DR. JENNIFER GARDY
BC CENTRE FOR DISEASE CONTROL
SCHOOL OF POPULATION & PUBLIC HEALTH
UNIVERSITY OF BRITISH COLUMBIA
@JENNIFERGARDY

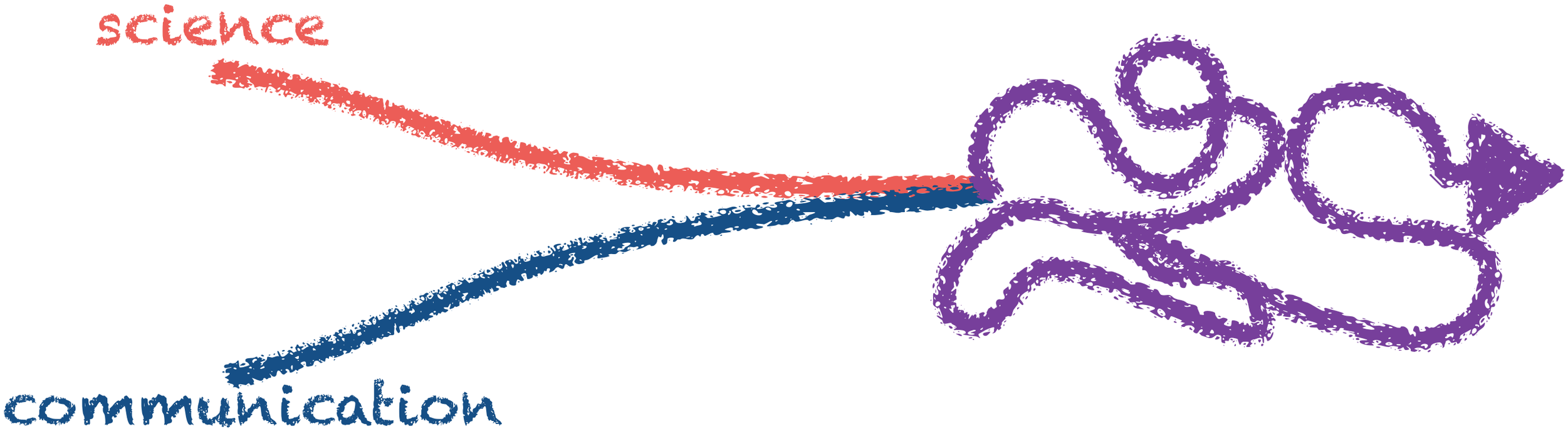


Figure 1. An accurate representation of my career path.

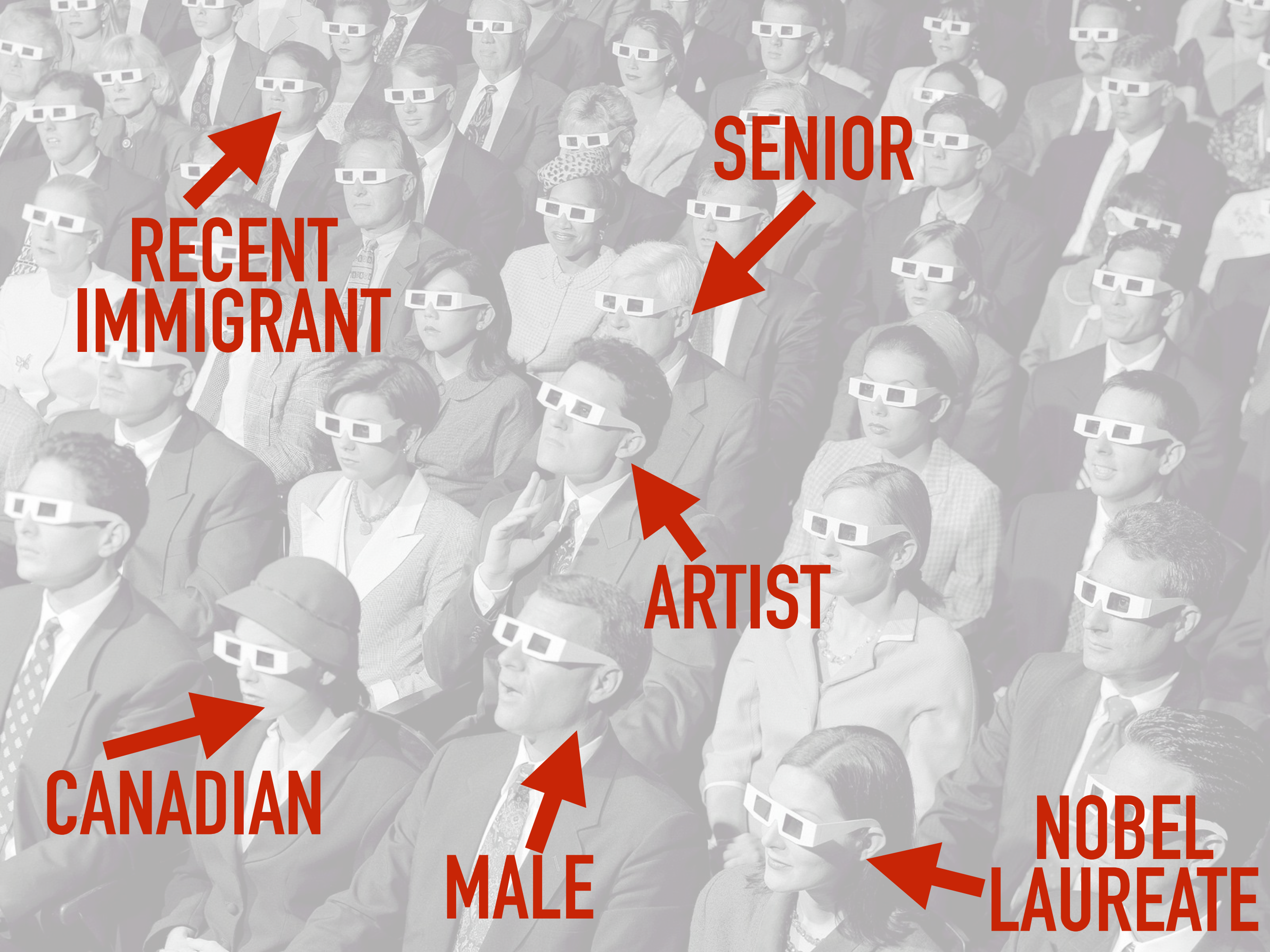
REASONS

OBLIGATION
INFORMED PUBLIC
IMPROVE OUR SCIENCE
SQUEAKY WHEEL GETS THE GREASE

5 LESSONS

KNOW YOUR AUDIENCE
CHOOSE YOUR MESSAGE
TELL A STORY
WATCH YOUR LANGUAGE
MAKE AWESOME VISUALS

Know Your *Audience*


RECENT IMMIGRANT
SENIOR
ARTIST
CANADIAN
MALE
NOBEL LAUREATE

- What are your audience's INTERESTS?
  - Not necessarily your interests!
- What does your audience WANT to know?
  - The answer is rarely facts.
- What does your story MEAN to them?
  - How will this affect their lives?
- What sort of BACKGROUND KNOWLEDGE do they have?
  - Cater your content and language to fit.

GROUP MEETING

CONFERENCE

PUBLIC TALK

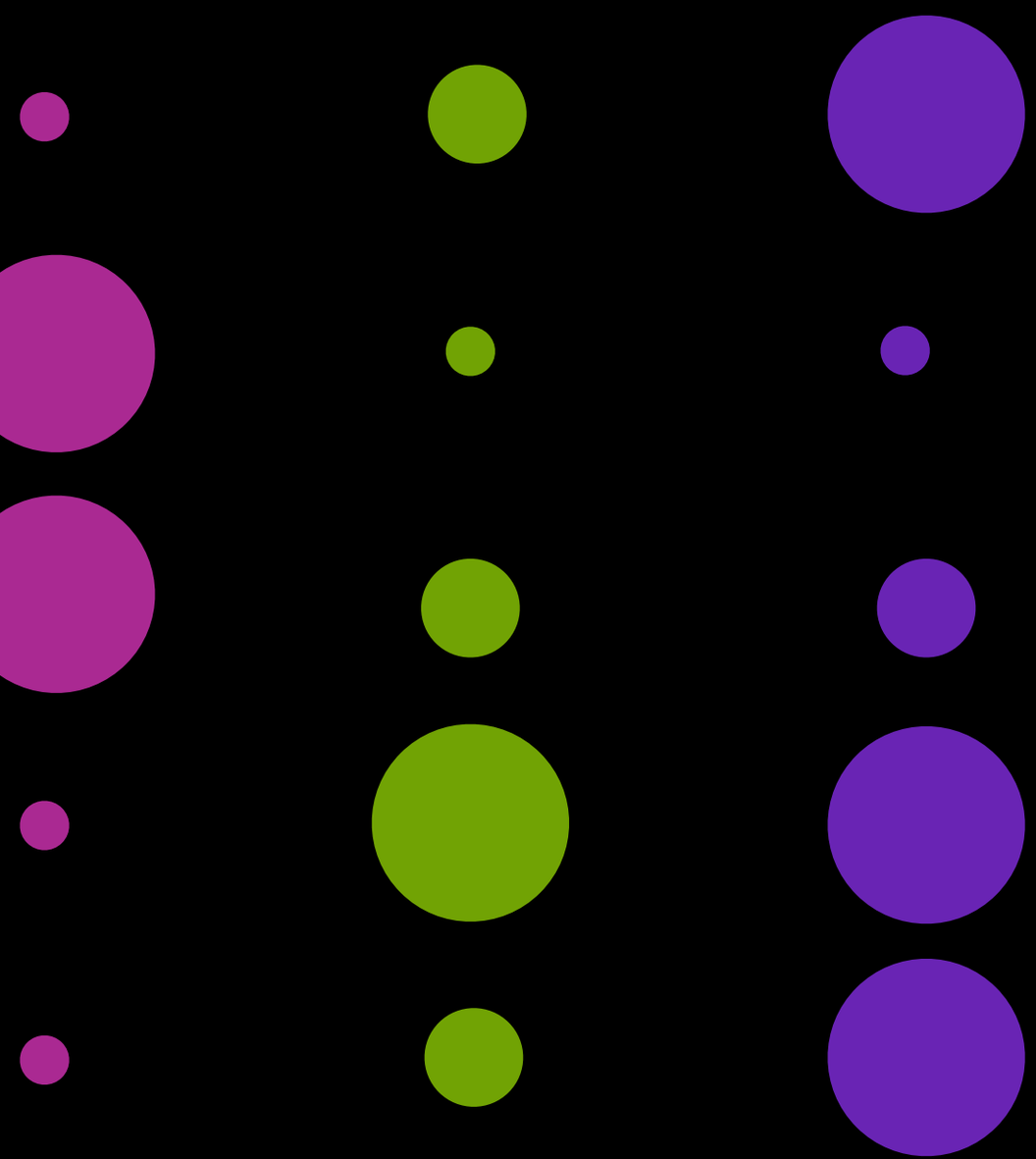
BACKGROUND

METHODS

RESULTS

CONCLUSIONS

BIG IMPACT



BRINGING GENOMICS HOME: YOUR DNA: A BLUEPRINT FOR BETTER HEALTH

Nov 12th 5:00 pm - 7:00 pm

Begbie Hall - Woodward Room - Royal Jubilee Hospital - 2101 Richmond Road Victoria, BC V8R 1J8

Genome BritishColumbia
Leading > Investing > Connecting

island health

BRINGING GENOMICS HOME

"Your DNA: A blueprint for better health"

Thank you for joining us in Victoria. Some presentations from the evening are available below:

Personalized Medicine: what's the prescription for BC in the next 5 years?
Brad Popovich PhD, Genome BC

Rare Disease: from diagnostic odyssey to tailored care
Clara van Karnebeek, MD PhD, Pediatrician and Biochemical Geneticist at BC Children's Hospital

The cancer genome through the eyes of the immune system
Brad Nelson PhD, Director and Distinguished Schientist, Deeley Research Centre

Better, Faster: how genomics is helping us diagnose and manage infectious disease
Jennifer Gardy PhD, Senior Scientist, BCCDC Communicable Disease Prevention and Control Services


“The public” isn’t a homogenous entity.
There are many different, unique publics.

Gateway Home
Aud
Can
Cha
Ent
Hea
Basics
Health Communication Science Digest
Research & Evaluation
Risk Communication
Tools & Templates +

CDC > Gateway Home

"Baby Boomers are more interested in experiences than possessions. Think about what they can "do" with a product rather than the product itself."

behavior. The more you know about your primary segment, the better you can reach them with messages,

"Moms are much more likely to follow unsolicited advice from their friends and family than anything they see, hear, or read via mass media channels."

Get Email Updates

To receive email updates about this page, enter your email address:

Wha

"Adults 64–84 prefer face-to-face or written communication."

These *Audience Insights* analyze different target audiences for public health so that you can more effectively communicate with them to influence their behavior.

Responsible Generation [1.0 MB, 8 pages]

Boomers [1.3 MB, 8 pages]

Family Physicians [1.1 MB, 8 pages]

Hispanics [1.2 MB, 23 pages]

Internists [844 KB, 8 pages]

Related Topics

THINK ABOUT YOUR MOST IMPORTANT

central message

HOW A SCIENTIST TELLS A STORY

THE INVERTED PYRAMID

MEDICINE MATTERS
The Vancouver Sun's Pamela Fayerman navigates through the medical system

Talk of miracles as heart pill used to wipe out cancer; gene sequencing pays off for costume designer who was facing death

March 10, 2015. 3:22 pm • Section: Medicine Matters

After multiple cancer relapses over the past five years, film industry costume designer Trish Keating knew that without a smash hit discovery, she had maybe only months to live.

Her “miraculous” reprieve came a few months ago in the most unlikely form: a blood pressure pill no one had ever used or even considered for cancer.

After multiple cancer relapses over the past five years, film industry costume designer Trish Keating knew that without a smash hit discovery, she had maybe only months to live.
Her “miraculous” reprieve came a few months ago in the most unlikely form: a blood pressure pill no one had ever used or even considered for cancer.
I met Keating at her home this week and she shared with me the history of horrible experiences she’s had with cancer since 2010 when it started in her colon. All the standard treatments she’s been given have been ineffective.
“I was months away from death. So this is really like a miracle. And so hard to believe,” said Keating in an interview at her home before joining her walking group for their usual two hour trek.
Keating looks like the picture of health now but she has plenty of scars and lingering side effects from five years of previous cancer treatments. Recurrences in other parts of her body were attacked with radiation, surgery and chemotherapy. Then her oncologist, Dr. Howie Lim, had to deliver the harsh news last fall that she was probably in the final, palliative stages.
But around the same time, the BC Cancer Foundation was making a concerted fundraising campaign for the newly launched Personalized Onco-Genomics Program (POG). It is a clinical trial enabling the sequencing of patients’ cancer genes. So far, only those patients with uncontrolled or incurable cancers are considered.
While biopsies and other pathology tests identify cancer types, the premise behind POG is that doctors can learn a lot more about the abnormal genes and biological engines fuelling each patient’s cancer; once that is known, experts can mine drug databases to find something tailored to each patient.
Late last fall, I wrote this exclusive article about the first “mystery” patient to have his cancer genome sequenced. The story about Dr. Don Rix, a biomedical and philanthropic superstar, was published the same day that a cancer foundation gala helped raised $5 million for POG. That has meant that the costs of sequencing Keating’s cancer and hundreds of other patients can be covered through a clinical trial protocol.
Lim said in an interview that before the sequencing, he suspected Keating’s last surgery to remove a tumour on her spine would relieve her pain, but not cure her. Sure enough, only a few months later, cancer cells were found in several lymph nodes throughout her body. He says:
“When I told her she was palliative, that our best option was to consider more chemotherapy to prolong lifespan, by two to three years, she felt I was giving her a death sentence.”
But then it was decided to offer Keating participation in the POG program. Keating knew the blood pressure medication was experimental but a “risk worth taking because the alternative was just more poisoning,” referencing the toxic effects of chemotherapy drugs.
Adds Lim:
“With POG, we are trying to figure out the blueprint of patients’ cancers, the (protein) pathways driving growth. Everyone’s cancer is different, genomically, so it’s helpful to try to individualize the treatment.”
Using gene sequencing information gleaned from the latest tumour removed from Keating’s spine, Marco Marra and his team of bioinformatic experts at the Michael Smith Genome Sciences Centre matched it to a blood pressure medication that blocks the abnormal proteins identified in the tumour sample.
Five weeks after taking it, Keating had sophisticated PET/CT imaging done which revealed a profoundly improved state. At a recent, two month mark, another PET/CT imaging scan showed she had “barely detectable” cancer.
Lim said he doesn’t want to give the impression that everyone will benefit from POG. It is still experimental, he cautions, and not all patients will have “durable” results.
“I would say Trish’s case has been a true outlier, right from the start,” he said, referring to the fact that when she was initially diagnosed, she had what was believed to be a “run of the mill” type of colorectal cancer that should have responded to standard treatment. But she did not.
Now Lim is busy writing up the case for publication in a medical journal so that doctors around the world can benefit from the blood pressure drug discovery and perhaps use it on other patients. (Lim is withholding the name of the drug until the case is published.)
“We’ve never tried this medication before, nor has anyone else to my knowledge. Yes, we hit a home run. But it takes a lot of steps and we could never do this without the Genome Sciences Centre.”
Lim said while everyone is excited about the possibilities of personalized cancer treatment, doctors and scientists must manage expectations so hopes don’t spiral out of control:
“I think, in general, in oncology, you make an educated guess about what treatment to offer. Genomic treatment helps us guess better.
“But we don’t know if every patient should have it, we have seen patients where it hasn’t helped. So in our research we are trying to answer what is the utility, and how often will it change treatment?”
Lim said he shares Keating’s shock, awe and happiness, especially since up until recently he was mostly giving her bad news.
“It’s been really empowering to finally offer some hope.”
“It’s very true that some amazing things have happened. I am shocked that this heart medication has worked so well,” Lim said, noting that Keating’s blood pressure has been closely monitored over the past three months to ensure the medication, which Keating believes she may be on for life, doesn’t lower it too much.

A common blood-pressure drug sent this woman’s cancer into remission

She was part of a unique cancer genome sequencing project

The genome data suggested the blood pressure medicine might target the tumor

Researchers are excited but must manage expectations

She will take the medicine for life

have a point. get to it.

Tell it like a *Story*

RESEARCH ARTICLE

NOSOCOMIAL INFECTION

Tracking a Hospital Outbreak of Carbapenem-Resistant *Klebsiella pneumoniae* with Whole-Genome Sequencing

Evan S. Snitkin,[1] Adrian M. Zelazny,[2] Pamela J. Thomas,[1] Frida Stock,[2]
NISC Comparative Sequencing Program,[3] David K. Henderson,[2]
Tara N. Palmore,[2]* Julia A. Segre[1]*

The Gram-negative bacteria *Klebsiella pneumoniae* is a major cause of nosocomial infections, primarily among immunocompromised patients. The emergence of strains resistant to carbapenems has left few treatment options, making infection containment critical. In 2011, the U.S. National Institutes of Health Clinical Center experienced an outbreak of carbapenem-resistant *K. pneumoniae* that affected 18 patients, 11 of whom died. Whole-genome sequencing was performed on *K. pneumoniae* isolates to gain insight into why the outbreak progressed despite early implementation of infection control procedures. Integrated genomic and epidemiological analysis traced the outbreak to three independent transmissions from a single patient who was discharged 3 weeks before the next case became clinically apparent. Additional genomic comparisons provided evidence for unexpected transmission routes, with subsequent mining of epidemiological data pointing to possible explanations for these transmissions. Our analysis demonstrates that integration of genomic and epidemiological data can yield actionable insights and facilitate the control of nosocomial transmission.

INTRODUCTION

The bacterial pathogen *Klebsiella pneumoniae* is responsible for roughly 15% of Gram-negative infections in hospital intensive care units (ICUs) (*1*), primarily affecting immunocompromised patients (*2*). In recent years, the threat posed by *K. pneumoniae* has markedly increased with the emergence of strains resistant to carbapenem antibiotics (*3*) and their worldwide dissemination (*4*, *5*). Infections caused by carbapenem-resistant strains have few treatment options (*6*, *7*) and are associated with mortality rates upwards of 50% (*8*, *9*). Although multiple resistance mechanisms have been identified (*10*), carbapenem resistance in the United States is primarily caused by the plasmid-encoded *K. pneumoniae* carbapenemase (KPC) gene (*5*).

Exacerbating the problems associated with the emergence of these highly resistant strains of *K. pneumoniae* is their propensity to cause outbreaks in health care institutions (*11*–*13*). As with most nosocomial pathogens, multiple-drug resistance offers inherent selective advantage (*11*), which allows such organisms to persist both in the flora of hospitalized patients and in the hospital environment, in which antibiotic usage is widespread. More specific to *K. pneumoniae* is its capacity to silently colonize patients or hospital personnel (*14*), that is, by establishing residence in the gastrointestinal tract without causing any signs of infection. Individuals can be silently colonized or asymptomatic carriers for long periods of time, with detection of these carriers often proving difficult (*12*). These silent carriers act as reservoirs for continued transmission that make spread difficult to control and outbreaks difficult to stop (*13*). In addition, *K. pneumoniae* can survive for several hours on the hands of hospital personnel, which likely facilitates nosocomial spread (*15*).

Effective control of *K. pneumoniae* outbreaks requires a detailed understanding of how transmission occurs. Molecular typing approaches, such as pulsed-field gel electrophoresis and multi-locus sequence typing, have been used to classify *K. pneumoniae* and thus understand its local and global dissemination (*16*, *17*). However, the high *K. pneumoniae* clonality (*16*, *18*) creates difficulty in tracking outbreaks because available methods may not provide sufficient resolution to distinguish intra-institutional spread from introduction of closely related strains from other health care facilities. In the United States, KPC–*K. pneumoniae* isolates are highly clonal, with 70% belonging to sequence type (ST) 258 (*16*).

With rapid technological advances, whole-genome sequencing is emerging as the gold standard in bacterial typing (*19*, *20*). Success in tracking worldwide epidemics (*21*–*24*), regional outbreaks (*23*, *25*), food-borne outbreaks (*26*, *27*), and bioterrorism agents (*28*) has demonstrated that the fine resolution provided by whole-genome sequencing facilitates our understanding of the spread of infectious agents. The continued improvements in turnaround time and accessibility of DNA sequencing technologies are now approaching a point where genomic data can be generated in a clinically relevant time frame. Genome sequencing has been applied recently to nosocomial strains (*29*–*32*) but with limited study size or scope in reconstructing transmission links during the course of the outbreak.

Here, we applied whole-genome sequencing to track an outbreak of carbapenem-resistant *K. pneumoniae* at the U.S. National Institutes of Health (NIH) Clinical Center that colonized 18 patients, with 6 deaths attributable to *K. pneumoniae* infection. We developed an algorithm to reconstruct the outbreak transmissions based on whole-genome sequencing of isolates and epidemiological data that tracked the location of patients throughout their hospital stays.

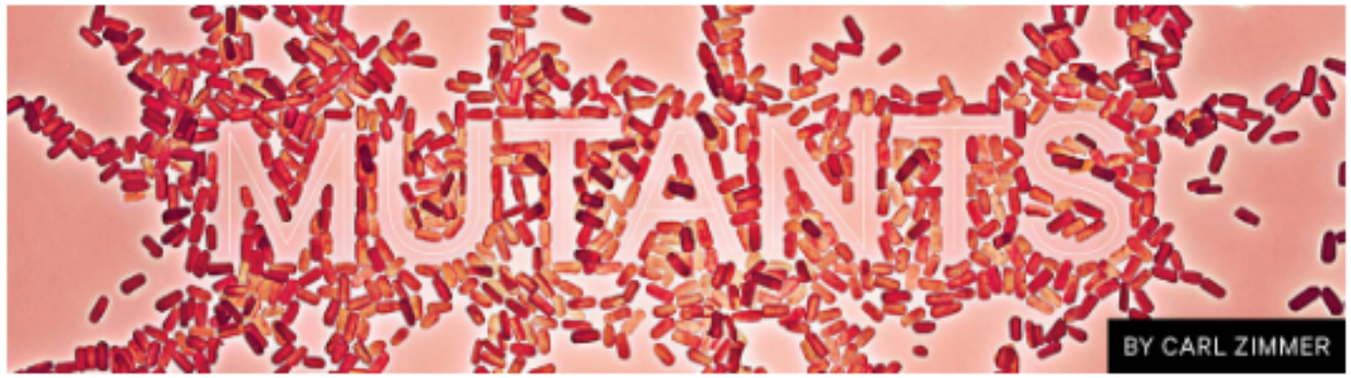
RESULTS

Overview of outbreak

On 13 June 2011, patient 1 was transferred to our ICU from a hospital in New York City and was discharged on 15 July. She was known to

[1]National Human Genome Research Institute, Bethesda, MD 20892, USA. [2]National Institutes of Health Clinical Center, Bethesda, MD 20892, USA. [3]National Institutes of Health Intramural Sequencing Center (NISC), Bethesda, MD 20892, USA.
*To whom correspondence should be addressed. E-mail: tpalmore@mail.nih.gov (T.N.P.); jsegre@nhgri.nih.gov (J.A.S.)

HOW SCIENTISTS STALKED A LETHAL SUPERBUG —WITH THE KILLER'S OWN DNA



A LETHAL BACTERIUM was running rampant at an NIH hospital. Antibiotics were useless. Then two scientists began a frantic race to track down the killer—with the superbug's own DNA.

http://www.wired.com/2013/01/ff-kpc-superbug-nih/

“Joshua Osborn, 14, lay in a coma at American Family Children’s Hospital in Madison, Wis. For weeks his brain had been swelling with fluid, and a battery of tests had failed to reveal the cause.”

–Carl Zimmer, New York Times, June 2014

Houston, We Have a Narrative

WHY SCIENCE NEEDS STORY

RANDY OLSON

When scientists tell us about their work, they pile one moment and one detail atop another moment and another detail—a stultifying procession of "and, and, and."

What we need instead is an understanding of the basic elements of story…which Olson boils down, brilliantly, to "And, But, Therefore," or ABT. At a stroke, the ABT approach introduces momentum ("And"), conflict ("But"), and resolution ("Therefore")—the fundamental building blocks of story.

W: THE DOBZHANSKY TEMPLATE

Nothing in _____
makes sense, except
in the light of _____ .

S: SENTENCE, THE ABT MODEL

- _____ and _____, but _____. Therefore, _____.

Agreement	*Contradiction*	*Consequence*
AND	BUT	THEREFORE
also	despite	so
equally	however	thus
identically	yet	consequently
uniquely	conversely	hence
like	rather	thereupon
moreover	whereas	accordingly
as well as	although	as a result
furthermore	otherwise	henceforth
likewise	instead	for this reason
similarly	albeit	in that case

P: PARAGRAPH, THE HERO'S JOURNEY

1. Call to adventure
2. Assistance
3. Departure
4. Trials
5. Approach
6. Crisis
7. Treasure
8. Result
9. Return
10. New life
11. Resolution
12. Status quo

OTHER HOOKS

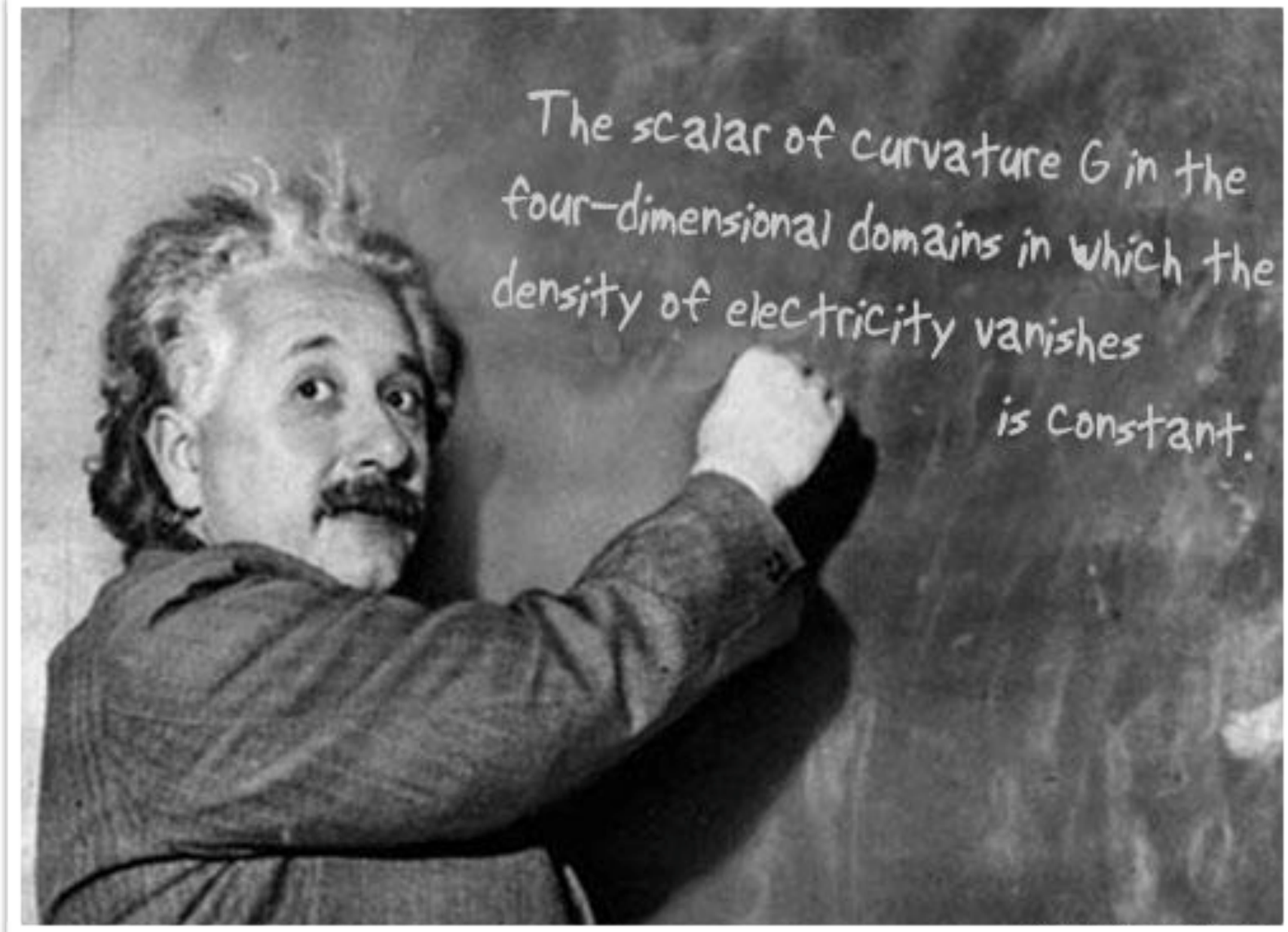
NOVELTY


IMPACT

CHARACTER

Find the story. Personalize the impersonal.

WATCH YOUR LANGUAGE



THE PARTY RULE


Simplifying
doesn't
mean you're
dumbing
things down.

lol my thesis

Summing up years of work in one sentence. Follow us on twitter: @lolmythesis

School/Field Search

About Random Submit

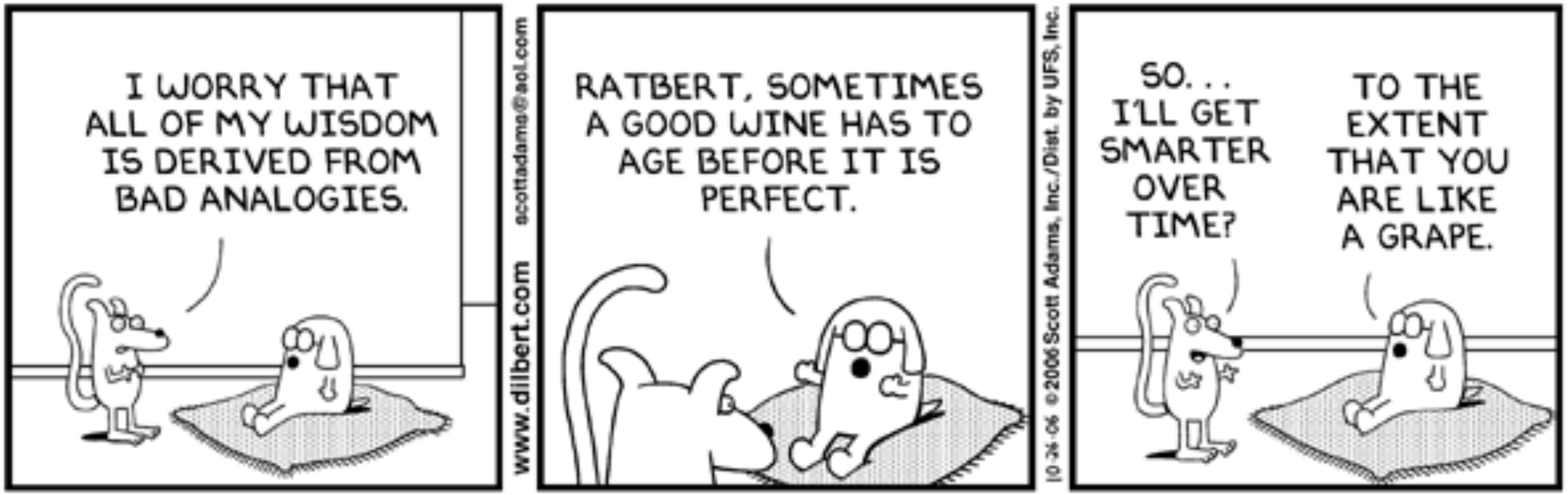
If you delete pieces of DNA, bad things happen.

Genetics, Dartmouth College

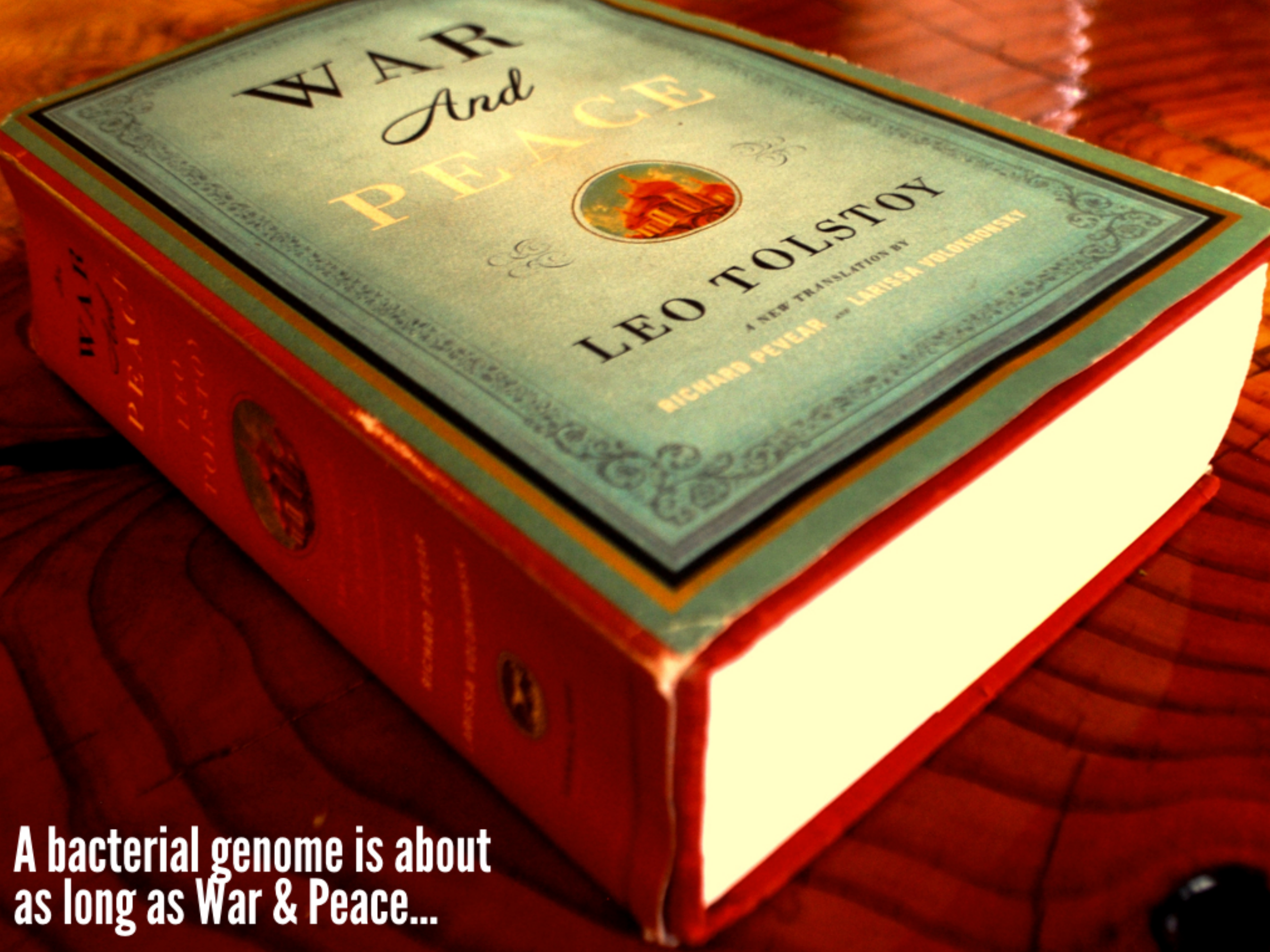
Using Zinc Finger Nucleases to Characterize the Regulation of c-MYC Transcription

Terms that have different meanings for scientists and the public		
Scientific term	**Public meaning**	**Better choice**
enhance	improve	intensify, increase
aerosol	spray can	tiny atmospheric particle
positive trend	good trend	upward trend
positive feedback	good response, praise	vicious cycle, self-reinforcing cycle
theory	hunch, speculation	scientific understanding
uncertainty	ignorance	range
error	mistake, wrong, incorrect	difference from exact true number
bias	distortion, political motive	offset from an observation
sign	indication, astrological sign	plus or minus sign
values	ethics, monetary value	numbers, quantity
manipulation	illicit tampering	scientific data processing
scheme	devious plot	systematic plan
anomaly	abnormal occurrence	change from long-term average

From Communicating the Science of Climate Change, RCJ Somerville and SJ Hassol, Physics Today, Oct. 2011
See also Andrew Thaler's http://www.southernfriedscience.com/?p=11584



metaphors, analogies

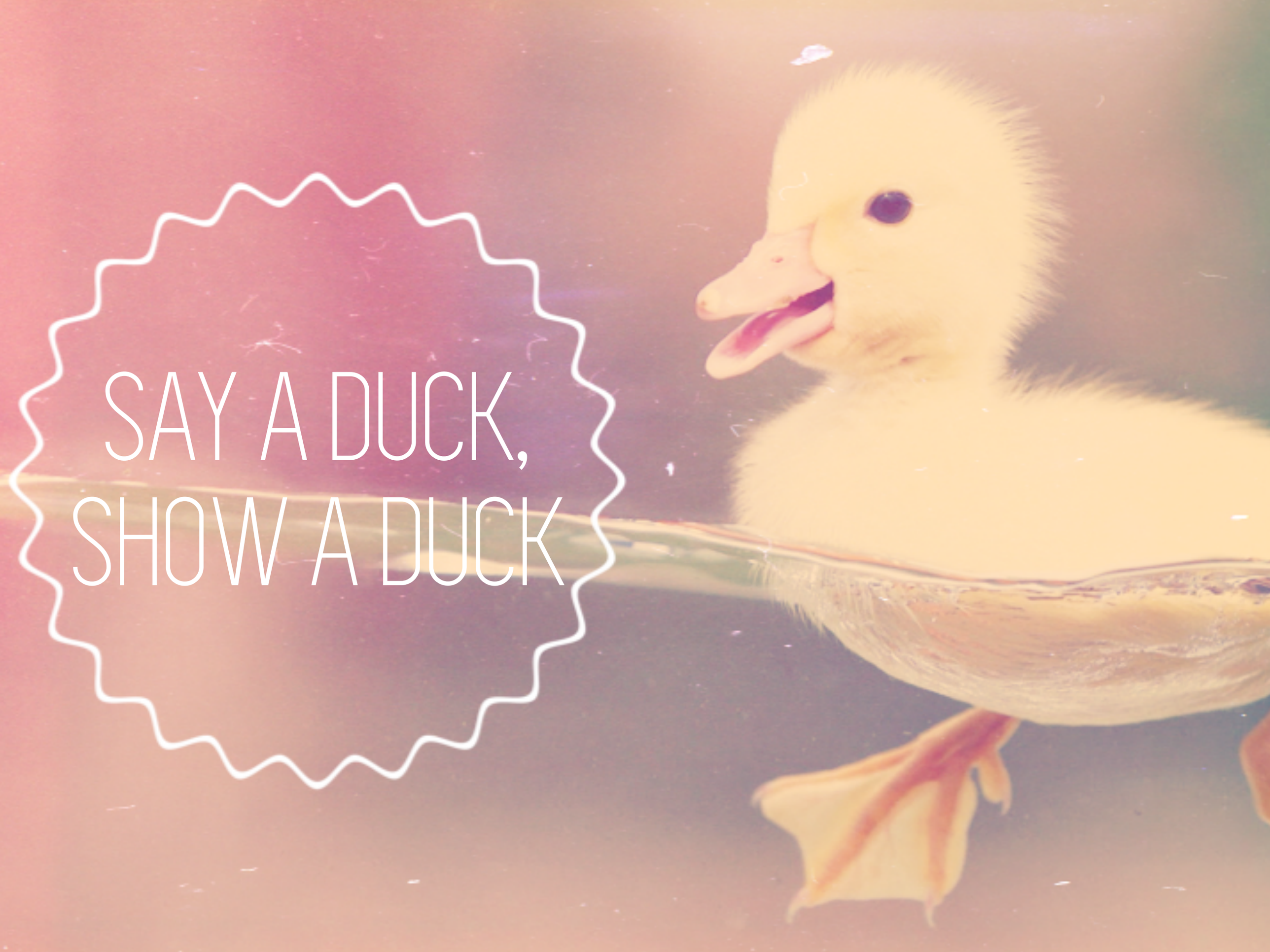

WAR
And
PEACE
LEO TOLSTOY
A NEW TRANSLATION BY
RICHARD PEVEAR
AND
LARISSA VOLOKHONSKY
A bacterial genome is about
as long as War & Peace...

TELEPHONE

ART BY DEVIANTART USER SCUMMY

Carefully review your choice of words. Edit.

SAY A DUCK, SHOW A DUCK



Break out of the Powerpoint box

WordArt is the devil's spawn

- It makes poor design choices
- We don't think in bullets, so why should we present that way?
- It tempts us to read our slides word-for-word off the screen
- And the clip art sucks

Oooh nice arrow

Chart Suggestions—A Thought-Starter

What would you like to show?

Comparison

Relationship

Two Variables

- Scatter Chart
- Bubble Chart

Three Variables

Distribution

Single Variable

- Few Data Points → Column Histogram
- Many Data Points → Line Histogram

Two Variables → Scatter Chart

Three Variables → 3D Area Chart

Composition

Changing Over Time

Few Periods

- Only Relative Differences Matter → Stacked 100% Column Chart
- Relative and Absolute Differences Matter → Stacked Column Chart

Many Periods

- Only Relative Differences Matter → Stacked 100% Area Chart
- Relative and Absolute Differences Matter → Stacked Area Chart

Static

- Simple Share of Total → Pie Chart
- Accumulation or Subtraction to Total → Waterfall Chart
- Components of Components → Stacked 100% Column Chart with Subcomponents

---

Variable Width Column Chart
Table or Table with Embedded Charts
Bar Chart
Column Chart
Circular Area Chart
Line Chart
Column Chart
Line Chart

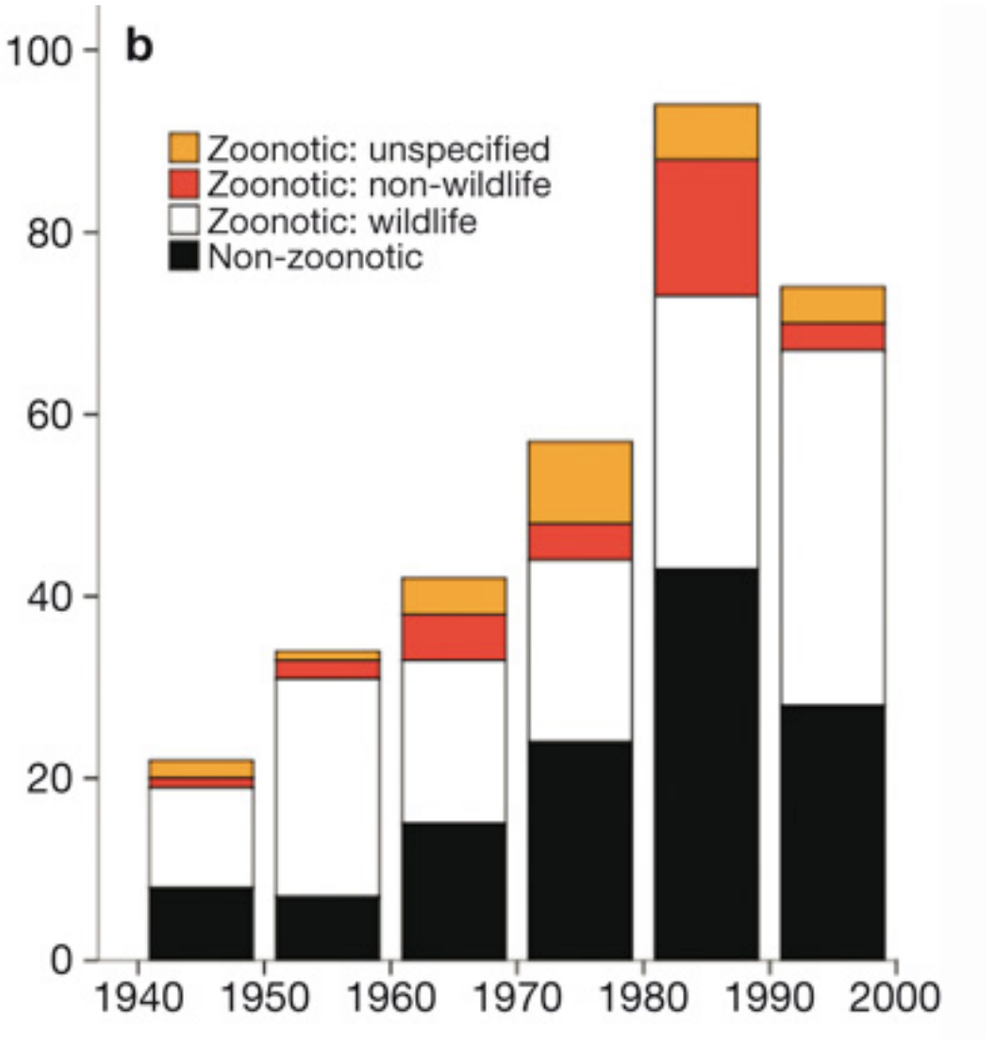
Two Variables per Item
Many Categories
Many Items
Few Items
Cyclical Data
Non-Cyclical Data
Single or Few Categories
Many Categories

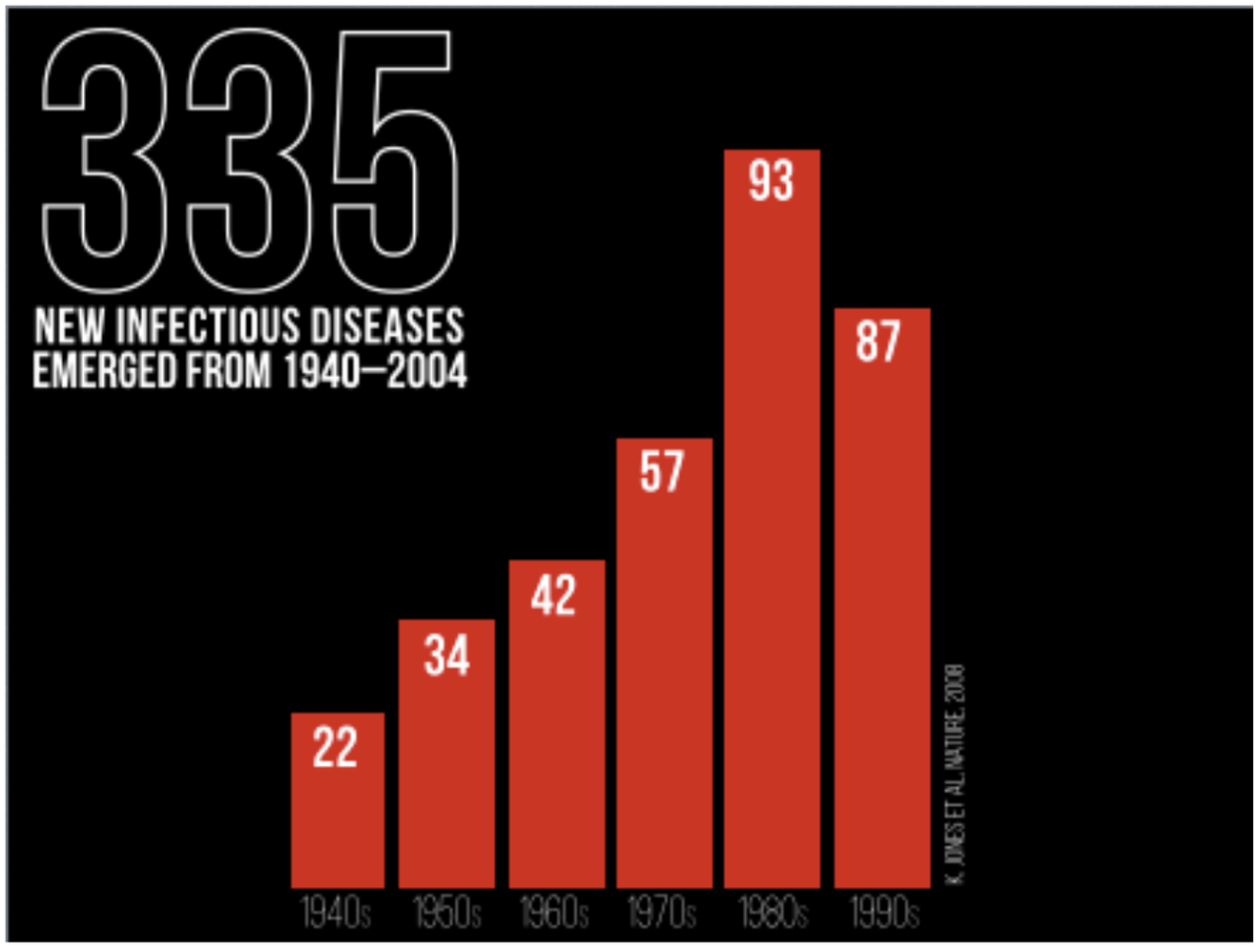
Few Categories
Many Periods
Few Periods
One Variable per Item
Over Time
Among Items

Remove
to improve
(the **data-ink** ratio)

Created by **Darkhorse Analytics**

www.**darkhorseanalytics**.com


b
100
80
60
40
20
0
Zoonotic: unspecified
Zoonotic: non-wildlife
Zoonotic: wildlife
Non-zoonotic
1940
1950
1960
1970
1980
1990
2000


335
NEW INFECTIOUS DISEASES
EMERGED FROM 1940–2004
22
34
42
57
93
87
1940s
1950s
1960s
1970s
1980s
1990s
K. JONES ET AL. NATURE, 2008

5 LESSONS

KNOW YOUR AUDIENCE
CHOOSE YOUR MESSAGE
TELL A STORY
WATCH YOUR LANGUAGE
MAKE AWESOME VISUALS