to make sure they are genuinely in the public interest.**

**Everyone in the country should be trained to be literate in biotechnology and the U.S. should be building the diverse training programs needed to grow the interdisciplinary bioeconomy workforce of the future.”**

**— Bioengineer Dr. Megan Palmer  
testifying before US Senate March  
2020**



# What capacities should be available to all citizens?

within limits either small or overcharged, and steeped in the vices which that situation generates. A government adapted to such men would be one thing; but a very different one that for the Man of these states. Here every one may have land to labor for himself if he chuses; or, preferring the exercise of any other industry, may exact for it such compensation as not only to afford a comfortable subsistence, but wherewith to provide for a cessation from labor in old age. Every one, by his property, or by his satisfactory situation, is interested in the support of law and order. And such men may safely and advantageously reserve to themselves a wholesome controul over their public affairs, and a degree of freedom, which in the hands of the Canaille of the cities of Europe, would be instantly perverted to the demolition and destruction of every thing public and private. The history of the last 25. years of France, and of the last 40. years in America, nay of it's last 200. years, proves the truth of both parts of this observation.

Proprietary  
Land  
Economic  
Participation

But even in Europe a change has sensibly taken place in the mind of Man. Science had liberated the ideas of those who read and reflect, and the American example had kindled feelings of right in the people. An insurrection has consequently

**Jefferson to  
Adams re:  
“natural  
aristocracy”  
October 1813**

>DQ208311.1 Influenza A virus (A/Brevig Mission/1/1918(H1N1)) polymerase PA (PA) mRNA, complete cds  
ATGGAAAGACTTGTGCGACAATGCTCAATCCGATGATTGTCGAGCTTGC GGAAAAAGCAATGAAAGAGT  
ATGGAGAGGACCTGAAAATCGAAACAAACAAATTGCAGCAATATGCACTCACTTGGAAAGTATGCTTCAT  
GTATTCA GATTTCACTTCATCAATGAGCGAGGCGAATCAATAATCGTAGAATCTGGCGATCCAAATGCA  
CTCTTGAAGCACAGATTGAAATAATCGAGGGAAAGAGATCGCACAATGGCCTGGACGGTGGTAAACAGTA  
TTTGCAACACTAACGCGCGTCAAGAACGCGAACGTTGCGCGACATGCTGATGTTGACAGCGACATGATT  
CATTGAGATCT  
GAGAAGAC TCTCG  
ATGAGGGAG GCCT  
CTGGGATT GAACA  
ATGCGCAG TGTGG  
ATGGATTCC GAAT  
TGAACCTT GGTCC  
AAATTCCCT CCGC  
TATATGATG CGA  
AAAGGGAA GAAT  
GAGGAGAA AATA  
TGGCACCA TGA  
ACCGGAAT ATTCA  
AGCTGGAT AGGA  
ATTATTTCA TAC  
TGCCTTGC AGA  
ACTAAGGA AATG  
ACACCGAC AATG  
GGAGAAGT GCCC  
ATGTTCTTC GTT  
GCCTCCTT ACAT  
GACCAAAGAATTCTTGAGAACAAATCAGAAACATGGCCCATTGGAGAGTCCCCCAAAGGAGTGGAGGAA  
GGTTCCATTGGGAAGGTCTGCAGGACTTGGCAAAATCGGTATTCAACAGCTTGTATGCATCTCCAC  
AACTAGAAGGATTCTCAGCTGAATCAAGAAAATGCTTCTTCAGGCTCTAGGGACAACCTGGA  
ACCTGGAACCTTGATCTGGGGCTATGAAGCAATTGAGGAGTGCCTGATTAATGATCCCTGGGTT  
TTGCTTAATGCGTCTGGTTCAACTCCTCACACATGCACTGAGATAG



Stanford students were required to wear masks as the Spanish Flu of 1918 struck campus.

(Courtesy Stanford Special Collections and University Archives)

[NYTimes.com](#)[Go to a Section](#)

SEARCH

NYT Since 1981

[Editorials/Op-Ed Home](#)[Editorials](#)[Columnists](#)[Contributors](#)

## OP-ED CONTRIBUTORS

## Recipe for Destruction

By RAY KURZWEIL and BILL JOY

Published: October 17, 2005

AFTER a decade of painstaking research, federal and university scientists have reconstructed the 1918 influenza virus that killed 50 million people worldwide. Like the flu viruses now raising alarm bells in Asia, the 1918 virus was a bird flu that jumped directly to humans, the scientists reported. To shed light on how the virus evolved, the United States Department of Health and Human Services published the full genome of the 1918 influenza virus on the Internet in the GenBank database.



This is extremely foolish. The genome is essentially the design of a weapon of mass destruction. No responsible scientist would advocate publishing precise designs for an atomic bomb, and in two ways revealing the sequence for the flu virus is even more dangerous.

First, it would be easier to create and release this highly destructive virus from the genetic data than it would be to build and detonate an atomic bomb given only its design, as you don't need rare raw materials like plutonium or enriched

[Sign In to E-Mail This](#) [Printer-Friendly](#) [Save Article](#)ARTICLE TOOLS  
SPONSORED BY  
I THINK  
**I LOVE MY WIFE**

# 1918 Flu and Responsible Science

The influenza pandemic of 1918 is estimated to have caused 50 million deaths worldwide; 675,000 in the United States. The reconstruction of the 1918 virus by the synthesis of all eight subunits and the generation of infectious virus are described on p. 77 of this issue,\* and the sequences of the final three gene segments of the virus are described in a concurrent *Nature* paper.† Predictably, but alarmingly, this virus is more lethal to mice than are other influenza strains, suggesting that this property of the 1918 virus has been recovered in the published sequence. The good news is that we now have the sequence of this virus, perhaps permitting the development of new therapies and vaccines to protect against another such pandemic. The concern is that a terrorist group or a careless investigator could convert this new knowledge into another pandemic.

Should the sequence of the 1918 virus have been published, given its potential use by terrorists? The dual-use nature of biological information has been debated widely since September 11, 2001. In 2003, a committee of the U.S. National Academies chaired by Gerald Fink considered this issue, weighing the benefits against the risks of restricting the publication of such biological information. They outlined the tradeoff between erring on the side of prudence, thus potentially hindering the progress of critical science, and erring on the side of disclosure, thus potentially aiding terrorists. The U.S. National Science Advisory Board for Biosecurity (NSABB) was established to advise governmental agencies and the scientific community on policies relative to public disclosure. This board has begun to deliberate, but the questions are complex, as typified by these papers on the 1918 virus. It is reassuring that the NSABB was asked to consider these papers before publication and concluded that the scientific benefit of the future use of this information far outweighs the potential risk of misuse. People may be reassured that the system is working, because agencies representing the public, the scientific community, and the publishing journals were involved in the decision.

I firmly believe that allowing the publication of this information was the correct decision in terms of both national security and public health. It is impossible to forecast how scientific observations might stimulate others to create new treatments or procedures to control future pandemics. For example, in the *Nature* article, sequence comparisons suggest that the 1918 virus was generated not by incremental changes in the polymerase genes, but by the movement of these genes, in total, from an avian source into a human influenza virus. The availability of these sequences will permit identification of their avian origin and should show why this particular set of genes was selected. Similarly, the results in the *Science* article suggest that the cleavage of a protein on the surface of the 1918 virus, a step critical for virulent infection, may occur by a previously unknown mechanism—a hint that could lead to new drugs for inhibiting this step and thus preventing future pandemic eruptions.

Influenza is highly infectious, and a new strain could spread around the world in a matter of months, if not weeks. The public needs confidence that the 1918 virus will not escape from research labs. All of the described experiments were done in a Biosafety Level 3 laboratory, a high-containment environment recommended by the U.S. Centers for Disease Control and Prevention and the National Institutes of Health on an interim basis, whose use should become a permanent requirement for such experiments. Current evidence suggests that some available drugs and possible future vaccines could suppress infections by the 1918 virus. Given the prospect of another natural influenza pandemic, the recent decision by the U.S. administration to stockpile antivirals for influenza treatment seems wise. Finally, although a sequence of the 1918 virus has been determined and is highly virulent in mice, this may not be the specific form of the virus that caused the pandemic of 1918. An article in the same issue of *Nature*‡ reports the existence of sequence variation in a natural population of influenza virus; yet we have only one sequence for the 1918 pandemic strain, and the reconstructed virus described in the *Science* article was built into the backbone of a laboratory strain. Because a pandemic infection is dependent on many unknown properties, there is no certainty that the reconstructed 1918 virus is capable of causing a pandemic.

Phillip A. Sharp

Philip A. Sharp is Institute Professor at the Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA 02139, USA.



NYTimes.com Go to a Section ▾

SEARCH

NYT Since 1981 ▾

Search

[Editorials/Op-Ed Home](#)[Editorials](#)[Columnists](#)[Contributors](#)

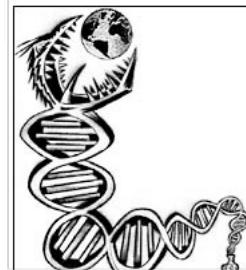
## OP-ED CONTRIBUTORS

**Recipe for Destruction**

By RAY KURZWEIL and BILL JOY

Published: October 17, 2005

AFTER a decade of painstaking research, federal and university scientists have reconstructed the 1918 influenza virus that killed 50 million people worldwide. Like the flu viruses now raising alarm bells in Asia, the 1918 virus was a bird flu that jumped directly to humans, the scientists reported. To shed light on how the virus evolved, the United States Department of Health and Human Services published the full genome of the 1918 influenza virus on the Internet in the GenBank database.



This is extremely foolish. The genome is essentially the design of a weapon of mass destruction. No responsible scientist would advocate publishing precise designs for an atomic bomb, and in two ways revealing the sequence for the flu virus is even more dangerous.

First, it would be easier to create and release this highly destructive virus from the genetic data than it would be to build and detonate an atomic bomb given only its design, as you don't need rare raw materials like plutonium or enriched

[Sign In to E-Mail This](#)[Printer-Friendly](#)[Save Article](#)

ARTICLE TOOLS

SPONSORED BY

I LOVE MY WIFE

**1918 Flu and Responsible Science**

The influenza pandemic of 1918 is estimated to have caused 50 million deaths worldwide; 675,000 in the United States. The reconstruction of the 1918 virus by the synthesis of all eight subunits and the generation of infectious virus are described on p. 77 of this issue,<sup>1</sup> and the sequences of the final three gene segments of the virus are described in a concurrent *Nature* paper.<sup>2</sup> Predictably, but alarmingly, this virus is more lethal to mice than are other influenza strains, suggesting that this property of the 1918 virus has been recovered in the published sequence. The good news is that we now have the sequence of this virus, perhaps permitting the development of new therapies and vaccines to protect against another such pandemic. The concern is that a terrorist group or a careless investigator could convert this new knowledge into another pandemic.

Should the sequence of the 1918 virus have been published, given its potential use by terrorists? The dual-use nature of biological information has been debated widely since September 11, 2001. In 2003, a committee of the U.S. National Academies chaired by Gerald Fink considered this issue, weighing the benefits against the risks of restricting the publication of such biological information. They outlined the tradeoff between erring on the side of prudence, thus potentially hindering the progress of critical science, and erring on the side of disclosure, thus potentially aiding terrorists. The U.S. National Science Advisory Board for Biosecurity (NSABB) was established to advise governmental agencies and the scientific community on policies relative to public disclosure. This board has begun to deliberate, but the questions are complex, as typified by these papers on the 1918 virus. It is reassuring that the NSABB was asked to consider these papers before publication and concluded that the scientific benefit of the future use of this information far outweighs the potential risk of misuse. People may be reassured that the system is working, because agencies representing the public, the scientific community, and the publishing journals were involved in the decision.

I firmly believe that allowing the publication of this information was the correct decision in terms of both national security and public health. It is impossible to forecast how scientific observations might stimulate others to create new treatments or procedures to control future pandemics. For example, in the *Nature* article, sequence comparisons suggest that the 1918 virus was generated not by incremental changes in the polymerase genes, but by the movement of these genes, in total, from an avian source into a human influenza virus. The availability of these sequences will permit identification of their avian origin and should show why this particular set of genes was selected. Similarly, the results in the *Science* article suggest that the cleavage of a protein on the surface of the 1918 virus, a step critical for virulent infection, may occur by a previously unknown mechanism—a hint that could lead to new drugs for inhibiting this step and thus preventing future pandemic eruptions.

Influenza is highly infectious, and a new strain could spread around the world in a matter of months, if not weeks. The public needs confidence that the 1918 virus will not escape from research labs. All of the described experiments were done in a Biosafety Level 3 laboratory, a high-containment environment recommended by the U.S. Centers for Disease Control and Prevention and the National Institutes of Health on an interim basis, whose use should become a permanent requirement for such experiments. Current evidence suggests that some available drugs and possible future vaccines could suppress infections by the 1918 virus. Given the prospect of another natural influenza pandemic, the recent decision by the U.S. administration to stockpile antivirals for influenza treatment seems wise. Finally, although a sequence of the 1918 virus has been determined and is highly virulent in mice, this may not be the specific form of the virus that caused the pandemic of 1918. An article in the same issue of *Nature*<sup>3</sup> reports the existence of sequence variation in a natural population of influenza virus; yet we have only one sequence for the 1918 pandemic strain, and the reconstructed virus described in the *Science* article was built into the backbone of a laboratory strain. Because a pandemic infection is dependent on many unknown properties, there is no certainty that the reconstructed 1918 virus is capable of causing a pandemic.



Phillip A. Sharp

Philip A. Sharp is Institute Professor at the Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA 02139, USA.



NYTimes.com Go to a Section ▾

SEARCH

NYT Since 1981 ▾

Search

[Editorials/Op-Ed Home](#)[Editorials](#)[Columnists](#)[Contributors](#)

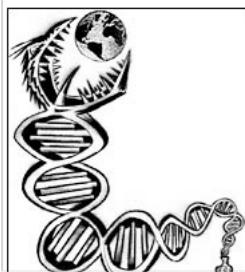
## OP-ED CONTRIBUTORS

## Recipe for Destruction

By RAY KURZWEIL and BILL JOY

Published: October 17, 2005

AFTER a decade of painstaking research, federal and university scientists have reconstructed the 1918 influenza virus that killed 50 million people worldwide. Like the flu viruses now raising alarm bells in Asia, the 1918 virus was a bird flu that jumped directly to humans, the scientists reported. To shed light on how the virus evolved, the United States Department of Health and Human Services published the full genome of the 1918 influenza virus on the Internet in the GenBank database.



This is extremely foolish. The genome is essentially the design of a weapon of mass destruction. No responsible scientist would advocate publishing precise designs for an atomic bomb, and in two ways revealing the sequence for the flu virus is even more dangerous.

First, it would be easier to create and release this highly destructive virus from the genetic data than it would be to build and detonate an atomic bomb given only its design, as you don't need rare raw materials like plutonium or enriched

[Sign In to E-Mail This](#)  
[Printer-Friendly](#)  
[Save Article](#)  
 ARTICLE TOOLS  
 SPONSORED BY  
**I LOVE MY WIFE**

## VACCINES

## Synthetic Generation of Influenza Vaccine Viruses for Rapid Response to Pandemics

Philip R. Dormitzer,<sup>1\*</sup> Pirada Suphaphiphat,<sup>1</sup> Daniel G. Gibson,<sup>2,3,4</sup> David E. Wentworth,<sup>2</sup> Timothy B. Stockwell,<sup>2</sup> Mikkel A. Algire,<sup>2</sup> Nina Alperovich,<sup>2</sup> Mario Barro,<sup>5</sup> David M. Brown,<sup>2</sup> Stewart Craig,<sup>1</sup> Brian M. Dattilo,<sup>5</sup> Evgeniya A. Denisova,<sup>2</sup> Ivana De Souza,<sup>1</sup> Markus Eickmann,<sup>6</sup> Vivien G. Dugan,<sup>2†</sup> Annette Ferrari,<sup>1</sup> Raul C. Gomila,<sup>1,7</sup> Ligu Han,<sup>1</sup> Casey Judge,<sup>1</sup> Sarthak Mane,<sup>1</sup> Mikhail Matrosovich,<sup>6</sup> Chuck Merryman,<sup>3</sup> Giuseppe Palladino,<sup>1</sup> Gene A. Palmer,<sup>1</sup> Terika Spencer,<sup>1,8</sup> Thomas Strecker,<sup>6</sup> Heidi Trusheim,<sup>8</sup> Jennifer Uhendorff,<sup>6</sup> Yingxia Wen,<sup>1</sup> Anthony C. Yee,<sup>2</sup> Jayshree Zaveri,<sup>2</sup> Bin Zhou,<sup>2</sup> Stephan Becker,<sup>6</sup> Armen Donabedian,<sup>5</sup> Peter W. Mason,<sup>1</sup> John I. Glass,<sup>2</sup> Rino Rappuoli,<sup>1,7</sup> J. Craig Venter<sup>2,3,4</sup>

During the 2009 H1N1 influenza pandemic, vaccines for the virus became available in large quantities only after

## Virus Attenuation by Genome-Scale Changes in Codon Pair Bias

J. Robert Coleman,<sup>3</sup> Dimitris Papamichail,<sup>2\*</sup> Steven Skiena,<sup>2</sup> Bruce Futcher,<sup>1</sup> Eckard Wimmer,<sup>1,†</sup> Steffen Mueller<sup>1</sup>

As a  
encod  
pair t  
statist  
under  
Unde  
conta  
custo  
This “  
kinds

## DNA synthesis and biological security

Hans Bügl, John P Danner, Robert J Molinari, John T Mulligan, Han-OH Park, Bas Reichert, David A Roth, Ralf Wagner, Bruce Budowle, Robert M Scripp, Jenifer A L Smith, Scott J Steele, George Church & Drew Endy

A group of academics, industry executives and security experts propose an oversight framework to address concerns over the security of research involving commercial DNA synthesis.

DNA synthesis allows the direct construction of genetic material starting from information and raw chemicals.<sup>1</sup> Improvements in synthesis technology are accelerating innovation across many areas of research, from the development of renewable energy to the production of fine chemicals. The potential of DNA synthesis to enable bioterrorism, and from agricultural productivity to breakthroughs in human health and medicine. Like any powerful technology, DNA synthesis has the potential to be purposefully misappropriated. Misuse of DNA-synthesis technology could give rise to both known and unknown threats to public health, national security and privacy. Current government oversight of the DNA-synthesis industry falls short of addressing this unfortunate reality.

Here, we outline a practical plan for developing an effective oversight framework for

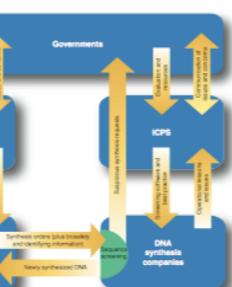


Figure 1. Our framework calls for the immediate and systematic implementation of a tiered DNA-synthesis order tracking process. To promote and sustain accountability, individual companies who place orders for DNA synthesis would be required to identify themselves, their home organization and all relevant bioterror information. Next, individual companies would use validated software tools to check synthesis orders against a set of select metrics or securities to help ensure regulatory compliance and mitigate potential misuse. Finally, synthesis and permitting agencies (both national and international) would work together through the IPCS and interface with appropriate government agencies (worldwide), to rapidly and continuously improve the underlying technologies used to screen orders and identify potentially dangerous sequences, as well as develop a clearly defined process to report behavior that falls outside of agreed-upon guidelines. IPCS, International Consortium for Polynucleotide Synthesis.

NATURE BIOTECHNOLOGY VOL 25 | NUMBER 6 | JUNE 2007

## 1918 Flu and Responsible Science

The influenza pandemic of 1918 is estimated to have caused 50 million deaths worldwide; 675,000 in the United States. The reconstruction of the 1918 virus by the synthesis of all eight subunits and the generation of infectious virus are described on p. 77 of this issue,<sup>1</sup> and the sequences of the final three gene segments of the virus are described in a concurrent *Nature* paper.<sup>2</sup> Predictably, but alarmingly, this virus is more lethal to mice than are other influenza strains, suggesting that this property of the 1918 virus has been recovered in the published sequence. The good news is that we now have the sequence of this virus, perhaps permitting the development of new therapies and vaccines to protect against another such pandemic. The concern is that a terrorist group or a careless investigator could convert this new knowledge into another pandemic.

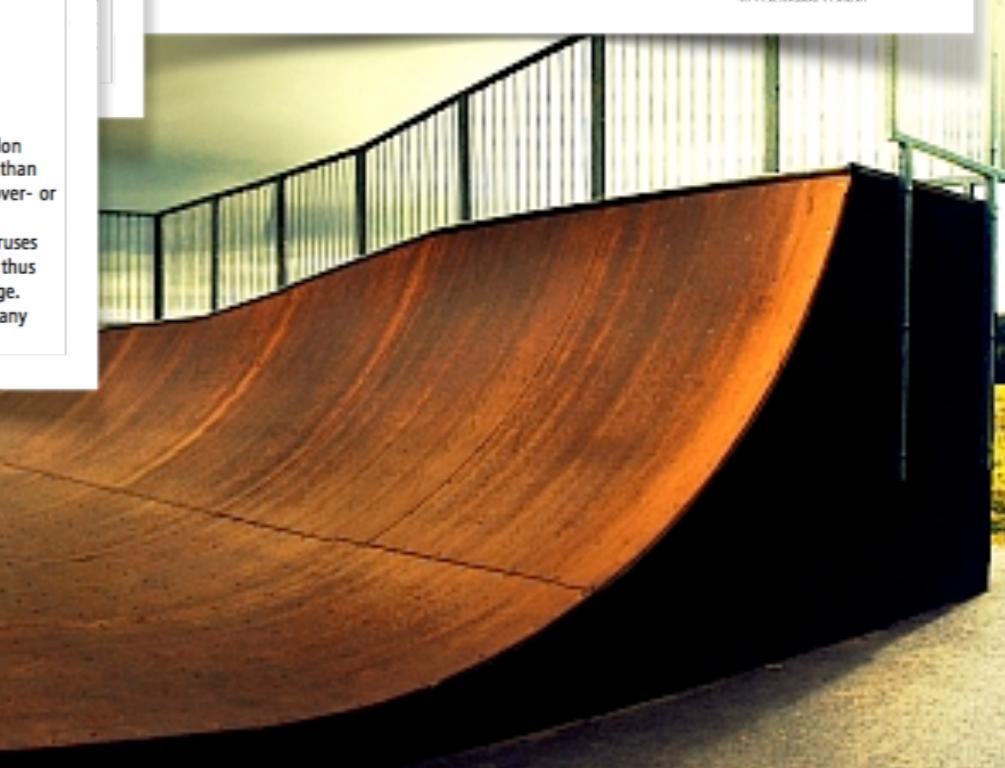
Should the sequence of the 1918 virus have been published, given its potential use by terrorists? The dual-use nature of biological information has been debated widely since September 11, 2001. In 2003, a committee of the U.S. National Academies chaired by Gerald Fink considered this issue, weighing the benefits against the risks of restricting the publication of such biological information. They outlined the tradeoff between erring on the side of prudence, thus potentially hindering the progress of critical science, and erring on the side of disclosure, thus potentially aiding terrorists. The U.S. National Science Advisory Board for Biosecurity (NSABB) was established to advise governmental agencies and the scientific community on policies relative to public disclosure. This board has begun to deliberate, but the questions are complex, as typified by these papers on the 1918 virus. It is reassuring that the NSABB was asked to consider these papers before publication and concluded that the scientific benefit of the future use of this information far outweighs the potential risk of misuse. People may be reassured that the system is working, because agencies representing the public, the scientific community, and the publishing journals are involved in the decision.

I firmly believe that allowing the publication of this information was a correct decision in terms of both national security and public health. It is impossible to forecast how scientific observations might stimulate others to create new treatments or procedures to control future epidemics. For example, in the *Nature* article, sequence comparisons suggest that the 1918 virus was generated not by incremental changes in the polymerase genes, but by the movement of these genes, in total, from an avian source into a human influenza virus. The availability of these sequences will permit identification of their avian origin and should show why this particular set of genes was selected. Similarly, the results in the *Science* article suggest that the cleavage of a protein on the surface of the 1918 virus, a step critical for virulent infection, may occur by a previously unknown mechanism—a hint that could lead to new drugs for inhibiting this step and thus preventing future pandemic eruptions.

Influenza is highly infectious, and a new strain could spread around the world in a matter of months, if not weeks. The public needs confidence that the 1918 virus will not escape from research labs. All of the described experiments were done in a Biosafety Level 3 laboratory, a high-containment environment recommended by the U.S. Centers for Disease Control and Prevention and the National Institutes of Health on an interim basis, whose use should become a permanent requirement for such experiments. Current evidence suggests that some available drugs and possible future vaccines could suppress infections by the 1918 virus. Given the prospect of another natural influenza pandemic, the recent decision by the U.S. administration to stockpile antivirals for influenza treatment seems wise. Finally, although a sequence of the 1918 virus has been determined and is highly virulent in mice, this may not be the specific form of the virus that caused the pandemic of 1918. An article in the same issue of *Nature*<sup>3</sup> reports the existence of sequence variation in a natural population of influenza virus; yet we have only one sequence for the 1918 pandemic strain, and a reconstructed virus described in the *Science* article was built into the backbone of a laboratory strain. Because a pandemic infection is dependent on many unknown properties, there is no certainty that the reconstructed 1918 virus is capable of causing a pandemic.

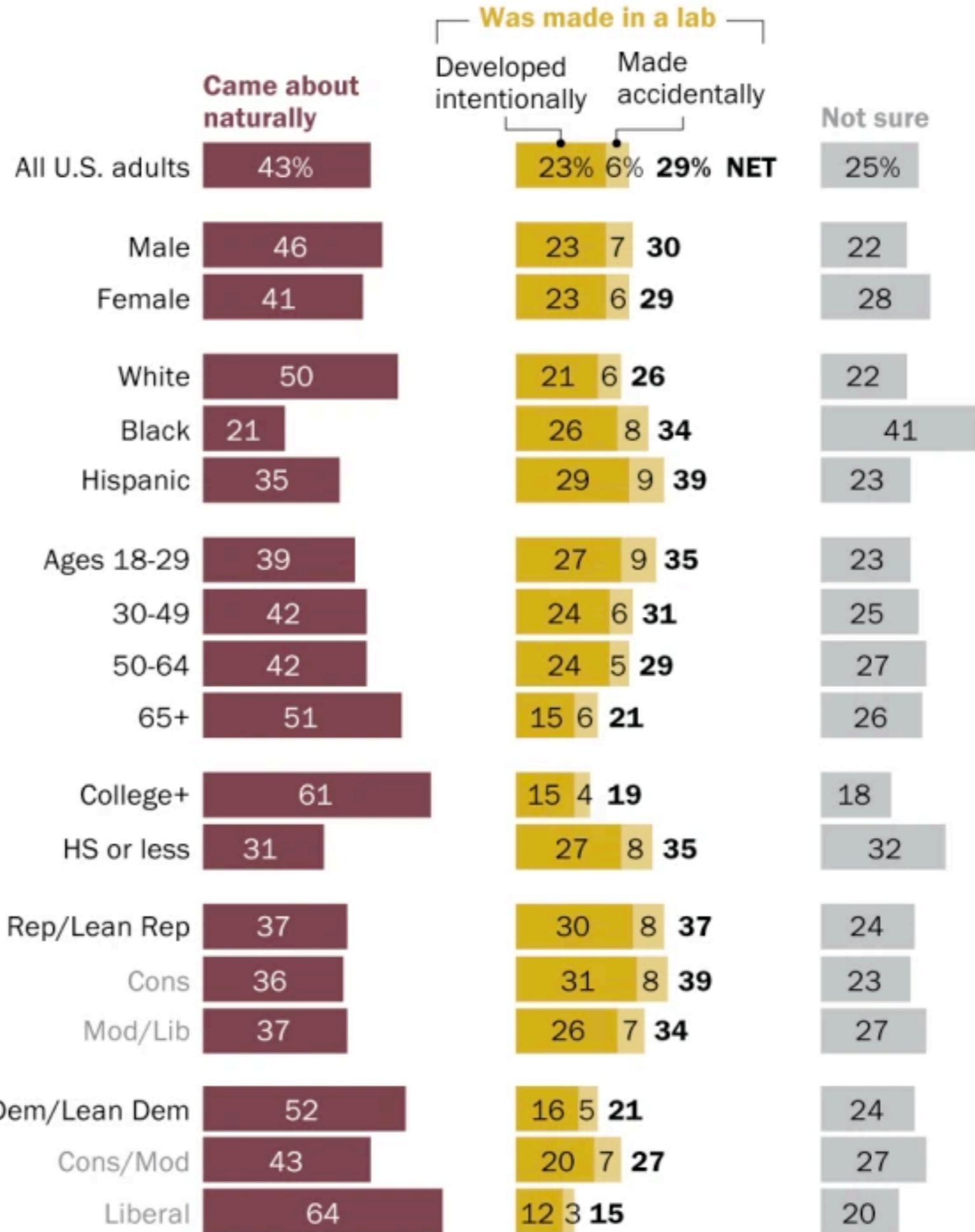
Phillip A. Sharp

Philip A. Sharp is Institute Professor at the Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, MA 02139, USA.



## Nearly three-in-ten Americans believe COVID-19 was made in a lab

BY KATHERINE SCHAEFFER



## Is COVID-19 a biological weapon?

# **Human Gene Editing Receives Science Panel's Support**

By AMY HARMON FEB. 14, 2017



An influential science advisory group formed by the [National Academy of Sciences](#) and the National Academy of Medicine on Tuesday lent its support to a once-unthinkable proposition: the modification of human embryos to create genetic traits that can be passed down to future generations.

The advisory group endorsed only alterations designed to prevent babies from acquiring genes known to cause “serious diseases and disability,” and only when there is no “reasonable alternative.” The report provides an explicit rationale for genetic research that the federal government has avoided supporting until now, although the work is being pursued in countries like Sweden and China.

Embryos being removed from cryogenic storage. An advisory group has endorsed the engineering of human eggs, sperm and embryos only to prevent babies from being born with genes known to cause serious diseases and disability. Universal Images Group, via Getty Images



123. If you think that big government interferes in your life too much NOW, just wait till the government starts regulating the genetic constitution of your children. Such regulation will inevitably follow the introduction of genetic engineering of human beings, because the consequences of unregulated genetic engineering would be disastrous. [19]

124. The usual response to such concerns is to talk about "medical ethics." But a code of ethics would not serve to protect freedom in the face of medical progress; it would only make matters worse. A code of ethics applicable to genetic engineering would be in effect a means of regulating the genetic constitution of human beings. Somebody (probably the upper-middle class, mostly) would decide that such and such applications of genetic engineering were "ethical" and others were not, so that in effect they would be imposing their own values on the genetic constitution of the population at large. Even if a code of ethics were chosen on a completely democratic basis, the majority would be imposing their own values on any minorities who might have a different idea of what constituted an "ethical" use of genetic engineering. The only code of ethics that would truly protect freedom would be one that prohibited ANY genetic engineering of human beings, and you can be sure that no such code will ever be applied in a technological society. No code that reduced genetic engineering to a minor role could stand up for long, because the temptation presented by the immense power of biotechnology would be irresistible, especially since to the majority of people many of its applications will seem obviously and unequivocally good (eliminating physical and mental diseases, giving people the abilities they need to get along in today's world). Inevitably, genetic engineering will be used extensively, but only in ways consistent with the needs of the industrial-technological system. [20]

# BREAKOUT DOWN W/ DISEASE

What should bioengineers do so that all infectious diseases are obsolete by 2030?

Hint — Try Framestorm & Futures Wheel Skills