
WHAT SORT OF DATA WERE YOU WANTING TO STORE, MR CLAUS?
GOOD GIRLS & BOYS
BAD GIRLS & BOYS

strategic science

International gambling repository: Discussion of value, issues, and concerns for science and society

April 5, 2013

Alberta Gambling Research Institute's 12th Annual Conference

Banff, Alberta

Presenters:

Chuck Humphrey, Data Library Coordinator, University of Alberta

Judith Glynn, Principal, Strategic Science


WE
PROTECT
& SERVE
DATA

Decade around data

- Data as an asset
- Data stewardship and governance
- Infrastructure

Why is data access important?

- Maximize scientific & social returns from public investment
- Encourage open, scientific inquiry, diversity of analysis
- Promote new research
- Facilitate education of new researchers
- Enables exploration of topics not envisioned by initial investigators
- Create new data sets when multiple sources combined

International Scan

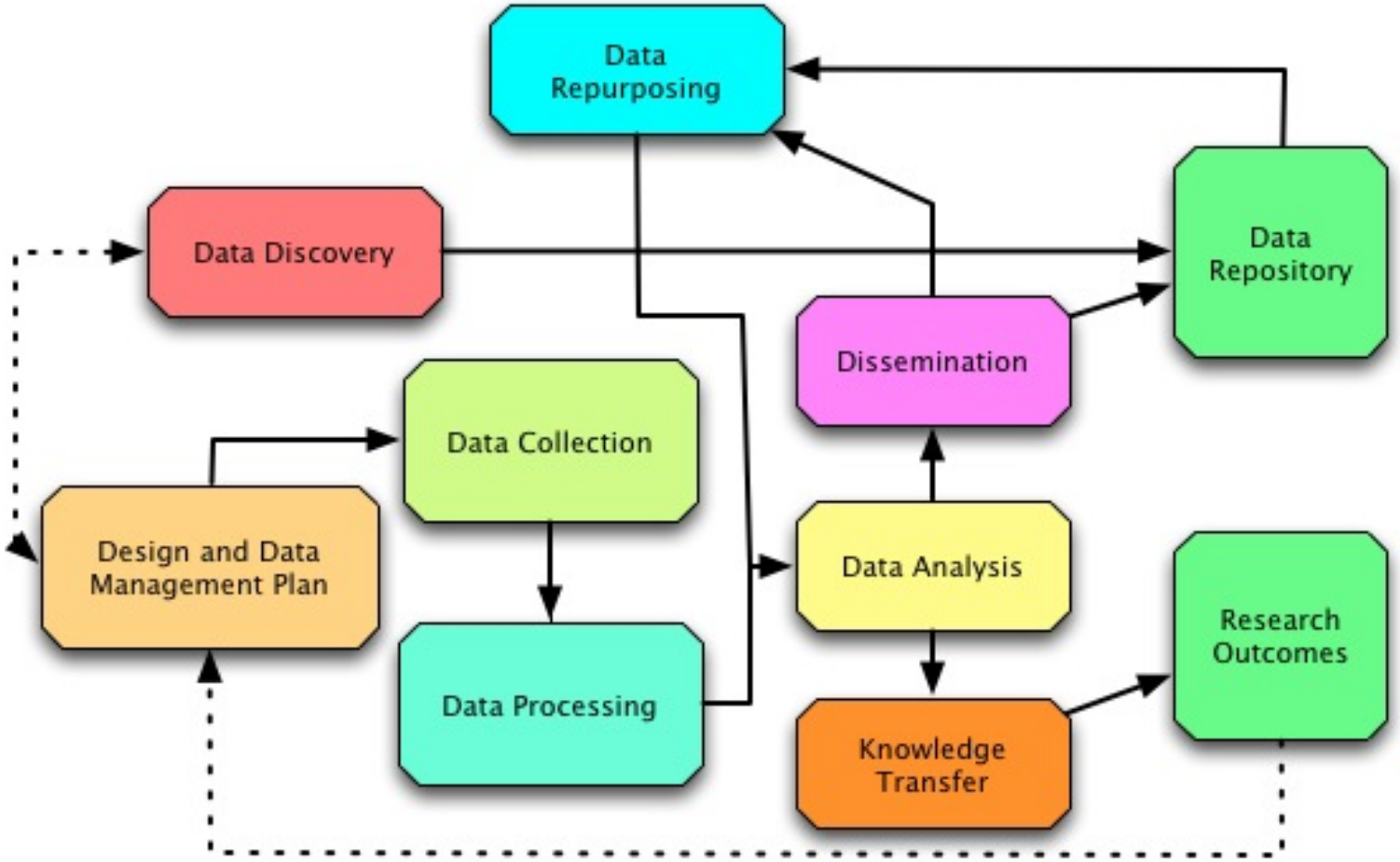
- Policy – Declaration on Access to Research Data from Public Funding (OECD, 2004)
- Community – UK - RIN – Stewardship of Research Data – community frame
- Practice – US - NIH and NSF require Data Management Plans – practice

National Scan

- National Data Archive consultation 2002 – 2 reports need. Models
- Canada signs OECD Declaration (2005)
- Consultation on access to scientific research data 2005
- Grassroots action – IPY

Problem Gambling Research Field Scan

Data Lifecycle



Nature – 1953

A Structure for Deoxyribose Nucleic Acid, J. D. Watson and F. H. C. Crick (1), April 25, 1953 (2), Nature (3), 171, 737-738

"We wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest."

1 page, 2 authors, 1 figure, no data

equipment, and to Dr. G. E. R. Deacon and the captain and officers of R.R.S. *Discovery II* for their part in making the observations.

[1] Young, F. B., Gerrard, H., and Jevons, W., *Phil. Mag.*, 40, 149 (1920).
[2] Longuet-Higgins, M. S., *Mon. Not. Roy. Astro. Soc., Geophys. Supp.*, 5, 285 (1949).
[3] Von Arx, W. S., Woods Hole Papers in Phys. Oceanog. Meteor., 11 (3) (1950).
[4] Ekman, V. W., *Arkiv. Mat. Astron. Fysik.* (Stockholm), 2 (11) (1905).

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey[1]. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons: (1) We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.

This figure is purely diagrammatic. The two ribbons symbolize the two phosphate—sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate diester groups joining β-D-deoxyribofuranose residues with 3',5' linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's[2] model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being roughly perpendi-

is a residue on each chain every 3·4 A. in the z-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 A. The distance of a phosphorus atom from the fibre axis is 10 A. As the phosphates are on the outside, cations have easy access to them.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two lie side by side with identical z-co-ordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: purine position 1 to pyrimidine position 1; purine position 6 to pyrimidine position 6.

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on one chain is given, then the sequence on the other chain is automatically determined.

It has been found experimentally[3,4] that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

The previously published X-ray data[5,6] on deoxyribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereochemical arguments.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.

Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on interatomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F.

International Human Genome Project

- 39 institutes from 18 countries
- Hundreds of scientists (200 in the U.S.)
- Identified all 20,000 – 25,000 genes in human DNA
- Decoding human DNA 2 years ahead of schedule

Impetus in PG Research Field

- 5 longitudinal studies
- 3 countries
- Many differences in implementation
- Common DV, many common IVs and assessment instruments

What is possible when we share?

LLLP & QLS - Two Prospective Studies in Canada

1. Leisure, Lifestyle, Lifecycle Study (LLLP)

PIs: N. el-Guebaly, MD, D. Hodgins, Ph.D., G. Smith, Ph.D., R. Williams, Ph.D. , D. Schopflocher, Ph.D., D. Casey, Ph.D., S. Currie, Ph.D.

2. Quinte Longitudinal Study (QLS)

PIs: Dr. R. Williams, University of Lethbridge & Mr. R. Hann, Robert Hann & Associates

- Developing an Etiological Model

LLLP Design

- A prospective, panel study of gambling behavior
  - 1808 Albertans over 5-year period
  - 5 age groups, stratified by region, oversampled for high frequency gamblers
  - 4 data collection points 2006-2011
  - Guided by bio-psycho-social conceptual model
  - Funded by AGRI

QLS Design

- Originally intended as an impact + longitudinal study (original name was the QERI Study)
  - 4,121 participants from Quinte region, Ontario
  - Sub sample at higher risk for PG
  - 5 data collection points 2006-2011
  - Funded by OPGRC

Dependent Variables: LLLP & QLS

	LLLP	QLS
CPGI (5+)	X	X
PPGM		X
DSM-IV-PY (3+)	X (adolescents)	X
DSM-IV-L	X	
Qualitative		X

- CPGI = Canadian Problem Gambling Index 5+
- PPGM = Problem and Pathological Gambling Measure (Williams & Volberg, 2010)
- DSM-IV–PY =NODS for QLS & Fisher DSM-IV-MR-Junior for LLLP
- DSM-IV-L = CIDI
- Qualitative data = everyone with a calculated CPGI 3+ during an assessment period was asked what caused their gambling problems = 1,310 open-ended responses

Approach to Developing an Etiological Model

1. Coordination of the QLS and LLLP analyses
   - 2 separate analyses, but using same analytic approach
   - Development of single etiological model that works for both data sets

2. Reducing # of IVs (from ~100) by identifying IVs that are:
   - Statistically correlated with PG status in the same year
   - Predictors of PG in the subsequent year
   - Predictors of IVs that predict subsequent PG
   - IVs need to have one or more of these features in both data sets

1. Using Structural Equation Modelling to test our theoretical model of PG

Variables Findings

- Determined most important & robust variables best predicting future PG from LLLP & QLS studies

  - Demographics
    - Non-caucasian (particularly East Indian)

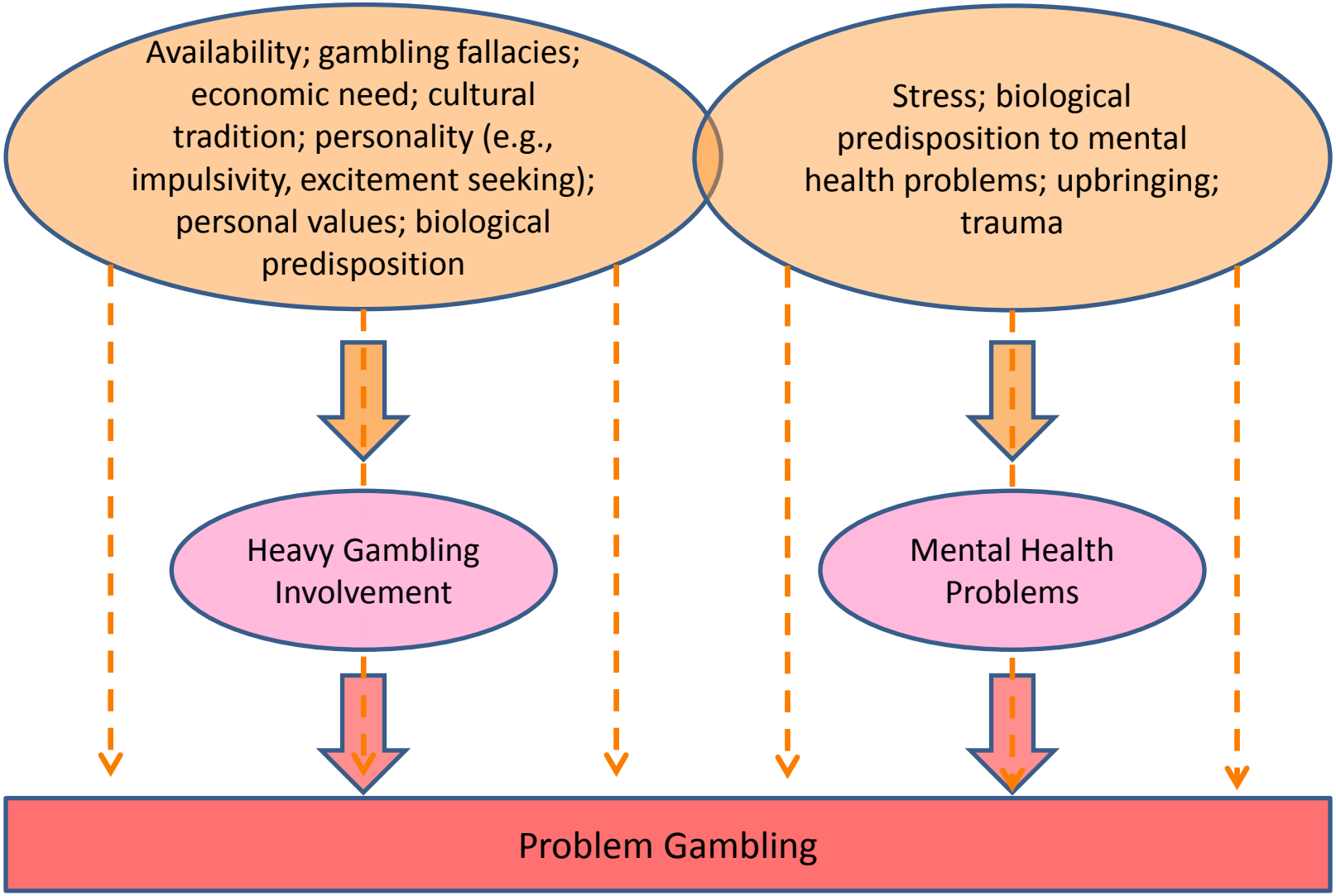
  - Gambling Involvement
    - Early big win
    - Family member(s) regular gamblers &/or problem gamblers
    - Gambling with family prior to 19
    - Number of formats engaged in
    - Overall Frequency of play
    - Overall Gambling expenditure
    - Membership in gambling rewards program
    - Gambling as a favoured leisure activity
    - Current friends/family with gambling problems

(…)

Variables Findings

- Determined most important & robust variables best predicting future PG from LLLP & QLS studies (…)
  - Mental Health
    - Lifetime history of addiction
    - Presence of any mental health disorder
    - Substance abuse or dependence
    - Presence of any behavioural addiction
  - Other
    - Illegal activities in past year
    - Below average intellect

Relevance to Model Development



Issues

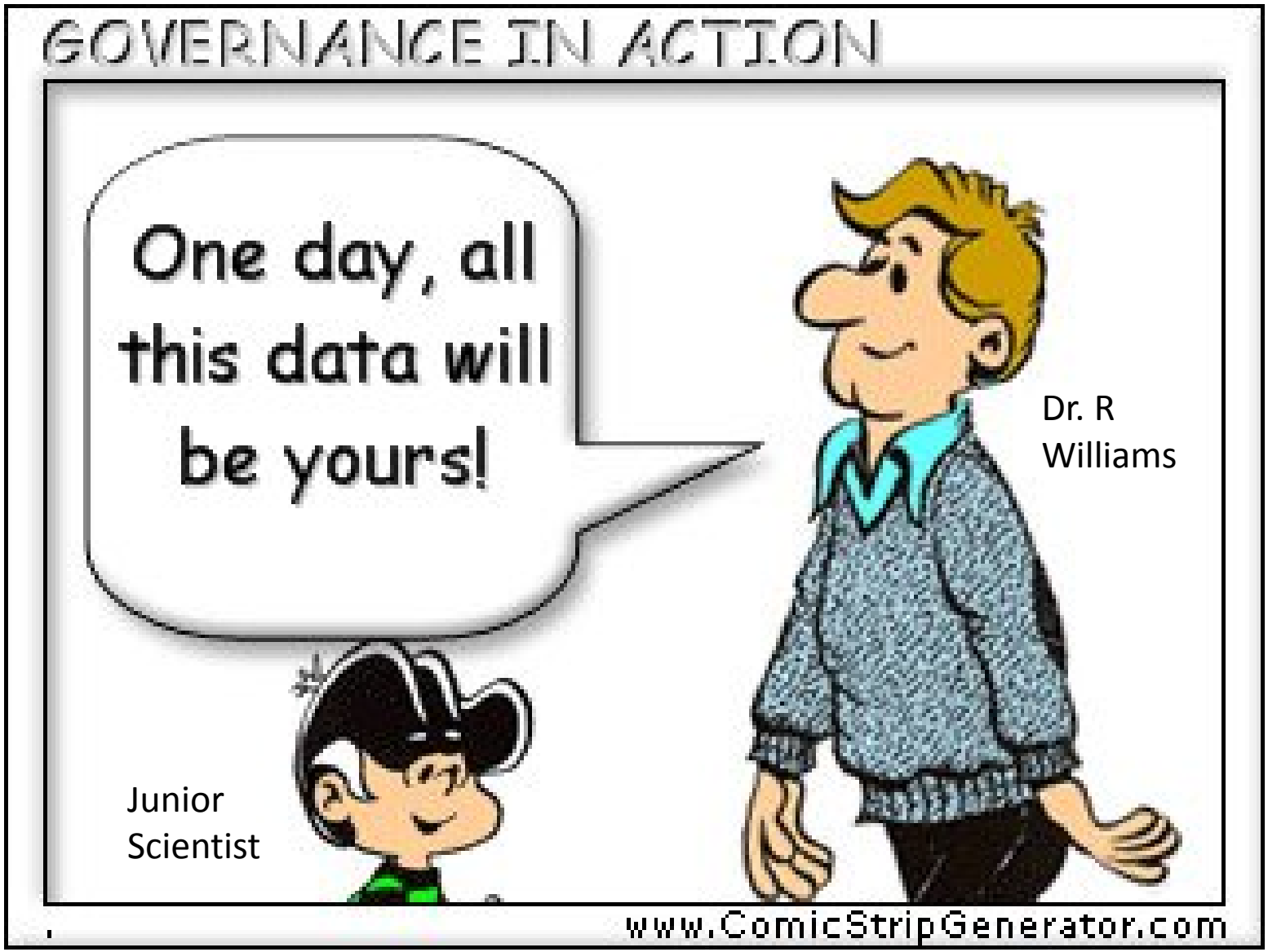
- Technological: security & ease of access
- Operational: flexibility to meet needs of researchers
- Resources: sustained $ and technical support
- Legal/Policy: intellectual property, privacy, consent, ERBs
- Cultural/Behavioural: Reward structures for promoting data access, e.g., tenure, recognition in publication

Questions

Opportunity for input

Online survey:

www.strategicscience.ca


GOVERNANCE IN ACTION
One day, all this data will be yours!
Dr. R Williams
Junior Scientist
www.ComicStripGenerator.com