



UNIVERSITY OF
LIVERPOOL

StatisticalHelp AI

*Helping health experts know enough statistical methodology to safely analyse their data with www.statsdirect.com since 1987.
Next Conversational Data Analytics with generative AIs...*



www.liverpool.ac.uk/statisticalhelp



buchan@liverpool.ac.uk



[@profbuchan](https://twitter.com/profbuchan)

Turning data into action for human health and wellbeing

What you will learn from this session

- Public **health** and healthcare needs to mobilise **data into action**
- The importance of **fusing** health (or other **domain** context) and statistical **methodology knowledge** when analysing data
- Learning from www.statsdirect.com software development journey since 1987 of how to **trap** common statistical **misconceptions** and help the user make a **reliable inference**
- Liverpool's Civic Health Innovation Labs' commitment to research and apply **Conversational Data Analytics AI**
- Building a **global reference site** of '**statistical conversations**' to test and harness generative AIs data analytic utility

The need

The following slides show examples of turning data into action in response to the COVID-19 pandemic and how healthcare AI can learn from data in joined-up ways with continuous learning loops linked across personal health, care provider and population health management...





GP, Social Care Sources



Hospital Sources



Community, Public Health Sources




Patient Sources

CIVIC DATA COOPERATIVE


TRUSTWORTHY LINKAGE, PSEUDONYMISATION, CODE EXECUTION

Health system 1...

Provider Data Processing



Integrated Care System Data Processing
Linked
Pseudonymised
Part-curated data




National Data Service
Trusted Third Party

- ❖ Key management
- ❖ Deidentification
- ❖ Reidentification

Approved Tools for Dataset production
Data curation
Analysis & Simulation

Actionable Analytic/Trustworthy Research/Secure Data Environment (TRE/SDE) in national grid / federation

Dataset Extraction and Curation Pipeline
Audited Execution of Code on Data
Population Health Management Linked to Care Workflow



SDE Network

API

COMMONS
Data Catalogue
Analytic Code Books
Algorithm Library
Terminology Services
Metadata Resources
Federated Analytics

APPROACH
Open Standards
Open Development
Open Assurance
Open Maintenance
Open Innovation

COMMUNITY
Dashboard exchange
Analytic load-balancing
Shared learning resources
Predictive cooperative

Mobilising data into action...

Spring 2019

Public Support for Data Uses

CivicDataCooperative.com

Summer 2020

Covid-19 intelligence system in 90 days for 2.7m population

CIPHA.nhs.uk

Autumn 2020

World-first voluntary mass testing

Covid-SMART

Spring 2021

First reopening of mass events

First Dance

Winter 2022

Mental Health Mission

M-RIC

Winter 2023 / Spring 2024

Research Centre, Birth Cohort, NHS Data-into-Action



CIVIC GOVERNANCE

Efficiently considering data access requests, processing agreements and monitoring data quality, curation and transferable value from innovative data processing – while driving patient, practitioner and public involvement within a region health system ‘diameter of trust & actionability’



OVERSIGHT

Strategic Data Insights
Steering Group

Role-based
Access



GOVERNED EXECUTION



OPEN DISCOVERY
OPEN IMPACT

- [Ainsworth J, Buchan I. Combining Health Data Uses to Ignite Health System Learning. Methods Inf Med. 2015;54\(6\):479-87](https://doi.org/10.1186/s12916-015-0479-8)
- [Buchan I, National Grid of Civic Data Cooperatives for Health in The Health of the Nation February 2020](https://www.nhs.uk/news/2020/02/18/national-grid-of-civic-data-cooperatives-for-health/)
- www.liverpool.ac.uk/coronavirus/research-and-analysis/covid-smart-pilot/

Covid-19 Wakeup Call for Action Ready Data

Tests & Cases

All Cheshire & Merseyside (C&M) residents tested at any Pillar 2 test site and non-C&M residents tested at a C&M test site

Note: this report does not include Pillar 1 data.

Note: positivity rate calculations do not follow PHE methodology

Show Filters

Clear Filters

Filters Applied



18,274,586

Tests Completed (LFT+PCR)

2,439,026

Individuals Tested (LFT+PCR)

803,196

Individuals Tested Positive (LFT+PCR)

3.22%

LFT Case Positivity Rate (Asymptomatic)

15.04%

PCR Case Positivity Rate (Symptomatic)

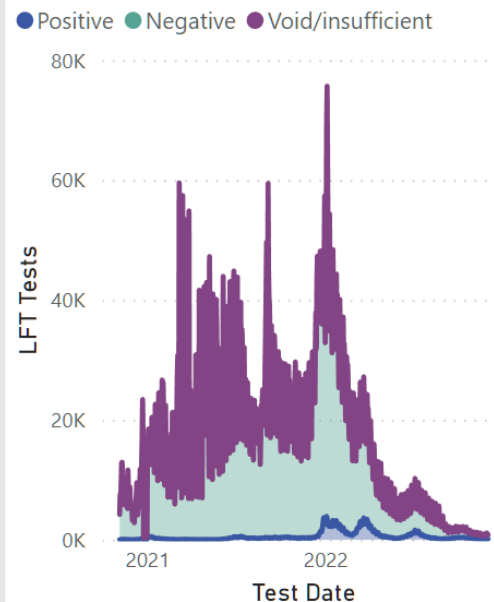
TEST COUNTS

Test Kit	Tests Completed	Positive Tests	Negative Tests	Void / Insufficient Tests
▲	406,360	21,834	369,056	15,470
LFT	13,394,612	430,575	12,948,537	15,500
PCR	4,473,614	659,790	3,726,918	86,906
Total	18,274,586	1,112,199	17,044,511	117,876

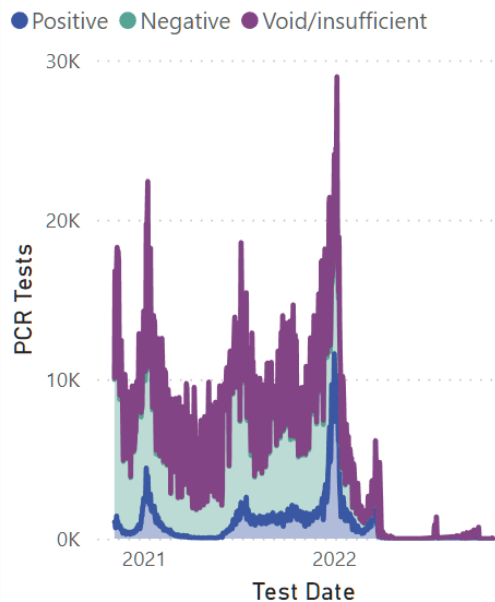
INDIVIDUALS TESTED POSITIVE

Test Kit	Individuals Tested	Individuals Tested Positive	Case Positivity Rate (Individuals)
▲	115,833	21,137	5.59%
LFT	1,666,102	315,295	3.22%
PCR	1,585,738	610,445	15.04%
Total	2,439,026	803,196	6.13%

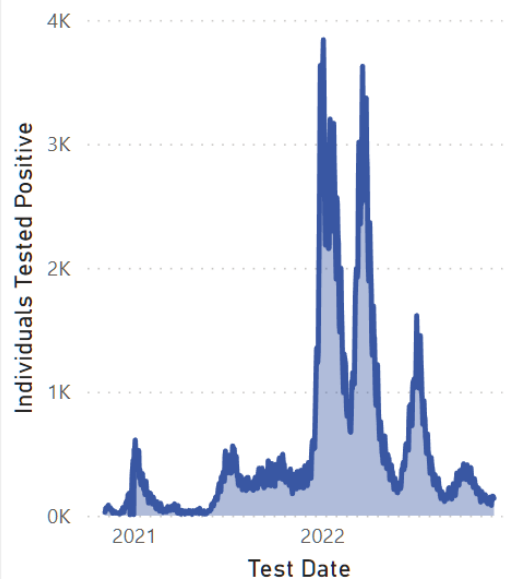
TESTS OVER TIME: LFT



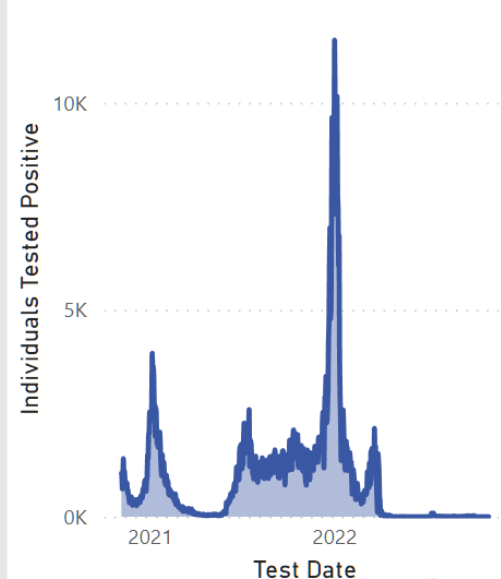
TESTS OVER TIME: PCR



INDIVIDUALS TESTED POSITIVE OVER TIME: LFT



INDIVIDUALS TESTED POSITIVE OVER TIME: PCR



Near real-time covid testing data for 2.7m people of Cheshire & Merseyside

Linked to GP and partial hospital and social care records

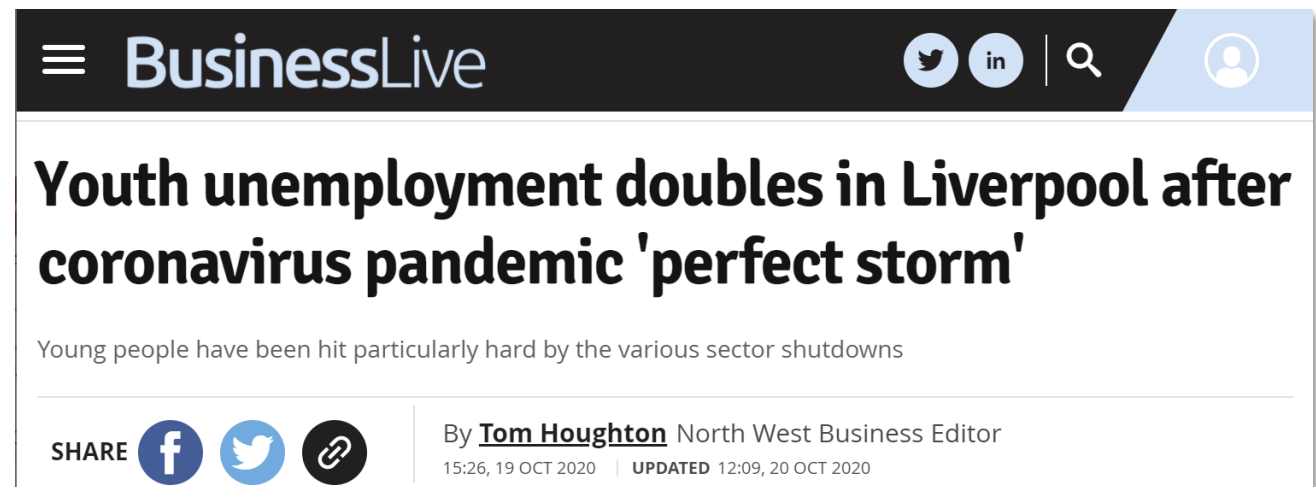
Dashboards for care, planning and research

Liverpool October 2020: Lives & Livelihoods

- COVID-19 **deaths** surge
- One of most **deprived** parts of UK
Third of children born in poverty
- **Job-losses** surge from
COVID-19 restrictions
- Visitors, hospitality and events
form **half** of Liverpool's **economy**
- **Lockdowns** a public health hazard
as well as SARS-CoV-2



The screenshot shows the ECHO Liverpool website. The header is red with the ECHO logo and a swan icon. Navigation links include NEWS, IN YOUR AREA, LIVERPOOL FC, EVERTON FC, WHAT'S ON, CELEBS, SPORT, and SPECIAL FEATURES. The main article headline is "Liverpool NHS Trust has highest number of coronavirus patients in the whole of England". The sub-headline reads: "Admissions of people with coronavirus are approaching the peak levels of last spring, city hospitals boss has warned". The article is by Luke Traynor (Chief Reporter) and Liam Thorp, dated 10:41, 10 OCT 2020. Social sharing icons for Facebook, Twitter, and LinkedIn are visible, along with a "SHARE" button and a "COMMENTS" section showing 9 comments.



The screenshot shows the BusinessLive website. The header is dark with the BusinessLive logo and social media icons for Twitter and LinkedIn. The main article headline is "Youth unemployment doubles in Liverpool after coronavirus pandemic 'perfect storm'". The sub-headline reads: "Young people have been hit particularly hard by the various sector shutdowns". The article is by Tom Houghton (North West Business Editor), dated 15:26, 19 OCT 2020, and updated 12:09, 20 OCT 2020. Social sharing icons for Facebook, Twitter, and LinkedIn are visible, along with a "SHARE" button.

Liverpool November 2020: Mass Testing Pilot

- World's **first city-wide pilot** of testing for people without COVID symptoms to save lives and livelihoods
- **Quarter** of population **volunteered** in a month despite external media negativity
- **Case detection increased** by a fifth
- **Known case rate fell** by a fifth
- **Hospitalisation fell** by a quarter

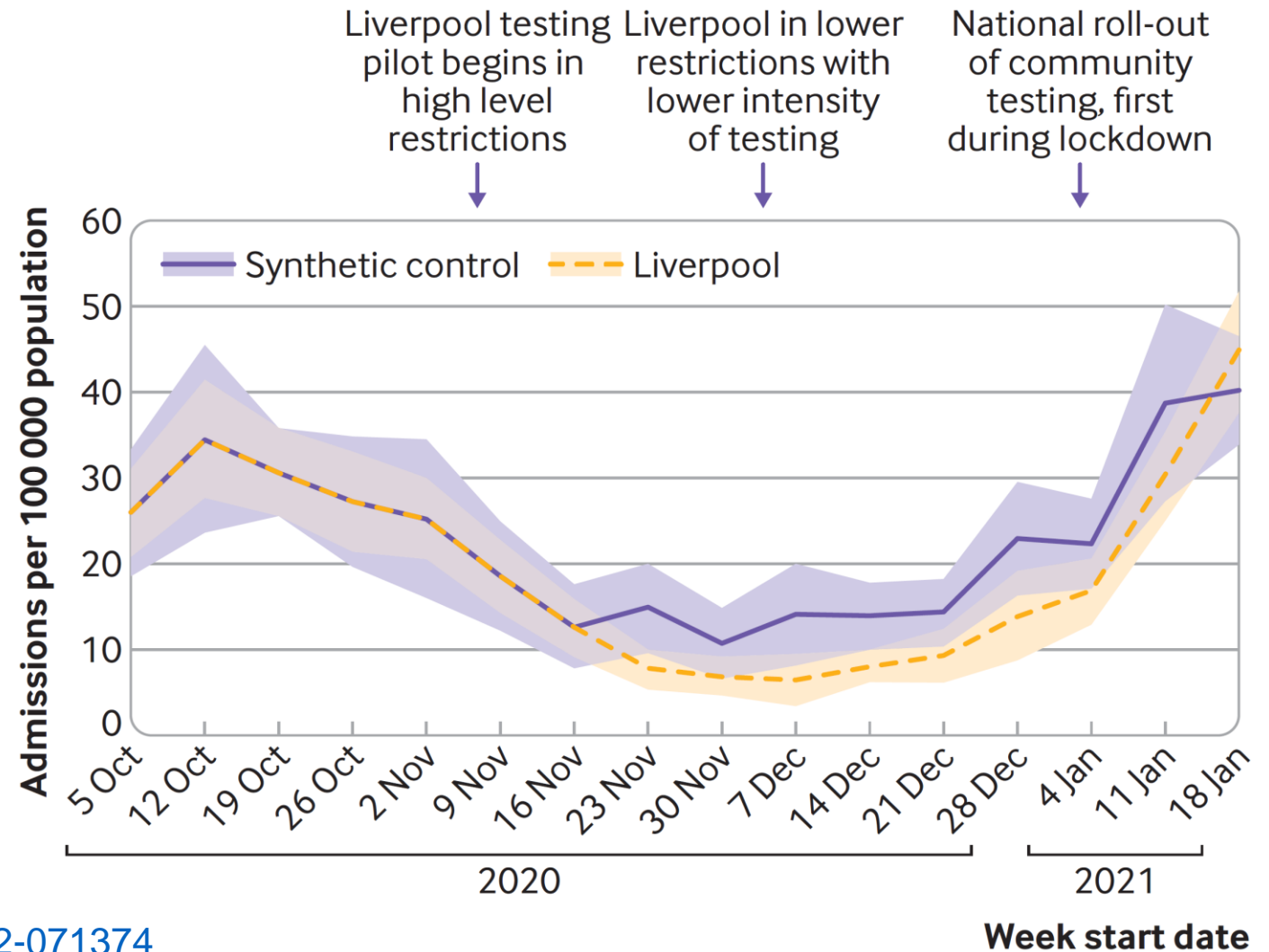
www.bmj.com/content/379/bmj-2022-071374

www.liverpool.ac.uk/coronavirus/research-and-analysis/covid-smart-pilot/



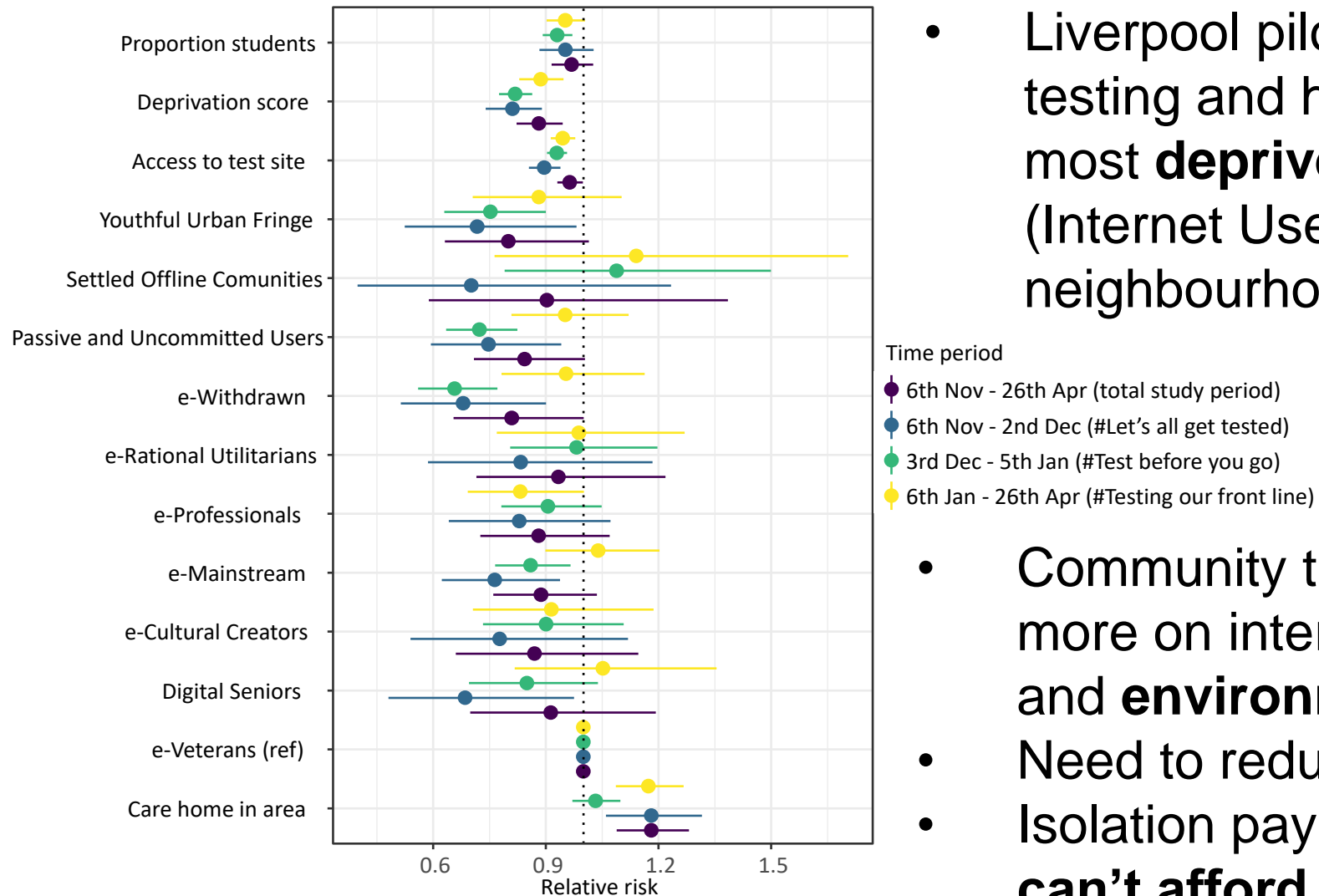
Impact of Mass Testing on Covid-19 Hospitalisations

- **Synthetic control** analysis making neighbourhoods similar in terms of background risks, epidemic and control measures
- Initial mass testing with military: **43%** (29% to 57%) **reduction** in COVID-19 hospital admissions
- Overall community testing pilot with handover to local services **25%** (11% to 35%) **reduction**



- Results: <https://www.bmj.com/content/379/bmj-2022-071374>
- Methodology: <https://www.bmj.com/content/379/bmj.o2712>
- Policy impacts: www.liverpool.ac.uk/coronavirus/research-and-analysis/covid-smart-pilot/

Digital Poverty → Low Test Uptake: Need Universal Access



- Liverpool pilot demonstrated **lower uptake** of testing and higher infection rates among the most **deprived** and the **digitally excluded** (Internet User Classification of neighbourhoods)

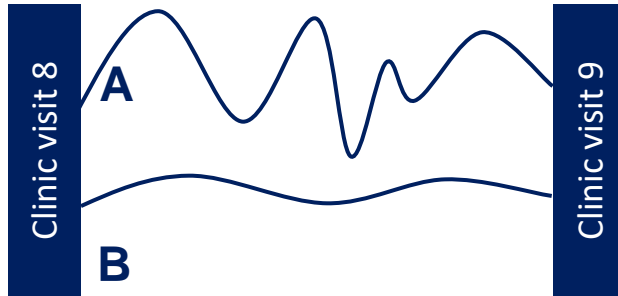
- Community testing roll-out advised to focus more on interactions of **biology, behaviour** and **environment** (end-to-end testing)
- Need to reduce **digital complexity**
- Isolation payments needed for those who **can't afford to isolate**

Digital Twin from Records or Self-experiment Avatar?



Sparse NHS records of clinical 'pit-stops'
Digital by-products of health, habits and self-care experiments
Rhythms of life to tap for discovery, engagement and intervention

Apps → Avatar Skills and Measurement Based Care

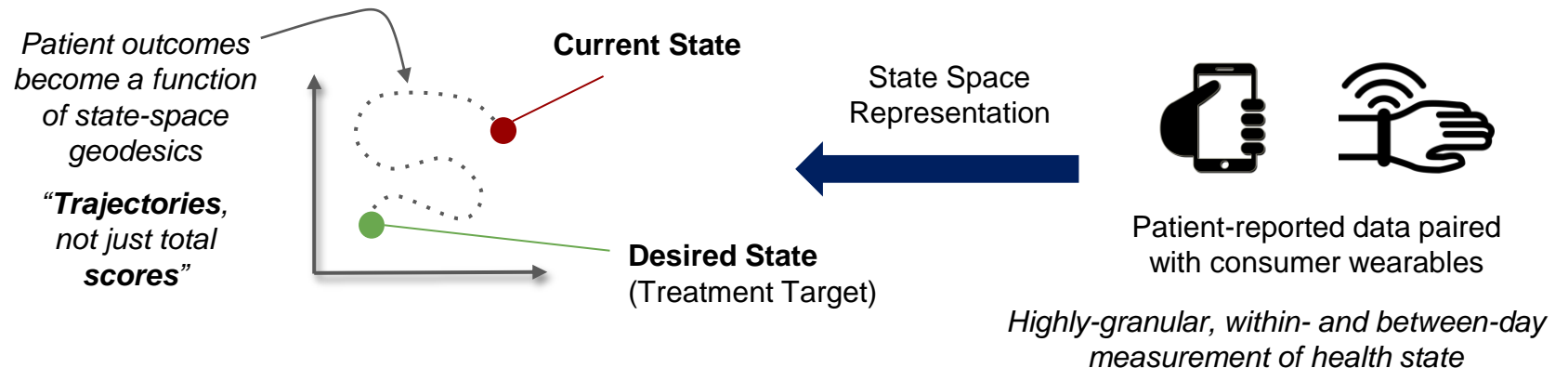
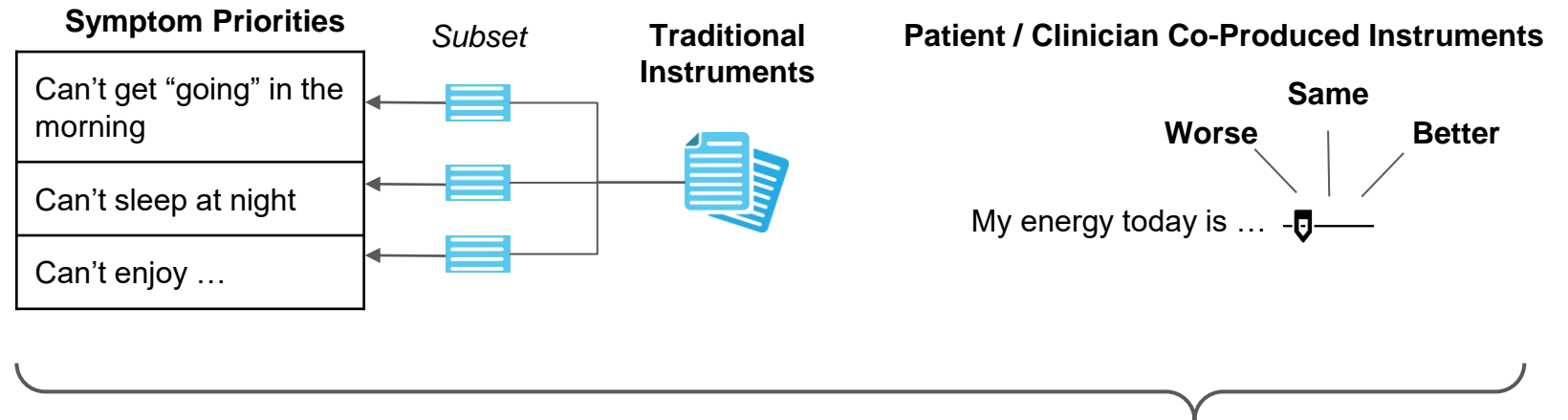


Two patients:

- Same diagnosis / treatment
- Different conditions / needs
- Key rhythms invisible to clinic

App market failure:

- Blizzard of apps for drugs, devices, clinics etc.
- Patient burden too high
- More people living longer with more than one condition
- Combinatorial explosion of complexity and confusion
- Lack of transparency & trust



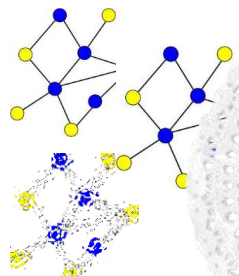
**TREAT THE PATIENT NOT THE DIAGNOSIS
AND MANAGE THE JOURNEY NOT THE VISIT**

Linked Digital Twins: Health Avatar & Learning Health System

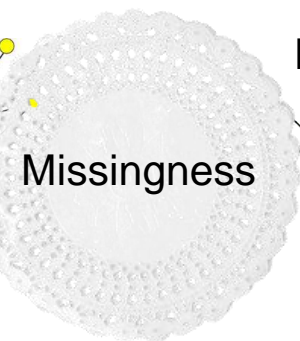
Health Avatar (interactive digital-self for healthcare) technology for tapping into the rhythms of life, sampling symptoms and biology adaptively – revealing mechanisms not manifest at clinic visits



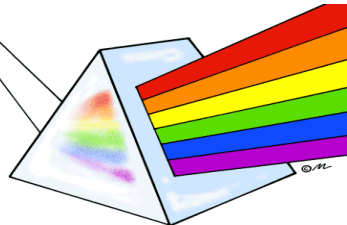
Mechanism knowledge



Missingness



Measurement Error

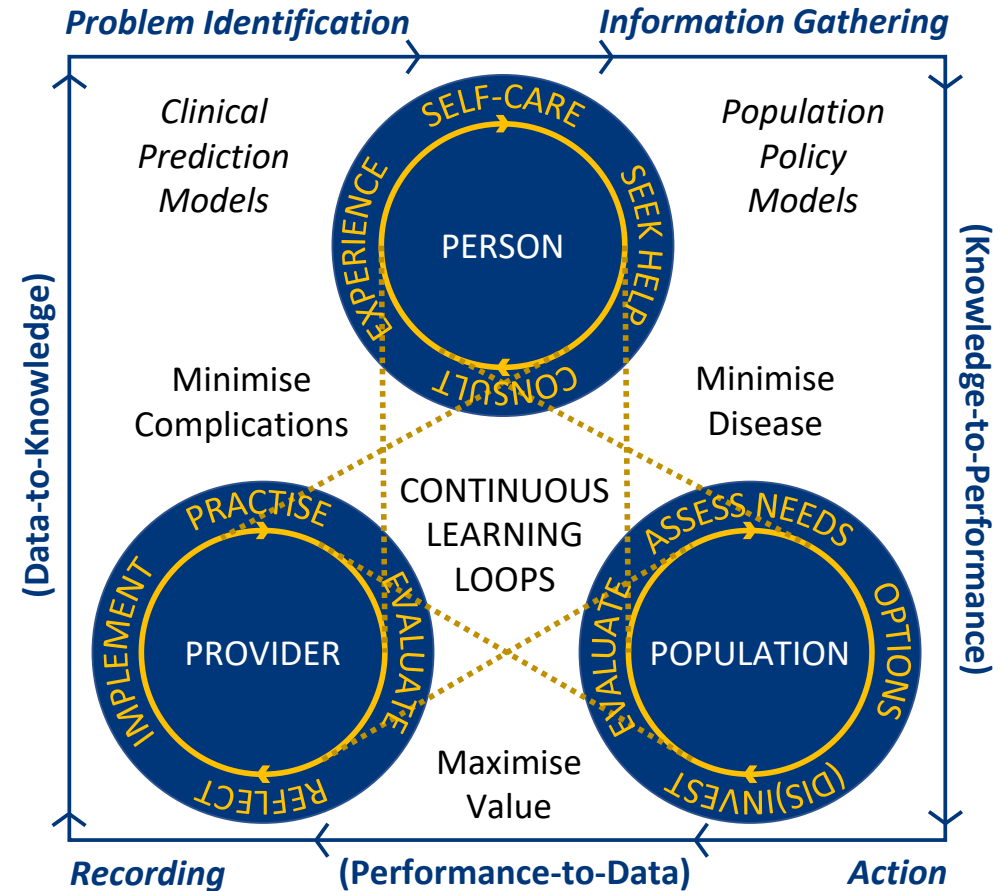


Data

A small table with multiple columns and rows of data. The columns are labeled with years from 1988 to 2008. The rows contain numerical values for various categories.

[Causal inference and counterfactual prediction in machine learning for actionable healthcare | Nature Machine Intelligence](#)

Millions of health avatars training and testing AIs in better care would reveal **temporal (transdiagnostic) patterns** and enable **adaptive observation** and **serial experimentation** for new discovery



The promise of **‘learning health systems’** will not be realised without **‘discovery grade’ data, causal inference** and **experiments**

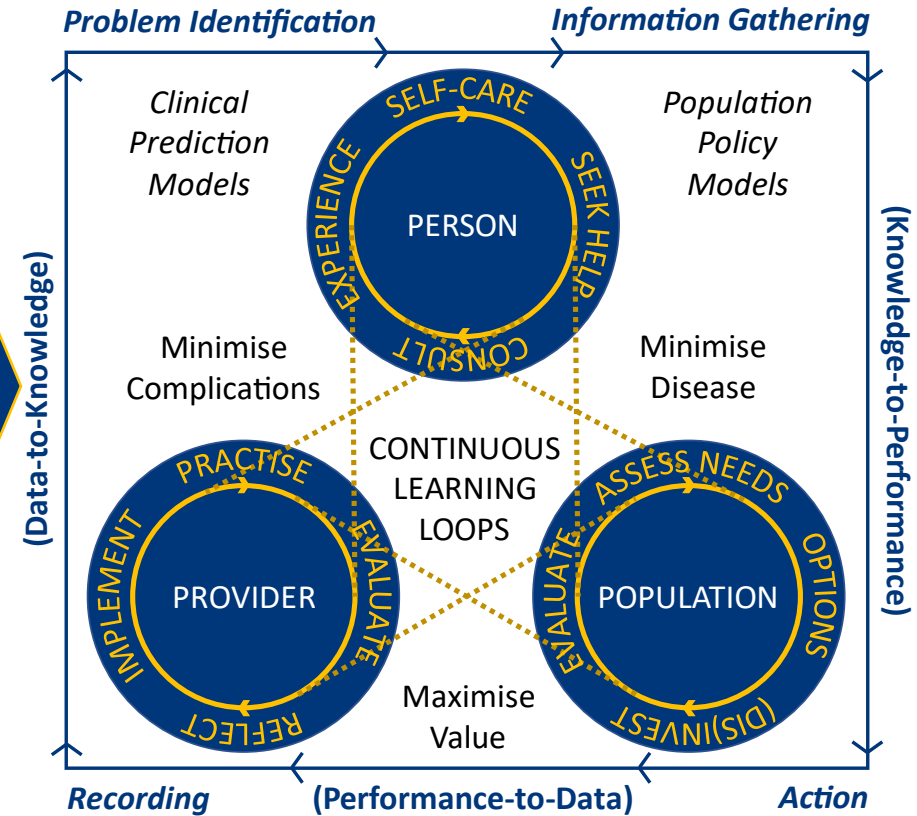
Optimising Healthcare Components vs Systems

Clinical Audit → Governance
(UK in 1980s/90s → 00s)

Learning Health Systems
(US rebranding in 2010s)

Health Systems
(Pop. Health Mgt. AI industry push 2020s)

- More people living longer with **multiple long-term conditions**
- Due to affect **68%** of **>65-year-olds** in UK by **2035** *
- Multi-condition pressures arise at **younger** ages in **deprived** areas
- Combined **mental-physical** problems more in **young** and **deprived**
- Existing **system pressures** higher in **deprived** areas
- Health and **social care** interdependency more in **deprived** areas
- Fewer resources for **prevention** accelerates **compound pressures**
- Climate/conflict/other **world pressures** denude available **funds**
- Population health management **AIs** trained/tested in **affluent** areas



Specialist registries/databases

Integrated clinical records

Wider civic (e.g. social care) data linkage

Crude predictive models
(baseline risk factor loaded)

Fuller longitudinal prediction
(difficulty learning models from data)

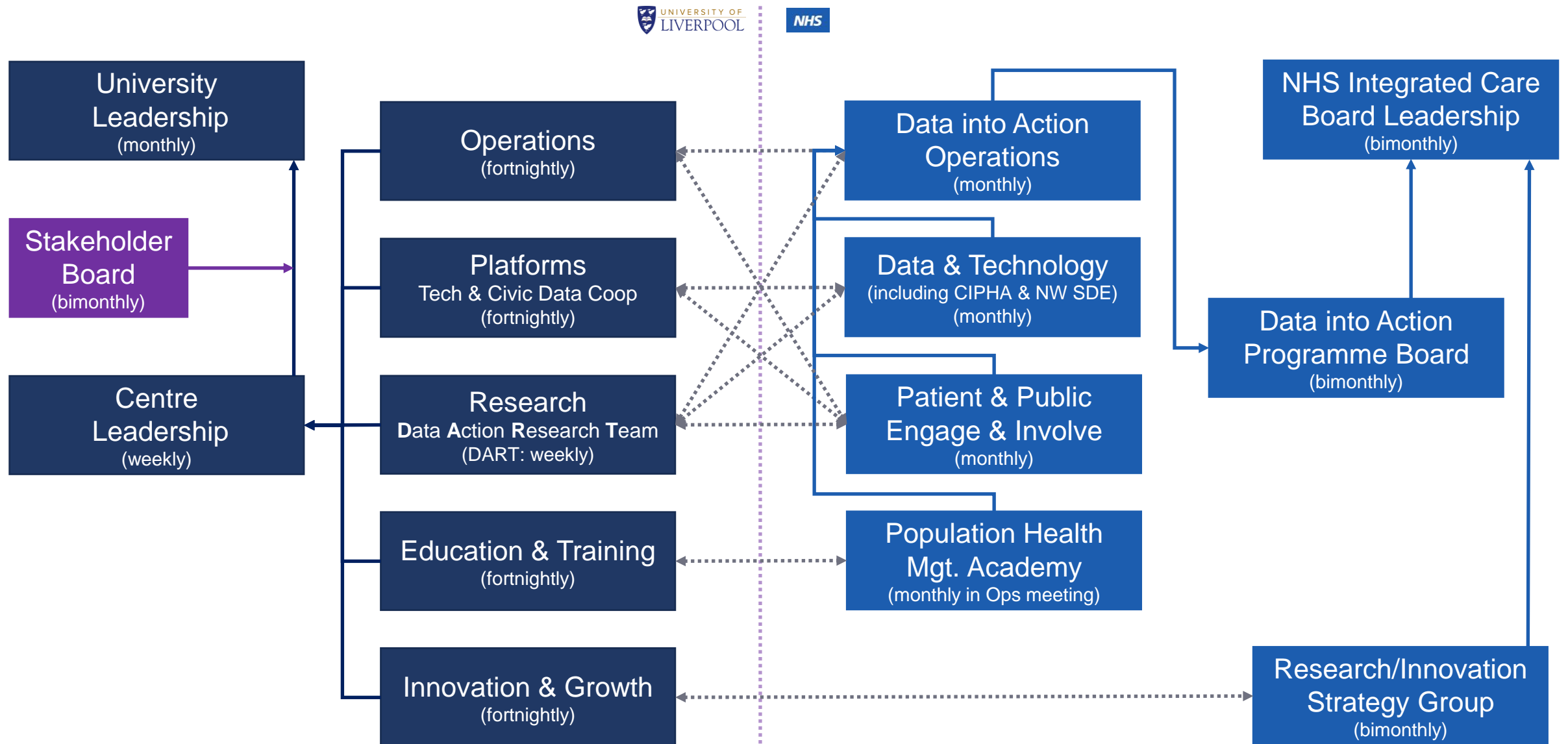
Multi-outcome prediction; complex interventions
(system dynamics; causal machine learning)

1-way translation
(trials evidence into practice)

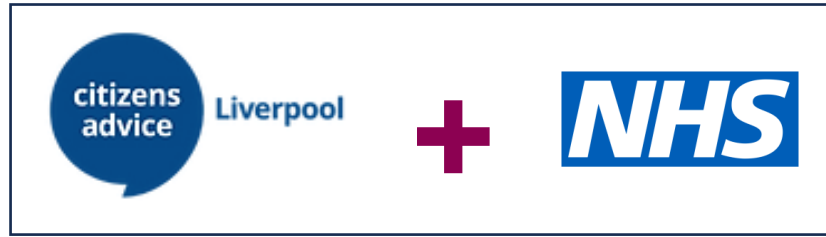
2-way translation aim
(+ practice-based evidence)

**Reverse-engineering actions to tackle
escalating/compound pressures**

CHIL Governance with NHS



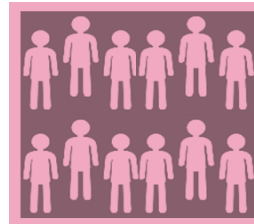
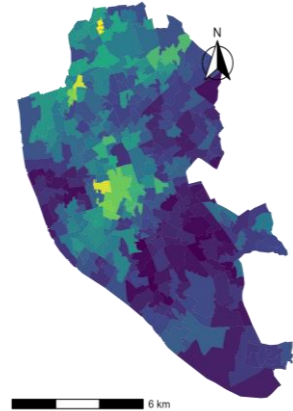
Citizens Advice on Prescription Does it improve mental health?



Large number of high need patients seen

- 65,000 people between 2018 and 2022
- 70% living in poverty
- 40% with at least 1 mental health problem
- 60% with multimorbidity
- Average 30 GP consultations per 100 clients in the 3 months before intervention

Number of people / 1000 population - 2022



Instrument
(provider preference)

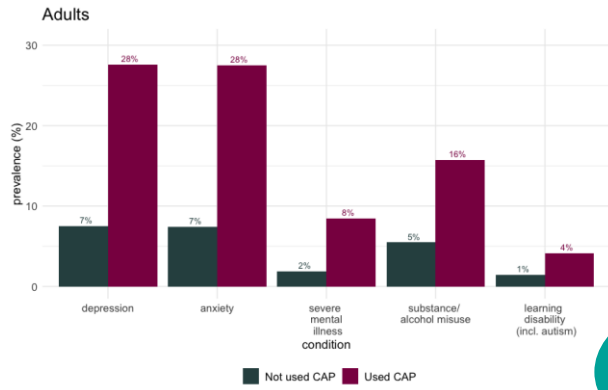


Referral to
Citizens Advice
on Prescription



Mental health care utilization:

- Antidepressant prescribing
- A&E attendances
- GP consultations
- Admissions



Cost per client was £141

Patient reported outcomes:
EQ-5D, SWEMWBS



- Reduced anxiety and depression
- Improved wellbeing

Impacts

- Reduction in Antidepressant prescribing by 73 ADQs per person per quarter (95% CI 25-121)
- 7 fewer A&E attendances per 100 clients per quarter (2-11)

Return on investment:
For every £1 invested in the CAP service,
£6.50 of value was generated

Themes: global challenges; system data-action hungry

HEALTH & CARE SYSTEMS (*pressure-resilience, equity, life-course, population health...*)

[C-GULL](#), [PHIRST LiLaC](#), [Data into Action](#), [Round E're](#), [SysteMatic](#), [M-RIC](#), [HDRC](#), [GroundsWell](#), [ARC NW Coast](#)

MENTAL HEALTH (*connected: digital, comorbidities, community/systems...*)

[M-RIC](#), Data Action Accelerator, CHI-Zone, [4M](#)

INFECTION RESILIENCE (*antimicrobial resistance, pandemic preparedness...*)

AMR-X, Data Action Accelerator, [CAMO-Net](#), [FluVue](#), [Pandemic Institute](#), [BRIT](#), CHI-Zone, [HPRU GI](#)

MEDICINES OPTIMISATION (*safety, genomics, companion-AI, polypharmacy, multimorbidity...*)

[DynAIRx](#), OLS Data Action Accelerator, CHI-Zone, [M-RIC](#), [SysteMatic](#)

METHODS & INFRASTRUCTURE (*training, methodology, digital infrastructure...*)

[CDC](#), [M-RIC](#), [HOD2](#), ARISTOTELES, [CIPHA/SDE](#), Data Action Accelerator



CHIL

Civic Health
Innovation Labs

On opening in December 2023:

"Collaboration within the research sector is essential if we want to tackle some of the largest health and care problems facing the world today, and centres like this make that a reality."

Professor Lucy Chappell

Chief Scientific Adviser DHSC
and CEO of NIHR

‘Safe Statistics’ – wakeup call in late 1980s

- **PC** revolution: more health researchers and professionals could **analyse their own data**
- Statistical **software** was written **for statisticians** not application domain experts and could easily be **misused**
- Knowledge about **mechanisms** needed to set up the best analysis was in the brain of the **domain expert**
- Knowledge about statistical **methods** to use and how to interpret the results was in the brain of the **statistician**
- “[Arcus ProStat](#)” **shareware** (for MS DOS in BASIC 7.1, FORTRAN, assembler; no external) written as **statistical knowledge support** and **data analytic tool** for common/simple methods



Personal Computer World - March 1994

Home > Browse Our Collection > Magazines > Personal Computer World Magazine > Personal Computer World - 1994 > Personal Computer World - March 1994

- Apple PowerBook Duo 270c
- Caere OmniScan Windows
- Virgin E DX2/66
- Tracker for Windows
- Trend Monitor e-Book
- Ezio FlexScan F780i
- OmniVerse 60
- Texas TravelMate 4000E Win486DX2/50
- Synergizer
- Trust FC2614 Colour Scanner
- Lexmark IJ4076 and LP4037 5E
- Digital Soup
- Q/Media for Windows
- InfoSource Word for Windows and Excel Seminars
- Arcus Pro-Stat 3**
- Radio Track
- Pro Tools Digital Audio 2
- Apple System 7 Pro
- ReelMagic video board
- Indigo E-Print 1000
- Microsoft Visual C+ +1.5
- OLE 2
- PC CAD software
- 50MHz DX2s
- Kodaks Cineon
- Sailmaking using computers
- Visual Basic Tutorial
- Converging the phone and the computer
- Fuzzy Logic Chips

Publication Date : 1st March 1994

This exhibit has a reference ID of CH690. Please quote this reference ID in any communication with the Centre for Computing History.



Click on the Image For Detail

'Safe Statistics' – typical user correction

- Typical 2-by-2 table from clinical audit
- Medic wants chi-squared test, but needs relative risk confidence interval

Exposure/ Outcome	New wound care	Usual wound care
Infected	3	38
Not infected	61	333

The screenshot shows a software interface for a 2 by 2 chi-square test. The main window has input fields for 'Characteristic' (Present: 3, Absent: 38) and 'Outcome' (Present: 61, Absent: 333). A confidence interval of 95% is selected. Below the input fields, there is a section for 'Expected values' and a 'Risk analysis (prospective)' section. A dialog box is open, asking 'Which type of study produced your data?' with options for 'Case-control study' and 'Cohort study'. The 'Cohort study' option is selected. The 'Risk analysis (prospective)' section displays the following results:

Risk analysis (prospective)

Outcome:	Characteristic factor:	
	Present	Absent
Positive	3	38
Negative	61	333

Risk ratio (relative risk in incidence study) = 0.457648
 Approximate (Koopman) 95% confidence interval = 0.151607 to 1.314979
 Approximate power (for 5% significance) = 15.58%

Risk difference = -0.055551
 Approximate (Miettinen) 95% confidence interval = -0.104474 to 0.030055

Fisher's exact test

Input table:

The help window, titled 'StatisticalHelp from StatsDirect', shows the 'Risk (prospective)' section. It explains that the function calculates relative risk, risk difference, and population attributable risk difference with confidence intervals. It provides the following 2x2 table for the risk analysis:

OUTCOME:	EXPOSURE:	
	EXPOSED	UNEXPOSED
YES	a	b
NO	c	d

Outcome rate exposed (P_e) = $a/(a+c)$
 Outcome rate not exposed (P_u) = $b/(b+d)$

Relative risk (RR) = P_e/P_u
 Risk difference (RD) = $P_e - P_u$

Estimate of population exposure (P_x) = $(a+c)/(a+b+c+d)$
 Population attributable risk % = $100 * (P_x * (RR - 1)) / (1 + (P_x * (RR - 1)))$

In retrospective studies where you select subjects by outcome not by group characteristic then you would use the odds ratio $((a/c)/(b/d))$ and not the relative risk. See [risk \(retrospective\)](#) for more information.

- From 20y old software (VB6, FORTRAN)
- User prompted to reflect on study design and correct method
- Help system helps interpret the right statistic: relative risk confidence interval not chi-square P-value

StatsDirect 2 dev-chain in
VB6, FORTRAN on XP VM

File Action Media Clipboard View Help



StatsDirect - Microsoft Visual Basic [design]

File Edit View Project Format Debug Run Query Diagram Tools Add-Ins Window Help

Ln 1, Col 1

X

General



abl



StatsDirect - meta (Code)

StatsDirect - ExactBB (Code)

(General)

(Declarations)

```
Option Explicit
Option Compare Text
```

```
' This is a bare-bones program which calculates the conditional maximum
' likelihood estimate, exact confidence limits, and exact P-values for
' either an odds ratio (given a series of 2x2 tables with person-count
' denominators) or a rate ratio (given a series of 2x2 tables with person-
' time denominators). It utilizes an efficient algorithm for calculating
' the coefficients of the conditional distribution as described in the
' references. To increase execution speed, the arithmetic is performed on
' the natural scale (not the log scale). If overflow occurs then a log
' scale is used.
```

```
' References
```

1. Martin,D Austin,H (1991) An efficient program for computing conditional maximum likelihood estimates and exact confidence limits for a common odds ratio. Epidemiology 2, 359-362.
2. Martin,DO Austin,H Exact estimates for a rate ratio. Submitted to Epidemiology.

```
' Author David O. Martin, MD, MPH
' Translation and extension (log scaling) by Iain Buchan
' Last mod 20/5/2001
```

```
Private Const MAXDEGREE As Long = 1000000           'Max degree of a polynomial
Private Const maxIter As Long = 300                 'Max # of iterations to bracket/converge to a root
Private Const TOLERANCE As Double = 0.000000000001 'Relative tolerance in results (do not use < 1e-15 if Pegasus rootfinder used)
```

```
Public Type Rec2x2 'Data for one "unique" 2x2 table
```

```
  a As Double
  m1 As Double
  n1 As Double
  n0 As Double
  freq As Long
  informative As Boolean
```

```
End Type
```

```
Private polyD() As Double 'The polynomial of conditional coefficients
Private degD As Long      'The degree of polyD
```

```
Private polyN() As Double 'The "numerator" polynomial in Func
Private degN As Long      'The degree of polyN
```

leva:

Project - StatsDirect

StatsDirect (StatsDirect.vbp)

- Forms
- Modules
 - anova (anova.bas)
 - CALCIT (CALCIT.BAS)
 - Comms (Comms.bas)
 - Coxreg (coxreg.bas)
 - describe (describe.bas)
 - dlg (dlg.bas)
 - ExactBB (ExactBB.bas)
 - FontDlg (FontDlg.bas)
 - FRMCODE (FRMCODE.BAS)
 - GraphConv (GraphConv.bas)
 - GRAPHIC (GRAPHIC.BAS)
 - Locale (Locale.bas)
 - MATHDBL (MATHDBL.BAS)
 - MESSAGE (MESSAGE.BAS)
 - meta (meta.bas)
 - nonparametric (nonparametric.bas)
 - parametric (parametric.bas)
 - power (power.bas)
 - random (random.bas)
 - rates (rates.bas)
 - REGRESS1 (REGRESS.BAS)
 - regressrpt (regressrpt.bas)
 - REVISION (REVISION.BAS)
 - ROC (ROC.BAS)
 - Routine2 (ROUTINE2.bas)
 - SUPPORT (SUPPORT.BAS)
 - survival (survival.bas)
 - tables (tables.bas)
 - xl (xl.bas)
- Class Modules

StatsDirect 4 dev-chain 100% C# in Visual Studio

```
ExactBB.cs -> X
StatsDirectUI
StatsDirect.Builtins.ExactBB
MAXDEGREE

347
348    /// <remarks>The interface between the polynomial solver and this should be far cleaner; Peter got partway through separating it.</remarks>
349    15 references | Richard Davies, 41 days ago | 1 author, 1 change
350    public class ExactBB : PolynomialSolver
351    {
352        // This is a bare-bones program which calculates the conditional maximum
353        // likelihood estimate, exact confidence limits, and exact P-values for
354        // either an odds ratio (given a series of 2x2 tables with person-count
355        // denominators) or a rate ratio (given a series of 2x2 tables with person-
356        // time denominators). It utilizes an efficient algorithm for calculating
357        // the coefficients of the conditional distribution as described in the
358        // references. To increase execution speed, the arithmetic is performed on
359        // the natural scale (not the log scale). If overflow occurs then a log
360        // scale is used.
361        //
362        // References
363        // 1. Martin,D Austin,H (1991) An efficient program for computing
364        //    conditional maximum likelihood estimates and exact confidence
365        //    limits for a common odds ratio. Epidemiology 2, 359-362.
366        // 2. Martin,DO Austin,H Exact estimates for a rate ratio.
367        //    Submitted to Epidemiology.
368        //
369        // Author David O. Martin, MD, MPH
370        // Translation and extension (log scaling) by Iain Buchan
371        // Last mod 20/5/2001
372
373        private const int MAXDEGREE = 1000000; // Max degree of a polynomial
374
375        /// <summary>
376        /// Data for one "unique" 2x2 table
377        /// </summary>
378        23 references | 0 changes | 0 authors, 0 changes
379        public struct Rec2X2
380        {
381            10 references | 0 changes | 0 authors, 0 changes
382            public double A { get; set; }
383            18 references | 0 changes | 0 authors, 0 changes
384            public double M1 { get; set; }
385            14 references | 0 changes | 0 authors, 0 changes
386            public double N1 { get; set; }
387            14 references | 0 changes | 0 authors, 0 changes
388            public double N0 { get; set; }
389            13 references | 0 changes | 0 authors, 0 changes
390            public int Freq { get; set; }
391            13 references | 0 changes | 0 authors, 0 changes
392            public bool IsInformative { get; set; }

```

Solution Explorer

Search Solution Explorer (Ctrl+)

- C# Agreement.cs
- C# Analysis.cs
- C# Anova.cs
- C# Calcit.cs
- C# CategoriseOptions.cs
- C# ChartExplorer.cs
- C# Chi.cs
- C# ConvertUnitsOptions.cs
- C# Coxreg.cs
- C# Describe.cs
- C# Distribution.cs
- C# DistributionOptions.cs
- C# DistributionType.cs
- C# DummyOptions.cs
- C# Exact.cs
- C# ExactBB.cs
- C# ExtractionOptions.cs
- C# Formula.cs
- C# GraphicsOptions.cs
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- C# Options.cs
- C# Parametric.cs
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- C# Random.cs
- C# Rates.cs
- C# Registry.cs
- C# Regress.cs
- C# Regress1.cs
- C# RegressRpt.cs
- C# Sheet.cs
- C# SimpleLinearRegressionContext.cs
- C# SortInPlaceOptions.cs

Solution Explorer Git Changes

Properties

0/0 3 net60 statsdirect3

100% No issues found

Error List

Entire Solution 0 Errors 0 Warnings 0 of 9 Messages Build + IntelliSense

Code	Description	Project	File	Line	Suppression State
------	-------------	---------	------	------	-------------------

StatsDirect 4 shared (soon open) GitHub

statsdirect / statsdirect4

Code Issues 20 Pull requests Actions Projects Wiki Security Insights

statsdirect4 Private Watch 2 Fork 0 Star 2

master 5 Branches 67 Tags

Go to file Add file Code

960 Commits

Key	Remove some secrets that shouldn't have been here	5 years ago
Layout	Revert to 4.6.*2*, not 4.6.*1*.	last year
ReleaseBuild	Add .gitignore and enough infrastructure to recreate Release...	5 years ago
RtfConverter	Allow compilation in VS2017	7 years ago
SDBootstrapper	Remove x86 builds	last year
SDInstaller	Remove x86 builds	last year
SDLicense	Revert to 4.6.*2*, not 4.6.*1*.	last year
Shell	Minor shell build fixes	12 years ago
StatsDirectCalculator	Remove BuildVersion from calculator project	6 months ago
StatsDirectUI	Add files via upload	4 days ago
bin	Start preparing for XML serialisation generation.	9 years ago
lib	Update to DX 15.1.7	9 years ago
packages	Update to more recent Antlr	8 years ago
.editorconfig	Turn off warnings about multidimensional arrays (we know ...	4 years ago
.gitignore	Ignore one extra file that can leak a password	4 years ago
StatsDirectUI.sln	Remove long-dead automation of build version	6 months ago
StatsDirectUI.sln.DotSettings	Add a few abbreviations to the approved list for method na...	6 years ago
UpgradeLog.htm	Start the process of moving from all builtins taking a ost to a...	5 years ago

About

StatsDirect source code version control

- Activity
- 2 stars
- 2 watching
- 0 forks

Releases

67 tags

Create a new release

Packages

No packages published

Publish your first package

Contributors 3

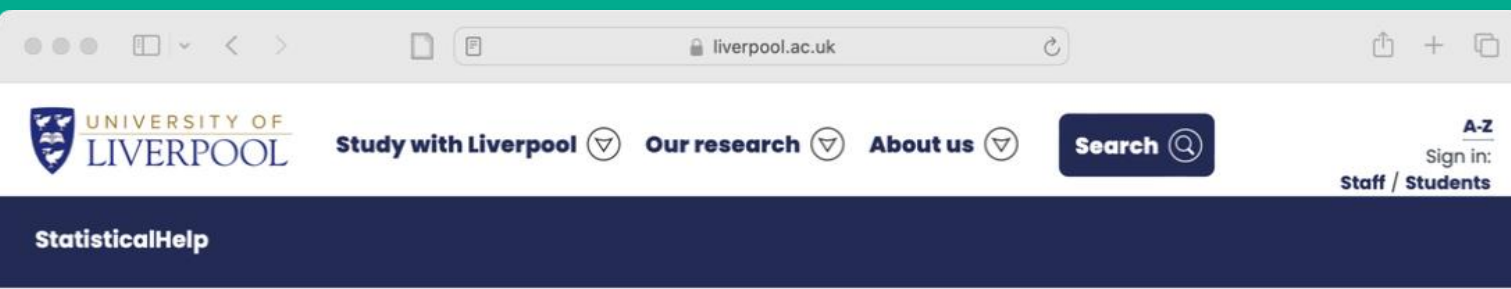
- statsdirect Professor iain E. Buchan at S...
- iain-buchan Prof iain E. Buchan
- richardvec Richard Davies

Languages

C# 98.7% Other 1.3%

Suggested workflows

Based on your tech stack



Software now free
for unrestricted use

[University home](#) > StatisticalHelp

StatisticalHelp

StatisticalHelp is a set of free, open resources to help you learn and use biostatistical methods.

StatsDirect software

StatsDirect is an easy-to-use desktop application tuned to the statistical analysis needs of clinical and public health researchers and professionals.

You can download the software from the **StatsDirect website**. It runs on Windows devices capable of running .Net 6 or later, and on Macs via **Vmware Fusion** or **Parallels**.

Biostatistical learning resources

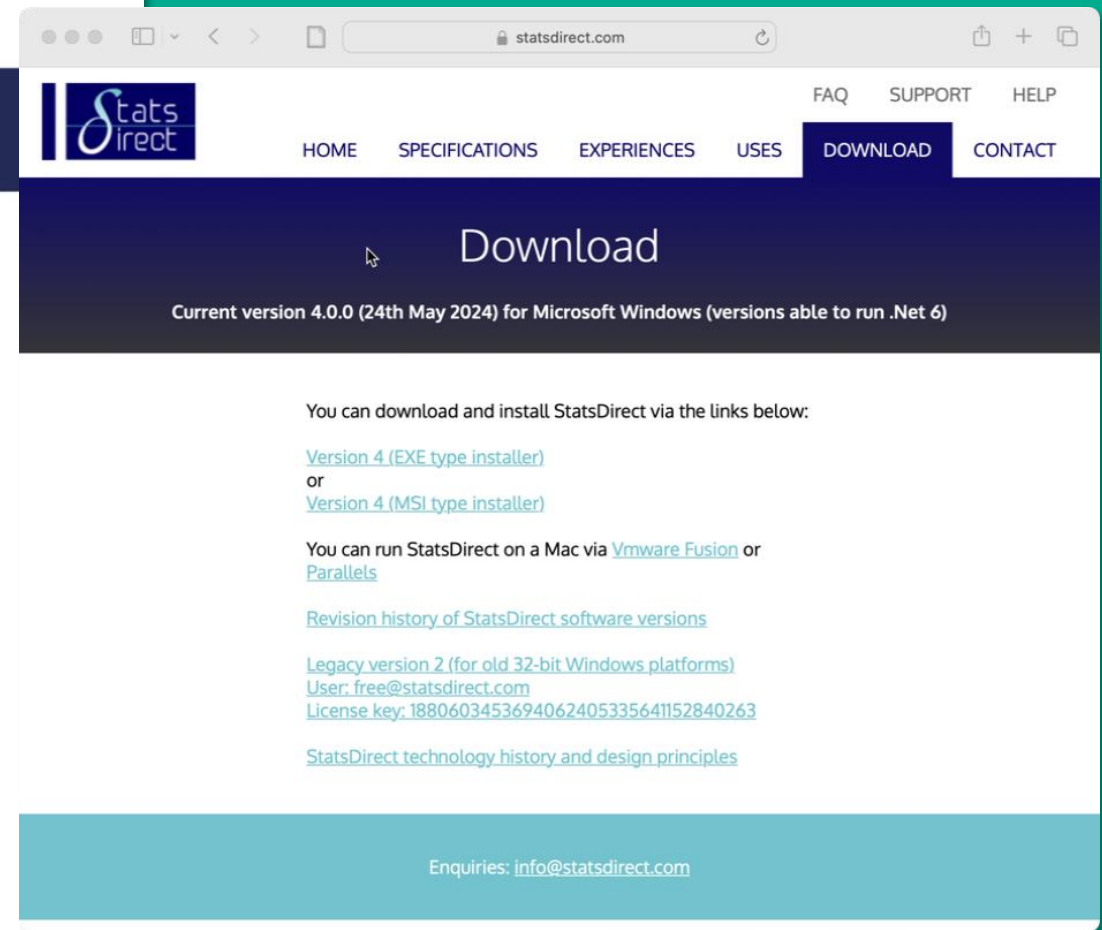
The help system in StatsDirect is also a **learning resource**. Embedding this learning in an easy-to-use data analysis tool addresses the need for health experts who are infrequent users of statistical methods to re-learn basic principles as they explore data, in turn preparing them to interact with statisticians.

Benefits

This system is designed to make it easy to analyse data while improving your statistical knowledge. Benefits include:

- **Quick and easy to use** – there's no programming required to use StatsDirect. The software uses interfaces that work like Microsoft Word and Excel. And it includes the statistical methods commonly used in health research.
- **Supports your knowledge** – it provides a robust research tool that's good for learning and employs prompts and explanations that helps to overcome common statistical misconceptions.
- **Reliable and trustworthy** – the software is a result of over 30 years of work and

Download the
Statsdirect
software



StatsDirect: Chi-square 2-by-2 table test - [Report 1]

File Edit Insert Format Data Analysis Graphics Tools Window Help

Return Help Run

Characteristic (press F1 for an example)

Present	Absent	Outcome:
3	38	Present
61	333	Absent

Which type of study produced your data?

Case-control study Cohort study Neither

Calculate Fisher exact test as well?

StatsDirect 4 UX

Auto-generated from XML 'functions'

Observed values and totals:

3	38	41
61	333	394
64	371	435

Expected values:

6.032184	34.967816
57.967816	336.032184

Uncorrected Chi² = 1.973081 P = 0.1601
 Yates-corrected Chi² = 1.376019 P = 0.2408
 Measures of association:
 Pearson's contingency = 0.067196
 Cramér's V (signed) = -0.067348

Risk analysis (prospective)

	Characteristic factor:	
Outcome:	Present	Absent
Positive	3	38
Negative	61	333

Risk ratio (relative risk in incidence study) = 0.457648
 Approximate (Koopman) 95% confidence interval = 0.151607 to 1.314979
 Approximate power (for 5% significance) = 15.58%
 Risk difference = -0.055551
 Approximate (Miettinen) 95% confidence interval = -0.104474 to 0.030055

Fisher's exact test

Input table:

3	38
61	333

Arranged table and totals:

3	38	41
61	333	394
64	371	435

Expectation of A = 6.032184
 One sided (lower tail) P = 0.1157 (doubled one sided P = 0.2314)
 Two sided (by summation) P = 0.2439
 One sided mid-P = 0.078
 Two sided mid-P = 0.1561

StatsDirect Help

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 - Risk (retrospective)
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- Sample size estimation
- Survival analysis and time series
- References

Risk (Prospective)

Menu location: Analysis_Clinical Epidemiology_Risk (Prospective).

This function calculates relative risk, risk difference and population attributable risk difference with confidence intervals.

You can examine the risk of an outcome, such as disease, given the incidence of the outcome in relation to an exposure, such as a suspected risk or protection factor for a disease. The study design should be [prospective](#). If you need information on retrospective studies see [risk \(retrospective\)](#).

The type of data used by this function is counts or frequencies (number of individuals with a study characteristic). If you want to analyse person-time data (e.g. months of follow up) instead of counts then please see [incidence rates](#).

In studies of the incidence of a particular outcome in two groups of individuals, defined by the presence or absence of a particular characteristic, the odds ratio for the resultant fourfold table becomes the relative risk. Relative risk is used for prospective studies where you follow groups with different characteristics to observe whether or not a particular outcome occurs:

		EXPOSURE	
		EXPOSED	UNEXPOSED
OUTCOME:	YES:	a	b
	NO:	c	d

Outcome rate exposed (Pe) = a/(a+c)
 Outcome rate not exposed (Pu) = b/(b+d)

Relative risk (RR) = Pe/Pu
 Risk difference (RD) = Pe-Pu

Estimate of population exposure (Px) = (a+c)/(a+b+c+d)
 Population attributable risk % = 100*(Px*(RR-1))/(1+(Px*(RR-1)))

In retrospective studies where you select subjects by outcome not by group characteristic then you would use the odds ratio ((a/c)/(b/d)) and not the relative risk. See [risk \(retrospective\)](#) for more information.

In addition to the relative measure of effect (relative risk) you may wish to express the absolute effect size in your study as the risk difference. Risk difference is sometimes referred to as [attributable risk](#) and when expressed in percent terms it is also referred to as attributable proportion. Attributable rate percent and prospective fraction. Attributable risk, risk difference is

Code-base History (www.statsdirect.com/technology.aspx)

- **1987-2000:** Gen 1 for MSDOS in BASIC PDS 7.1, FORTRAN, MS assembler – no external components – hand crafted spreadsheet
- **2000-2013:** Gen 2 for Windows in VB6, FORTRAN – external spreadsheet and report editor for familiar UX
- **2013-2024:** Gen 3 for Windows on .Net Framework in C# - similar spreadsheet and report editor external components
- **2024-:** Gen 4 for Windows on .Net 6.1 in C# - external components easily replaced – aiming for cross-platform (easy refactor)
- **2025....:** Generative AI integration with help system to wean advanced users onto deeper analytic programming in R

StatsDirect 4 Coding Priorities 2024

- Replace CHM with HTML5 help (content ready at <https://github.com/iain-buchan/statisticalhelp> – needs integrating)
- Move report editor from RTF/WMF to HTML/SVG (classes written) by shifting from DevExpress RichEdit to <https://developer.microsoft.com/en-gb/microsoft-edge/webview2/> with <https://www.tiny.cloud/>
- Continue cross-platform preparation
- Explore native MacOS options
- Explore browser-based simple function embedding in HTML5 help system (Madcap Flare project above)

Conversational Data Analytics

Statistical Help

Contents

- Basic statistical principles
- Preparing your data
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- Descriptive statistics and tabulations
- Agreement analysis
- Analysis of variance
- Chi-square tests
- Clinical epidemiology calculations
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- Exact tests on counts
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- Parametric methods**
 - Paired t test
 - Single sample t test
 - Unpaired (two sample) t test
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 - F (variance ratio) test
 - z (normal distribution) tests
 - Reference range
 - Poisson confidence interval
 - Normality tests
 - Proportions analysis
 - Randomization
 - Rates analysis and standardization
 - Regression and correlation
 - Sample size estimation
 - Survival analysis and time series
 - References

Example
From [Armitage and Berry \(1994, p. 111\)](#).
Test workbook (Parametric worksheet: Low Protein, High Protein).

Consider the gain in weight of 19 female rats between 28 and 84 days after birth. 12 were fed on a high protein diet and 7 on a low protein diet.

High protein	Low protein
134	70
146	118
104	101
119	85
124	107
161	132
107	94
83	
113	
129	
97	
123	

To analyse these data in StatsDirect first prepare them in two workbook columns and label these columns appropriately. Alternatively, open the test workbook using the file open function of the file menu. Then select the unpaired t test from the parametric methods section of the analysis menu. [Select](#) the columns marked "High protein" and "Low protein" when prompted for data.

For this example:

Unpaired t test
Mean of High Protein = 120 (n = 12)
Mean of Low Protein = 101 (n = 7)

Assuming equal variances
Combined standard error = 10.045276
df = 17
t = 1.891436
One sided P = 0.0379
Two sided P = 0.0757

95% confidence interval for difference between means = -2.193679 to 40.193679

Power (for 5% significance) = 82.25%

Assuming unequal variances
Combined standard error = 9.943999
df = 13.081702
t(d) = 1.9107

Write me the R code for comparing these two groups using an unpaired, two-sample Student t-test

High protein Low protein

134 70

146 118

104 101

119 85

124 107

161 132

107 94

83

113

129

97

123

Certainly! Below is the R code for performing an unpaired, two-sample Student t-test on the two groups "High protein" and "Low protein":

```
r
# Create vectors for the two groups
high_protein <- c(134, 146, 104, 119, 124, 161, 107, 83, 113, 129, 97, 123)
low_protein <- c(70, 118, 101, 85, 107, 132, 94)

# Perform the unpaired two-sample t-test
t_test_result <- t.test(high_protein, low_protein, var.equal = TRUE)

# Print the result
print(t_test_result)
```

This code assumes that the variances of the two groups are equal. If you suspect that the variances might not be equal, you can use `var.equal = FALSE` instead.

Two Sample t-test

```
data: high_protein and low_protein
t = 1.8914, df = 17, p-value = 0.07573
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -2.193679 40.193679
sample estimates:
mean of x mean of y
      120          101
```



Question from a user who knows what method to use but doesn't have enough R coding skills to get started...

Compare these two groups using an unpaired, two-sample Student t-test

High protein	Low protein
134	70
146	118
104	101
119	85
124	107
161	132
107	94
83	
113	
129	
97	
123	

Certainly! I'll run an unpaired, two-sample Student t-test on the provided data using R. Below is the R code for this analysis, along with the steps to handle the missing data in the "Low protein" group.

```
r
# Create vectors for the two groups
high_protein <- c(134, 146, 104, 119, 124, 161, 107, 83, 113, 129, 97, 123)
low_protein <- c(70, 118, 101, 85, 107, 132, 94)

# Perform the unpaired two-sample t-test
t_test_result <- t.test(high_protein, low_protein, var.equal = TRUE)

# Print the result
print(t_test_result)
```

To provide a complete result, I'll explain how to interpret the output once you run the code in your R environment.

Interpretation of the t-test Result

When you run the above code, you'll get an output similar to this:

```
yaml
Two Sample t-test

data: high_protein and low_protein
t = t-value, df = degrees of freedom, p-value = p-value
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 conf_low conf_high
sample estimates:
mean of x mean of y
mean_high mean_low
```

```
Two Sample t-test

data: high_protein and low_protein
t = 1.8914, df = 17, p-value = 0.07573
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -2.193679 40.193679
sample estimates:
mean of x mean of y
    120     101
```

Key Components of the Output

- t-value:** This is the calculated t-statistic.
- degrees of freedom (df):** This indicates the number of independent values that can vary in the data.
- p-value:** This value helps you determine the statistical significance of your results.
 - If the p-value is less than the significance level (commonly 0.05), you reject the null hypothesis, indicating a significant difference between the two groups.
- Confidence Interval:** This gives you a range within which the true difference between the group means lies with 95% confidence.
- Means of x and y:** These are the mean values of the "High protein" and "Low protein" groups, respectively.

To run this test with **unequal variances** you can modify the `var.equal` parameter:

```
r
# Perform the unpaired two-sample t-test with unequal variances
t_test_result <- t.test(high_protein, low_protein, var.equal = FALSE)

# Print the result
print(t_test_result)
```

Running either version of the test will allow you to compare the two groups and determine if there is a significant difference between their means.

User thinks a P-value < 0.05 is the answer to their question as a "statistically significant": not so in this example, however, given more knowledge support they would place more emphasis on the width of the confidence interval and consider collecting more data

Statistical knowledge support needs conversation segways for different users

3 patients with a new wound care regime got infected where 61 did not, where 38 patients with the usual wound care regime got infected where 333 did not, is there a statistically significant difference?

4. Calculate the z-score:

- $z = \frac{\hat{p}_1 - \hat{p}_2}{SE}$

5. Determine the p-value from the z-score and compare it to the significance level (commonly 0.05) to decide if we reject the null hypothesis.

Let's perform these calculations.

Here are the results of the calculations:

1. Sample proportions:

- Proportion of infections with the new wound care regime (\hat{p}_1): 0.046875
- Proportion of infections with the usual wound care regime (\hat{p}_2): 0.1024

2. Combined proportion (\hat{p}):

- 0.0943

3. Standard error (SE):

- 0.0395

4. Z-score:

- 1.405

5. P-value:

- 0.1601

Since the p-value (0.1601) is greater than the common significance level ($\alpha = 0.05$), we fail to reject the null hypothesis. This means there is no statistically significant difference between the infection rates of the new wound care regime and the usual wound care regime. [-]

3 patients on a new wound care regimen got infected when 61 did not, and 38 patients with usual wound care got infected when 333 did not, is there a statistically significant difference?

To determine if there is a statistically significant difference between the infection rates of the two wound care regimes, we can perform a hypothesis test for the difference between two proportions.

In this case, we can use a two-proportion z-test.

Let's define the groups as follows:

- Group 1: New wound care regime
 - Infected: $x_1 = 3$
 - Not infected: $n_1 - x_1 = 61$
 - Total: $n_1 = 3 + 61 = 64$
- Group 2: Usual wound care regime
 - Infected: $x_2 = 38$
 - Not infected: $n_2 - x_2 = 333$
 - Total: $n_2 = 38 + 333 = 371$

We will test the null hypothesis H_0 that there is no difference between the proportions of infections in the two regimes, against the alternative hypothesis H_a that there is a difference.

The steps are as follows:

1. Calculate the sample proportions:

- $\hat{p}_1 = \frac{x_1}{n_1} = \frac{3}{64}$
- $\hat{p}_2 = \frac{x_2}{n_2} = \frac{38}{371}$

2. Calculate the combined proportion \hat{p} :

- $\hat{p} = \frac{x_1 + x_2}{n_1 + n_2} = \frac{3 + 38}{64 + 371}$

3. Calculate the standard error (SE) of the difference between the two proportions:

- $SE = \sqrt{\hat{p} \cdot (1 - \hat{p}) \cdot \left(\frac{1}{n_1} + \frac{1}{n_2}\right)}$ ↓

show me this as a relative risk with 95% confidence interval

To calculate the relative risk (RR) and its 95% confidence interval, we'll use the following steps:

1. Calculate the relative risk (RR):

$$RR = \frac{\hat{p}_1}{\hat{p}_2}$$

where \hat{p}_1 is the infection rate for the new wound care regime and \hat{p}_2 is the infection rate for the usual wound care regime.

2. Calculate the standard error (SE) of the log of the relative risk:

$$SE(\ln(RR)) = \sqrt{\frac{1}{x_1} - \frac{1}{n_1} + \frac{1}{x_2} - \frac{1}{n_2}}$$

3. Calculate the 95% confidence interval for $\ln(RR)$:

$$\ln(CI) = \ln(RR) \pm Z \times SE(\ln(RR))$$

where Z is the z-value for a 95% confidence interval (approximately 1.96).

4. Exponentiate the bounds to obtain the 95% confidence interval for the relative risk:

$$CI = \left(e^{\ln(CI_{lower})}, e^{\ln(CI_{upper})} \right)$$

Let's perform these calculations.

Here are the results for the relative risk and its 95% confidence interval:

1. Relative Risk (RR):

$$RR = 0.458$$

2. 95% Confidence Interval for RR:

$$(0.146, 1.438)$$

This means that the relative risk of infection with the new wound care regime compared to the usual wound care regime is approximately 0.458. The 95% confidence interval ranges from 0.146 to 1.438, indicating that we do not have enough evidence to conclusively state that the new wound care regime significantly reduces or increases the risk of infection compared to the usual regime, as the

show me this as a relative risk with 95% confidence interval

Analysis

```
python Always show details Copy code

import numpy as np

# Calculate the relative risk
RR = p1 / p2

# Calculate the standard error of the log of the relative risk
SE_log_RR = np.sqrt((1/x1) - (1/n1) + (1/x2) - (1/n2))

# 95% confidence interval for the log of the relative risk
z = 1.96
log_CI_lower = np.log(RR) - z * SE_log_RR
log_CI_upper = np.log(RR) + z * SE_log_RR

# Exponentiate to get the 95% confidence interval for the relative risk
CI_lower = np.exp(log_CI_lower)
CI_upper = np.exp(log_CI_upper)

RR, (CI_lower, CI_upper)
```

Result
(0.4576480263157895, (0.1456203...

Risk analysis (prospective)

	Characteristic factor:	
Outcome:	Present	Absent
Positive	3	38
Negative	61	333

Risk ratio (relative risk in incidence study) = 0.457648
 Approximate (Koopman) 95% confidence interval = 0.151607 to 1.314979
 Approximate power (for 5% significance) = 15.58%
 Risk difference = -0.055551
 Approximate (Miettinen) 95% confidence interval = -0.104474 to 0.030055

Analysis

```
python Always show details Copy code

# Calculate the Koopman method confidence interval for RR

# Lower bound
CI_lower_koopman = RR * np.exp(-1.96 * np.sqrt((1/x1) + (1/x2)))

# Upper bound
CI_upper_koopman = RR * np.exp(1.96 * np.sqrt((1/x1) + (1/x2)))

(RR, (CI_lower_koopman, CI_upper_koopman))
```

Result
(0.4576480263157895, (0.14127009512778288, 1.4825622917666437))

use the koopman method for the confidence interval

The Koopman method for calculating the confidence interval for the relative risk (RR) involves using the exact method for the binomial distribution. This approach is often more accurate for small sample sizes or when the event rates are low.

Here's how we can calculate the confidence interval for RR using the Koopman method:

1. Calculate the relative risk (RR):

$$RR = \frac{\hat{p}_1}{\hat{p}_2}$$

where \hat{p}_1 is the infection rate for the new wound care regime and \hat{p}_2 is the infection rate for the usual wound care regime.

2. Calculate the lower and upper bounds for the confidence interval using the Koopman method:

$$\text{Lower bound} = \frac{\hat{p}_1}{\hat{p}_2} \cdot e^{-1.96 \cdot \sqrt{\frac{1}{x_1} + \frac{1}{x_2}}}$$

$$\text{Upper bound} = \frac{\hat{p}_1}{\hat{p}_2} \cdot e^{1.96 \cdot \sqrt{\frac{1}{x_1} + \frac{1}{x_2}}}$$

ns.

Using the Koopman method, the relative risk (RR) and its 95% confidence interval are as follows:

1. Relative Risk (RR):

$$RR = 0.458$$

2. 95% Confidence Interval for RR (Koopman method):

$$(0.141, 1.483)$$

This means that the relative risk of infection with the new wound care regime compared to the usual wound care regime is approximately 0.458. The 95% confidence interval, calculated using the Koopman method, ranges from 0.141 to 1.483. This interval still includes 1.0, indicating that we do

To calculate the relative risk (RR) and its 95% confidence interval, we'll use the following steps:

1. Calculate the relative risk (RR):

$$RR = \frac{\hat{p}_1}{\hat{p}_2}$$

where \hat{p}_1 is the infection rate for the new wound care regime and \hat{p}_2 is the infection rate for the usual wound care regime.

2. Calculate the standard error (SE) of the log of the relative risk:

$$SE(\ln(RR)) = \sqrt{\frac{1}{x_1} - \frac{1}{n_1} + \frac{1}{x_2} - \frac{1}{n_2}}$$

3. Calculate the 95% confidence interval for $\ln(RR)$:

$$\ln(CI) = \ln(RR) \pm Z \times SE(\ln(RR))$$

where Z is the z-value for a 95% confidence interval (approximately 1.96).

4. Exponentiate the bounds to obtain the 95% confidence interval for the relative risk:

$$CI = \left(e^{\ln(CI_{lower})}, e^{\ln(CI_{upper})} \right)$$

Let's perform these calculations.

Here are the results for the relative risk and its 95% confidence interval:

1. Relative Risk (RR):

$$RR = 0.458$$

2. 95% Confidence Interval for RR:

$$(0.146, 1.438)$$

This means that the relative risk of infection with the new wound care regime compared to the usual wound care regime is approximately 0.458. The 95% confidence interval ranges from 0.146 to 1.438, indicating that we do not have enough evidence to conclusively state that the new wound care regime significantly reduces or increases the risk of infection compared to the usual regime, as the

The Koopman method for calculating the confidence interval is the exact method for the binomial distribution with unequal sample sizes or when the event rates are low.

Here's how we can calculate the confidence interval for the relative risk (RR) using the Koopman method:

```

Analysis
python
Always show details
Copy code
# Calculate the Koopman method confidence interval for RR
# Lower bound
CI_lower_koopman = RR * np.exp(-1.96 * np.sqrt((1/x1) + (1/x2)))
# Upper bound
CI_upper_koopman = RR * np.exp(1.96 * np.sqrt((1/x1) + (1/x2)))
(RR, (CI_lower_koopman, CI_upper_koopman))

Result
(0.4576480263157895, (0.14127009512778288, 1.4825622917666437))
    
```

1. Calculate the relative risk (RR):

where \hat{p}_1 is the infection rate for the new wound care regime and \hat{p}_2 is the infection rate for the usual wound care regime.

2. Calculate the lower and upper bounds of the confidence interval using the Koopman method:

$$\text{Lower bound} = \frac{\hat{p}_1}{\hat{p}_2} \cdot e^{-1.96 \cdot \sqrt{\frac{1}{x_1} + \frac{1}{x_2}}}$$

$$\text{Upper bound} = \frac{\hat{p}_1}{\hat{p}_2} \cdot e^{1.96 \cdot \sqrt{\frac{1}{x_1} + \frac{1}{x_2}}}$$

Let's perform these calculations.

Using the Koopman method, the relative risk (RR) and its 95% confidence interval are as follows:

1. Relative Risk (RR):

$$RR = 0.458$$

2. 95% Confidence Interval for RR (Koopman method):

$$(0.141, 1.483)$$

This means that the relative risk of infection with the new wound care regime compared to the usual wound care regime is approximately 0.458. The 95% confidence interval, calculated using the Koopman method, ranges from 0.141 to 1.483. This interval still includes 1.0, indicating that we do not have sufficient evidence to conclude that the new regime is better.

Let Y_1 and Y_2 be multinomial random variables with parameters n_1, π_{1i} , and n_2, π_{2i} , respectively; where $i = \{1, 2, 3, \dots, r\}$. This encompasses the binomial case in which $r = 1$. We define the true selection ratio for the i th resource of r total resources to be:

$$\theta_i = \frac{\pi_{1i}}{\pi_{2i}}$$

where π_{1i} and π_{2i} represent the proportional use and availability of the i th resource, respectively. Note that if $r = 1$ the selection ratio becomes relative risk. The maximum likelihood estimators for π_{1i} and π_{2i} are the sample proportions:

$$\hat{\pi}_{1i} = \frac{y_{1i}}{n_1},$$

$$\hat{\pi}_{2i} = \frac{y_{2i}}{n_2}$$

and

← Hallucinated

where y_{1i} and y_{2i} are the observed counts for use and availability for the i th resource. The estimator for θ_i is:

$$\hat{\theta}_i = \frac{\hat{\pi}_{1i}}{\hat{\pi}_{2i}}$$

Method	Algorithm
Katz-log	$\hat{\theta}_i \times \exp(\pm z_1 - \alpha/2\hat{\sigma}_W)$, where $\hat{\sigma}_W^2 = \frac{(1-\hat{\pi}_{1i})}{\hat{\pi}_{1i}n_1} + \frac{(1-\hat{\pi}_{2i})}{\hat{\pi}_{2i}n_2}$.
Adjusted-log	$\hat{\theta}_{Ai} \times \exp(\pm z_1 - \alpha/2\hat{\sigma}_A)$, where $\hat{\theta}_{Ai} = \frac{y_{1i}+0.5/n_1+0.5}{y_{2i}+0.5/n_2+0.5}$, $\hat{\sigma}_A^2 = \frac{1}{y_1+0.5} - \frac{1}{n_1+0.5} + \frac{1}{y_2+0.5} - \frac{1}{n_2+0.5}$.
Bailey	$\hat{\theta}_i \left[\frac{1 \pm z_1 - (\alpha/2)(\hat{\pi}'_{1i}/y_{1i} + \hat{\pi}'_{2i}/y_{2i} - z_1 - (\alpha/2)^2 \hat{\pi}'_{1i} \hat{\pi}'_{2i} / 9y_{1i}y_{2i})^{1/2} / 3}{1 - z_1 - (\alpha/2)^2 \hat{\pi}'_{2i} / 9y_{2i}} \right]^3$, where $\hat{\pi}'_{1i} = 1 - \hat{\pi}_{1i}$, and $\hat{\pi}'_{2i} = 1 - \hat{\pi}_{2i}$.
Inv. hyperbolic sine	$\ln(\hat{\theta}_i) \pm \left[2 \sinh^{-1} \left(\frac{z(1-\alpha/2)}{2} \sqrt{\frac{1}{y_{1i}} - \frac{1}{n_1} + \frac{1}{y_{2i}} - \frac{1}{n_2}} \right) \right]$
Koopman	Find $X^2(\theta_0) = \chi^2_1(1 - \alpha)$, where $\tilde{\pi}_{1i} = \frac{\theta_0(n_1+y_{2i})+y_{1i}+n_2 - \{[\theta_0(n_1+y_{2i})+y_{1i}+n_2]^2 - 4\theta_0(n_1+n_2)(y_{1i}+y_{2i})\}^{0.5}}{2(n_1+n_2)}$, $\tilde{\pi}_{2i} = \frac{\tilde{\pi}_{1i}}{\theta_0}$, and $X^2(\theta_0) = \frac{(y_{1i}-n_1\tilde{\pi}_{1i})^2}{n_1\tilde{\pi}_{1i}(1-\tilde{\pi}_{1i})} \left\{ 1 + \frac{n_1(\theta_0-\tilde{\pi}_{1i})}{n_2(1-\tilde{\pi}_{1i})} \right\}$.
Noether	$\hat{\theta}_i \pm z_1 - \alpha/2\hat{\sigma}_N$, where $\hat{\sigma}_N^2 = \hat{\theta}_i^2 \left(\frac{1}{y_{1i}} - \frac{1}{n_1} + \frac{1}{y_{2i}} - \frac{1}{n_2} \right)$.

Slight tweak to question and different ChatGPT4 session:

3 patients on a new wound care regimen got infected when 61 did not, where 38 patients with usual wound care got infected when 333 did not, is there a statistically significant difference?

To determine if there is a statistically significant difference between the infection rates of the two wound care regimens, we can perform a chi-square test of independence. This test will help us understand if the observed differences in infection rates between the two groups are due to chance or if there is a statistically significant association between the type of wound care regimen and infection rates.

Let's set up the contingency table based on the given data:

	Infected	Not Infected	Total
New Wound Care Regimen	3	61	64
Usual Wound Care	38	333	371
Total	41	394	435

Now, we'll perform the chi-square test.

The chi-square test statistic is approximately 1.38, and the p-value is approximately 0.24.

Since the p-value is greater than the common significance level of 0.05, we fail to reject the null hypothesis. This means there is no statistically significant difference in infection rates between the new wound care regimen and the usual wound care regimen. The observed difference in infection rates could be due to chance. [\[-\]](#)

c.f. ...

3 patients with a new wound care regime got infected where 61 did not, where 38 patients with the usual wound care regime got infected where 333 did not, is there a statistically significant difference?

To determine if there is a statistically significant difference between the infection rates of the two wound care regimens, we can perform a hypothesis test for the difference between two proportions. In this case, we can use a two-proportion z-test.

Let's define the groups as follows:

- Group 1: New wound care regime
 - Infected: $x_1 = 3$
 - Not infected: $n_1 - x_1 = 61$
 - Total: $n_1 = 3 + 61 = 64$
- Group 2: Usual wound care regime
 - Infected: $x_2 = 38$
 - Not infected: $n_2 - x_2 = 333$
 - Total: $n_2 = 38 + 333 = 371$

We will test the null hypothesis H_0 that there is no difference between the proportions of infections in the two regimes, against the alternative hypothesis H_a that there is a difference.

The steps are as follows:

1. Calculate the sample proportions:

- $\hat{p}_1 = \frac{x_1}{n_1} = \frac{3}{64}$
- $\hat{p}_2 = \frac{x_2}{n_2} = \frac{38}{371}$

2. Calculate the combined proportion \hat{p} :

- $\hat{p} = \frac{x_1 + x_2}{n_1 + n_2} = \frac{3 + 38}{64 + 371}$

3. Calculate the standard error (SE) of the difference between the two proportions:

- $SE = \sqrt{\hat{p} \cdot (1 - \hat{p}) \cdot \left(\frac{1}{n_1} + \frac{1}{n_2}\right)}$ ↓

And pressing for the relative risk confidence interval:

c.f. ...

show me the associated relative risk and 95% confidence interval

To calculate the relative risk (RR) and its 95% confidence interval (CI), we will use the following formulas:

1. Relative Risk (RR):

$$RR = \frac{\text{Incidence rate in the treatment group}}{\text{Incidence rate in the control group}} = \frac{\frac{3}{64}}{\frac{38}{371}}$$

2. Standard Error (SE) for log(RR):

$$SE = \sqrt{\frac{1}{a} - \frac{1}{a+b} + \frac{1}{c} - \frac{1}{c+d}}$$

where:

- a is the number of infected in the tre;
- b is the number of not infected in the
- c is the number of infected in the con
- d is the number of not infected in the

1. Compute the relative risk:

$$RR = \frac{a/(a+b)}{c/(c+d)}$$

2. Compute the confidence interval using the following bounds:

$$\text{Lower bound} = \frac{RR}{\exp(SE \cdot Z_{\alpha/2})}$$

$$\text{Upper bound} = \frac{RR}{\exp(-SE \cdot Z_{\alpha/2})}$$

where $Z_{\alpha/2}$ is the critical value from the standard normal distribution for a 95% confidence interval (typically 1.96).

Let's perform these calculations.

The relative risk (RR) is approximately 0.46, and the 95% confidence interval calculated using the Koopman method is (0.15, 1.44).

This confidence interval is the same as the one obtained earlier, indicating that the infection rate for the new wound care regimen is not statistically significantly different from the usual wound care regimen, with considerable uncertainty about the true effect. [↔](#)

Semantic equivalence

Same asymptotic approximation of variance reported when alternative methods requested

show me this as a relative risk with 95% confidence interval

To calculate the relative risk (RR) and its 95% confidence interval, we'll use the following steps:

1. Calculate the relative risk (RR):

$$RR = \frac{\hat{p}_1}{\hat{p}_2}$$

where \hat{p}_1 is the infection rate for the new wound care regime and \hat{p}_2 is the infection rate for the usual wound care regime.

2. Calculate the standard error (SE) of the log of the relative risk:

$$SE(\ln(RR)) = \sqrt{\frac{1}{x_1} - \frac{1}{n_1} + \frac{1}{x_2} - \frac{1}{n_2}}$$

3. Calculate the 95% confidence interval for $\ln(RR)$:

$$\ln(CI) = \ln(RR) \pm Z \times SE(\ln(RR))$$

where Z is the z-value for a 95% confidence interval (approximately 1.96).

4. Exponentiate the bounds to obtain the 95% confidence interval for the relative risk:

$$CI = (e^{\ln(CI_{\text{lower}})}, e^{\ln(CI_{\text{upper}})})$$

Let's perform these calculations.

Here are the results for the relative risk and its 95% confidence interval:

1. Relative Risk (RR):

$$RR = 0.458$$

2. 95% Confidence Interval for RR:

$$(0.146, 1.438)$$

This means that the relative risk of infection with the new wound care regime compared to the usual wound care regime is approximately 0.458. The 95% confidence interval ranges from 0.146 to 1.438,

Statistica/Help Test Battery for Generative AIs

- At the end of each www.statisticalhelp.org worked example add a 'chat' that reproduces the answers given the data and question
- Compare ChatGPT and Gemini, varying hallucination settings
- Give a red (failed), amber (part-answered) and green (answered) rating for the AIs tested (by version and date)
- Construct an overall score from a battery of ratings
- Consider how to jump in and out of a generative AI supported by best practice statistical examples matching the user's data/questions

Thank You

To collaborate in the *StatisticalHelp* challenge
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