Practical data management for modern open science

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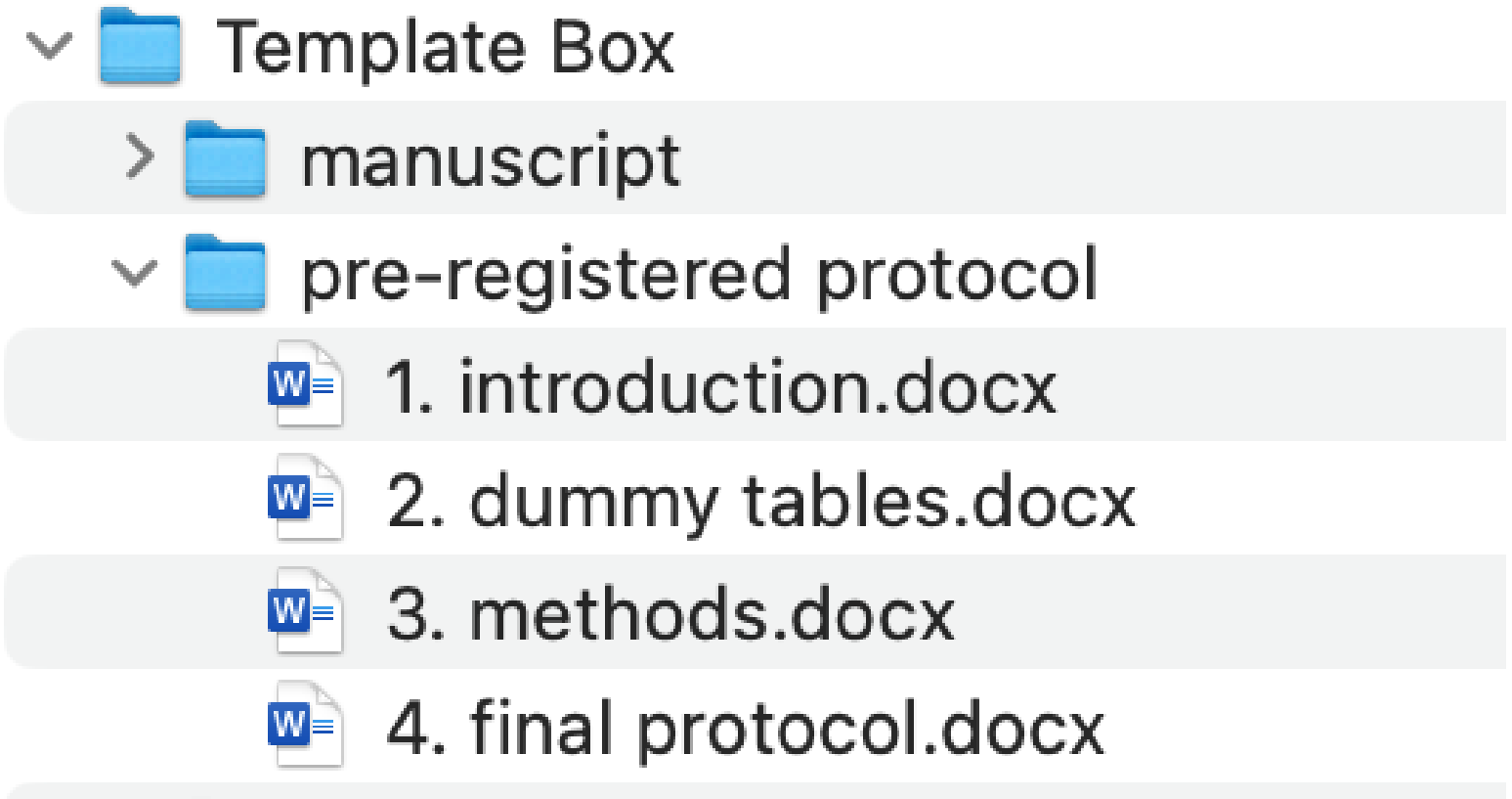
Starting a new article

Aim: Frontload all of your problems before you invest time in running analyses



Introduction

Introduction

Background
Around 18% of births in Sweden are by caesarean section, half of these planned, the other half emergency. Emergency caesarean sections (EmCS) have an increased risk of lung related issues for the infant when comparing to planned. On the other hand, emergency cesarean have a higher risk of excessive bleeding, infection, reoperation, PTSD, etc and overall higher mortality and morbidity risk for both mother and child.

Previous studies
Previous prediction models for EmCS, sfincter rupture or apgar score (evaluates health in newborns) under 7 have been made in Sweden. These looked at BMI, the womens height and age for first time mothers(nulliparious), women who have previously given birth(multiparius) and have previously had a caesarean section. They have also looked at the risk for these groups if they have diabetes, gestational diabetes, high blood pressure, epilepsi or IVF pregnancy(1).

Canadian researchers developed a predictive model for the risk of emCS with the six variables hypertensive disorders of pregnancy, antenatal depression, previous vaginal delivery, age, height and BMI and achieved an accuracy of 85% in the validation set(2).

Several studies have linked fear of childbirth as a risk factor for EmCS. Other studies have looked at depressive symptoms, antidepressants, personality traits, stress, child maltreatment, sleep, worry with some contradictory results and some correlations to increased risk of cesarean in general.

Aim
This study will include other possibly predictive markers that have not yet been tested together, such as personality, resilience, fear of childbirth and well-being during pregnancy. We want to investigate whether a combination of these markers, that includes a comprehensive list of psychological factors, in the form of a model can help in screening pregnant women with a particularly high risk of emergency caesarean section so that the birth planning can be adjusted accordingly.

1. https://www.socialstyrelsen.se/kunskapsstod-och-regler/regler-och-riktlinjer/nationella-riktlinjer/nationella-riktlinjer-graviditet-forlossning-och-tiden-efter/rekommendationer/oversikt-graviditet/planera-for-kejsarsnitt/
2. https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0268229

Dummy tables/figures

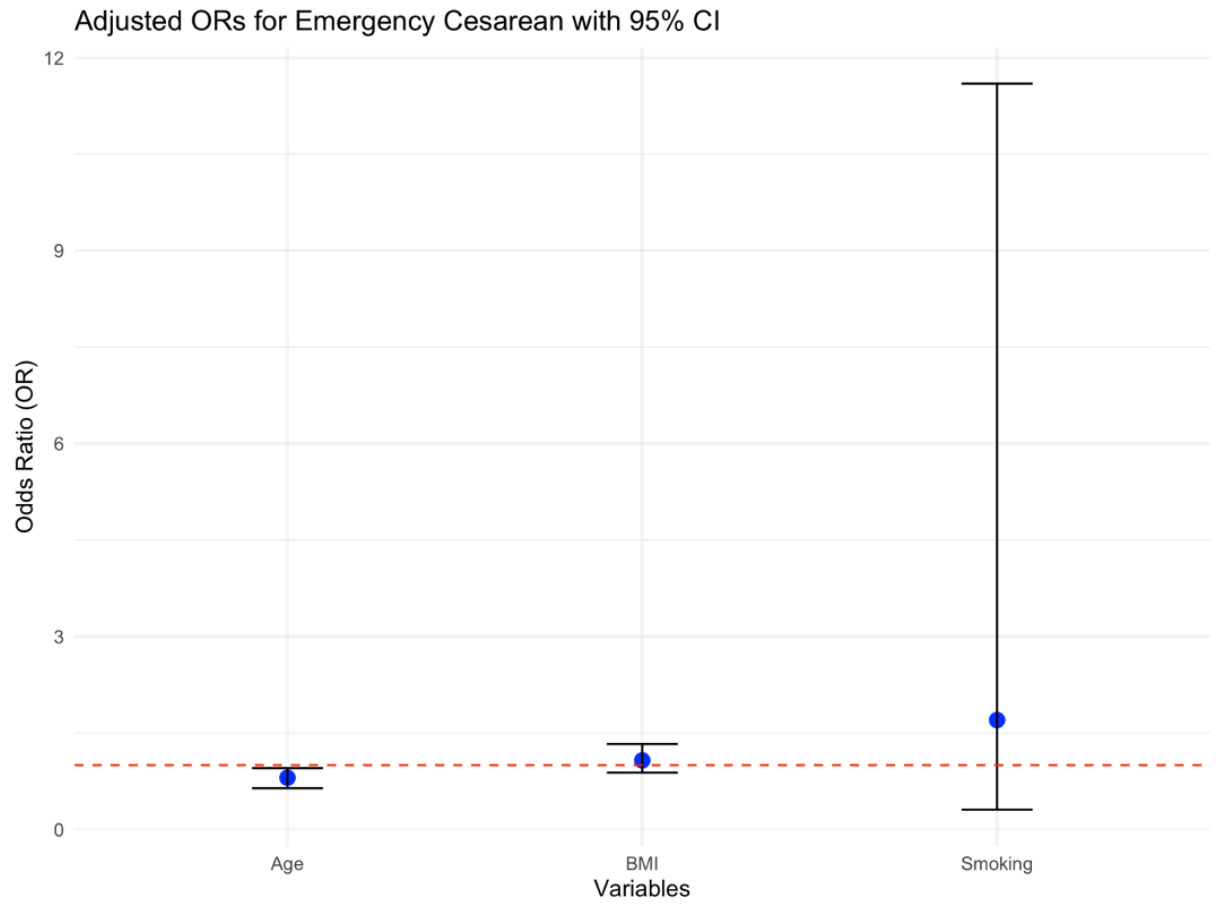
Table 1

characteristics of study population

Variable	Study population (n=x)(%)	Vaginal delivery(n=x)(%)	Emergency casarean(n=x)(%)	P value
Mean age(years)	x±			
Height	x±			
BMI before pregnancy (kg/m^2)	x±			
Infant sex Male female	 X(%) X(%)	 X(%) X(%)	 X(%) X(%)	

Dummy tables/figures

Figure 2. Forrest plot of adjusted OR (LASSO) for the variables in the training dataset



Dummy tables/figures

Table 2

Confusion matrix (based off the cutoff chosen in Figure 3)

TRAINING		Real	Real
		Vaginal delivery	EmCS
Predicted	Vaginal	0	0
Predicted	EmCS	0	200
VALIDATION		Real	Real
		Vaginal delivery	EmCS
Predicted	Vaginal	0	0
Predicted	EmCS	0	200

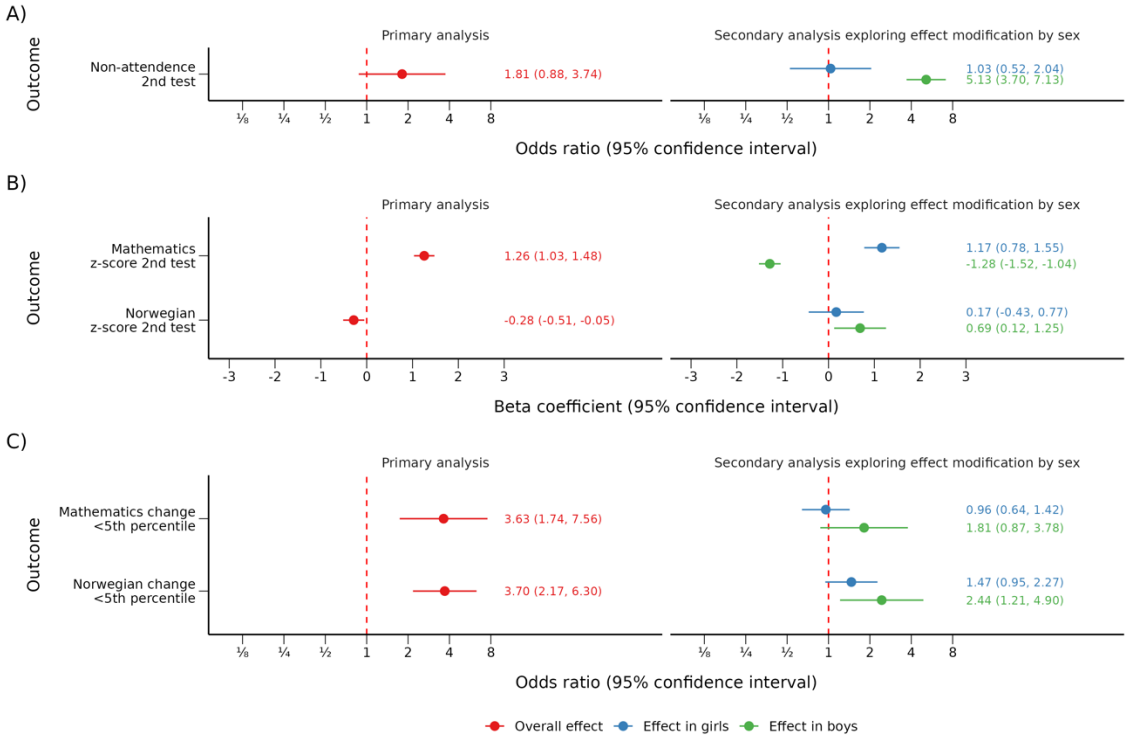
Supplemental table 1

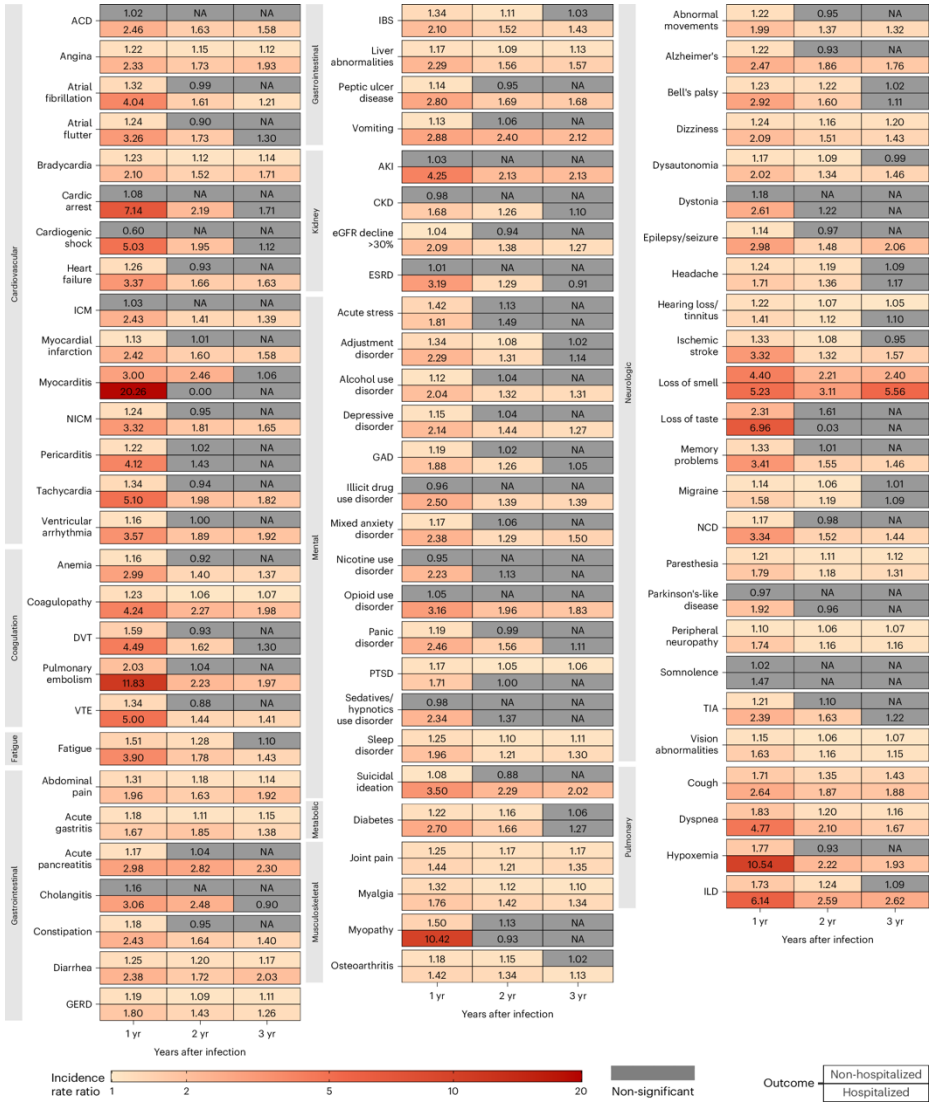
characteristics of study population

	TRAINING	TRAINING	VALIDATION	VALIDATION
Variable	Vaginal delivery(n=x)(%)	Emergency casarean(n=x)(%)	Vaginal delivery(n=x)(%)	Emergency casarean(n=x)(%)
Mean age(years)				
Height				
BMI before pregnancy (kg/m^2)				
Infant sex Male female	 X(%) X(%)	 X(%) X(%)	 X(%) X(%)	 X(%) X(%)

Dummy tables/figures

↓ ↓ ↓ 480 analyses ↓ ↓ ↓





Methods

Figure 1. To develop the prediction model, penalized multivariable logistic regression using the Least Absolute Shrinkage and Selection Operator (LASSO) was employed to exclude irrelevant variables. N variables from the univariable analysis were initially included in the LASSO regression model. Hyperparameter tuning using 10-fold cross-validation was used to determine the optimal value for the penalty parameter (λ), minimizing the classification error while selecting the most relevant predictors for emCS. Once the optimal λ was selected, the model coefficients were used to calculate adjusted odds ratios (ORs) for the selected variables in a Forest Plot.

Figure 2. To assess the performance of the LASSO-based logistic regression model, a Receiver Operating Characteristic (ROC) curve was generated for the training dataset. The optimal cut-off point (x) was selected based on maximizing the Youden index (sensitivity + specificity - 1).

Table 2. A confusion matrix was created to compare the predicted mode of delivery with the actual outcomes in the validation set. The matrix provided counts for: TP, TN, FP, FN

Table 3. From the confusion matrix, sensitivity, specificity, PPV, NPV were calculated. These metrics were compared between the training and validation sets to evaluate the models generalizability.

Final protocol

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Academic achievement in non-syndromic craniosynostosis

Public registration ▾ Updates ▾

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Open practice resources

- Data
- Analytic code
- Materials
- Papers
- Supplements

Study Information

Hypotheses

The purpose of the present study is to test for the existence of a link between single-suture craniosynostosis (SSC) and educational attainment in comparison to a cohort of matched individuals. Based on previous findings in the field and known effects of demographic variables on academic achievement in the general population, the present study therefore intends to address the following:

Is the presence of SSC associated with poorer educational attainment in comparison with individuals without SSC?

Is this effect moderated by sex or psychiatric comorbidity?

In individuals with sagittal SSC, is older age at primary surgery for the condition associated with poorer educational attainment?

Design Plan

Study type

Observational Study - Data is collected from study subjects that are not randomly assigned to a treatment. This includes surveys, "natural experiments," and regression discontinuity designs.

Blinding

No blinding is involved in this study.

Is there any additional blinding in this study?

No response

Study design

Between subjects design with 1 primary predictor (SSC/no SSC) and 3 main outcomes (school grade scores, scores on national standardized tests and obtaining of a university degree).

No files selected

Randomization

SSC participants are not randomized since they include all patients operated for the condition within the sampling frame described in the sampling plan, but the comparison group has been randomly selected from the swedish total population before we received the data.

Contributors

Karl Olsson, Mia Ramklint, Daniel Nowinski, Richard A White, Fotios C Papadopoulos, and Matilda A. Frick

Description

A registry study on acadmic achievement in individuals with non-syndromic craniosynostosis (NSC).

Registration type

OSF Preregistration

Date registered

November 10, 2023

Date created

November 10, 2023

Associated project

osf.io/ubd4j

Internet Archive link

https://archive.org/details/osf-registrations-mbjf3-v1

Category

Project

Registration DOI

https://doi.org/10.17605/OSF.IO/MBJF3

Subjects

Psychology

Social and Behavioral Sciences

Congenital, Hereditary, and Neonatal Diseases and Abnormalities

Developmental Psychology

Medicine and Health Sciences

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Registered Reports

The format is offered for hypothesis-driven quantitative research with primary research data.

We also welcome submissions in those fields proposing secondary analyses of existing data sets, provided that the authors have had no prior access to the data in question. Note that we do not consider systematic reviews and meta-analyses for the Registered Report format. High quality protocols are provisionally accepted for publication before data collection (or data analysis, for submissions involving secondary analyses of existing datasets) commences.

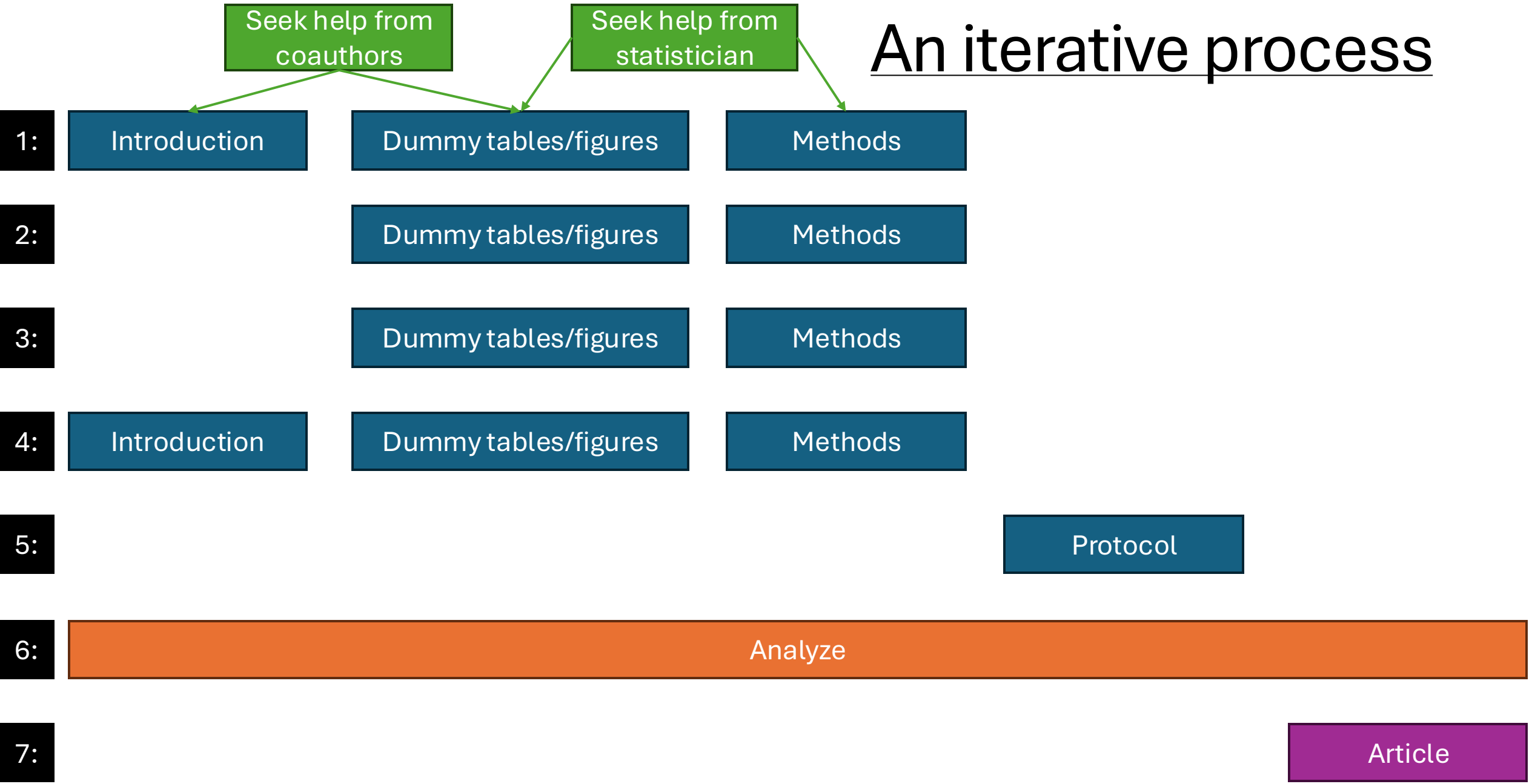
This format is designed to minimize publication bias and research bias in hypothesis-driven research, while also allowing the flexibility to conduct exploratory (unregistered) analyses and report serendipitous findings.

Registered Reports are peer reviewed in two stages - before and after data collection.

Following Stage 1 peer review, manuscripts will either be rejected outright, offered the opportunity to revise, or in-principle accepted (IPA).

An IPA decision indicates that the article will be published pending completion of the approved methods and analytic procedures, passing of all pre-specified quality checks, and a defensible interpretation of the results. Stage 1 protocols are not published in the journal following IPA. Instead they are registered by the authors in a recognised repository (either publicly or under embargo until Stage 2) and integrated into a single completed article following approval of the final Stage 2 manuscript. We have created a dedicated space on figshare to host Stage 1 protocols in-principle accepted at *Nature Communications* and offer

An iterative process



Future plans

Gather all of the previous examples and collate a series of “best examples” that people can use as templates for their own studies.

Dataset creation

The analysis dataset can be extremely tricky to construct, when variables are based off other variables that exist in different registries

Date of first gender dysphoria diagnosis	Date of second gender dysphoria diagnosis	Education level at first gender dysphoria diagnosis	Hormones within 3 months of first gender dysphoria diagnosis	Death of myocardial infarction within 3 months of hormone initiation after gender dysphoria diagnosis
Patient registry	Patient registry	Patient registry	Patient registry	Patient registry
		Education registry	Prescription registry	Prescription registry
				Cause of death registry

Education level at second gender dysphoria diagnosis (F64.0/8/9)

Patient reg.

ID	Date	ICD-10 code
1	2020-01-01	F64.0
1	2021-02-01	F64.0
3	2020-04-01	F64.0

ID	Date of 2nd diag	Year of 2nd diag
1	2021-02-01	2021

Edu. reg. 2020

ID	education
1	highschool
2	tertiary
3	highschool

Edu. reg. 2021

ID	education
1	tertiary
2	tertiary
3	highschool

ID	Year	education
1	2020	highschool
1	2021	tertiary
2	2020	tertiary
2	2021	tertiary
3	2020	highschool
3	2021	highschool

Education level at second gender dysphoria diagnosis (F64.0/8/9)

Patient reg. (edited)

ID	Date of 2nd diag	Year of 2nd diag
1	2021-02-01	2021

+

Edu. reg. (edited)

ID	Year	education
1	2020	highschool
1	2021	tertiary
2	2020	tertiary
2	2021	tertiary
3	2020	highschool
3	2021	highschool

→

Final

ID	Date of 2nd diag	Year of 2nd diag	Education at 2nd diag
1	2021-02-01	2021	tertiary

↑

What happened to people 2 and 3?

Dataset creation

Repeat that process for every variable.

This process becomes exponentially more complicated when:

- More datasets are included
- More complicated conditions (3rd diagnosis after university education…)
- The datasets are larger than your RAM
- A coauthor asks for a new variable/sensitivity analysis

“Skeleton” concept

Get good bones and attach the flesh

“Good bones”

Guaranteed to include all people and all dates!

Skeleton

ID	Date
1	2020-01-01
1	2020-01-02
1	2020-01-03
1	2020-01-04
1	2020-01-05
…	…
1	2023-12-28
1	2023-12-29
1	2023-12-30
1	2023-12-31

Patient reg.

ID	Date	ICD-10 code
1	2020-01-01	F64.0
1	2021-02-01	F64.0
3	2020-04-01	F64.0

Can be edited independently of all other datasets

ID	Date	is_gender_dysphoria
1	2020-01-01	TRUE
1	2021-02-01	TRUE
3	2020-04-01	TRUE

“Skeleton” concept

Get good bones and attach the flesh

Skeleton

ID	Date
1	2020-01-01
1	2020-01-02
1	2020-01-03
1	2020-01-04
1	2020-01-05
…	…
1	2023-12-28
1	2023-12-29
1	2023-12-30
1	2023-12-31

+

Patient reg. (edited)

ID	Date	is_gender_dysphoria
1	2020-01-01	TRUE
1	2021-02-01	TRUE
3	2020-04-01	TRUE

Can be edited independently of all other datasets

→

ID	Date	is_gd
1	2020-01-01	TRUE
1	2020-01-02	FALSE
1	2020-01-03	FALSE
1	2020-01-04	FALSE
1	2020-01-05	FALSE
…	…	
1	2023-12-28	FALSE
1	2023-12-29	FALSE
1	2023-12-30	FALSE
1	2023-12-31	FALSE

“Skeleton” concept

Each dataset has been analyzed independently of the others, then merged

skeleton		patient	education	prescription	cause of death
ID	**Date**	**is_gd**	**education**	**is_hormones**	**is_dead_mi**
1	2020-01-01	TRUE	highschool	FALSE	FALSE
1	2020-01-02	FALSE	highschool	FALSE	FALSE
1	2020-01-03	FALSE	highschool	FALSE	FALSE
1	2020-01-04	FALSE	highschool	TRUE	FALSE
1	2020-01-05	FALSE	highschool	TRUE	FALSE
…	…				
1	2023-12-28	FALSE	tertiary	TRUE	FALSE
1	2023-12-29	FALSE	tertiary	TRUE	FALSE
1	2023-12-30	FALSE	tertiary	TRUE	FALSE
1	2023-12-31	FALSE	tertiary	TRUE	FALSE

Three kinds of datasets:

1. One time -> date of birth
2. Annual -> education/salary
3. Daily -> diagnoses/death

“Skeleton” concept

Start to make the dataset more “interesting” → variables across registries

ID	Date	is_gd	gd_#	education	Educ at first gd diag	is_hormones	is_dead_mi
1	2020-01-01	TRUE	1	highschool	highschool	FALSE	FALSE
1	2020-01-02	FALSE	1	highschool	highschool	FALSE	FALSE
1	2020-01-03	FALSE	1	highschool	highschool	FALSE	FALSE
1	2020-01-04	FALSE	1	highschool	highschool	TRUE	FALSE
1	2020-01-05	FALSE	1	highschool	highschool	TRUE	FALSE
…	…						
1	2023-12-28	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-29	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-30	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-31	FALSE	2	tertiary	highschool	TRUE	FALSE

“Skeleton” concept

Start to make the dataset more “interesting” → variables across registries

ID	Date	is_gd	gd_#	education	Educ at first gd diag	is_hormones	is_dead_mi
1	2020-01-01	TRUE	1	highschool	highschool	FALSE	FALSE
1	2020-01-02	FALSE	1	highschool	highschool	FALSE	FALSE
1	2020-01-03	FALSE	1	highschool	highschool	FALSE	FALSE
1	2020-01-04	FALSE	1	highschool	highschool	TRUE	FALSE
1	2020-01-05	FALSE	1	highschool			FALSE
…	…						
1	2023-12-28	FALSE	2	tertiary			FALSE
1	2023-12-29	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-30	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-31	FALSE	2	tertiary	highschool	TRUE	FALSE

Easy to calculate complicated variables
Education 3 days after first GD diagnosis

“Skeleton” concept

	Row dependent				Row independent	Row dependent	
ID	**Date**	**is_gd**	**gd_#**	**education**	**Educ at first gd diag**	**is_hormones**	**is_dead_mi**
1	2020-01-01	TRUE	1	highschool	highschool	FALSE	FALSE
1	2020-01-02	FALSE	1	highschool	highschool	FALSE	FALSE
1	2020-01-03	FALSE	1	highschool	highschool	FALSE	FALSE
1	2020-01-04	FALSE	1	highschool	highschool	TRUE	FALSE
1	2020-01-05	FALSE	1	highschool	highschool	TRUE	FALSE
…	…						
1	2023-12-28	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-29	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-30	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-31	FALSE	2	tertiary	highschool	TRUE	FALSE

“Skeleton” concept — ready to analyze

Perfect for time-series analysis with time-varying covariates!

ID	Date	is_gd	gd_#	education	Educ at first gd diag	is_hormones	is_dead_mi
1	2020-01-01	TRUE	1	highschool	highschool	FALSE	FALSE
1	2020-01-02	FALSE	1	highschool	highschool	FALSE	FALSE
1	2020-01-03	FALSE	1	highschool	highschool	FALSE	FALSE
1	2020-01-04	FALSE	1	highschool	highschool	TRUE	FALSE
1	2020-01-05	FALSE	1	highschool	highschool	TRUE	FALSE
…	…						
1	2023-12-28	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-29	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-30	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-31	FALSE	2	tertiary	highschool	TRUE	FALSE

“Skeleton” concept — ready to analyze

Can collapse down to one row per person after generating all variables

ID	Date	is_gd	gd_#	education	Educ at first gd diag	is_hormones	is_dead_mi
1	2020-01-01	TRUE	1	highschool	highschool	FALSE	FALSE
1			1	highschool	highschool		FALSE
1			1	highschool	highschool		FALSE
1			1	highschool	highschool		FALSE
1	2020-01-05	FALSE	1	highschool	highschool	TRUE	FALSE
…	…						
1	2023-12-28	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-29	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-30	FALSE	2	tertiary	highschool	TRUE	FALSE
1	2023-12-31	FALSE	2	tertiary	highschool	TRUE	FALSE

Only cells that I care about?

Only cells that I care about?

“Skeleton” concept — big data

A) More granular skeletons:

1. Make skeleton by week instead of by day.
2. Don’t make it by month -> unequal # of days

B) Batch it:

1. Identify 10,000 ID numbers
2. After loading in datasets, restrict all datasets to those 10,000 ID numbers
3. Create a 10,000 person skeleton (per day/week)
4. Collapse to 1-week, 2-weeks, 4-weeks, 8-weeks or 1 row per person

Append all the collapsed skeletons

Analyze!

The skeleton concept scales:

- Many different datasets
- Datasets can be:
  - One time
  - Annual
  - Daily
- Large number of people
- Complicated variables
- Easy to add in new variables
- All analyses possible

Writing code

swereg (R package) assists in:

1. Skeleton creation
2. Constant datasets
3. Annual datasets
4. Daily datasets:
    1. Cause of death
    2. Diagnoses
    3. Operations
    4. Prescriptions

Writing code — Skeleton creation

```
# Initial setup----
# create the initial skeleton
skeleton <- swereg::create_skeleton(
  ids = ids,
  date_min = "2000-01-01",
  date_max = "2023-12-31"
)
```

Writing code — One time datasets

```
# One-time demos ----------------------------
## DOB & country of birth----
d <- haven::read_sas(
  fs::path(org::project$data_raw, "SCB/fp_lev_grunduppgifter.sas7bdat"),
  col_select = c("lopnr", "fodelselandgrupp", "fodelseman", "DodDatum")
) %>%
  swereg::make_lowercase_names() %>%
  dplyr::filter(lopnr %in% ids) %>%
  setDT()

swereg::add_onetime(
  skeleton,
  d,
  id_name = "lopnr"
)
```

Writing code — Annual datasets

```
# Annual demographics ----------------------------------------------
## Family type ----
for(i in 1990:2023){
  filename <- paste0("SCB/fp_lev_famtyp",i,".sas7bdat")
  #}
  d <- haven::read_sas(
    fs::path(org::project$data_raw, filename)
  ) %>%
    swereg::make_lowercase_names() %>%
    dplyr::filter(lopnr %in% ids) %>%
    setDT()

  # renaming FTYP90 to FamTyp (if it exists)
  if("ftyp90" %in% names(d)) setnames(d, "ftyp90", "famtyp")
  if("ftyp91" %in% names(d)) setnames(d, "ftyp91", "famtyp")
  if("ftyp92" %in% names(d)) setnames(d, "ftyp92", "famtyp")
  if("ftyp93" %in% names(d)) setnames(d, "ftyp93", "famtyp")
  if("ftyp94" %in% names(d)) setnames(d, "ftyp94", "famtyp")
  if("ftyp95" %in% names(d)) setnames(d, "ftyp95", "famtyp")
  if("ftyp96" %in% names(d)) setnames(d, "ftyp96", "famtyp")
  if("ftyp97" %in% names(d)) setnames(d, "ftyp97", "famtyp")

  swereg::add_annual(
    skeleton,
    d,
    id_name = "lopnr",
    isoyear = i
  )
}
```

Writing code — Cause of death

```
swereg::add_cods(
  skeleton,
  causedeath,
  id_name = "lopnr",
  cod_type = "underlying", # "underlying", "multiple"
  cods = list(
    "death_certain_infectious_parasitic_diseases"= c(
      "A",
      "B"
    ),
    "death_tumors" = c(
        "C",
        sprintf("D%02d", 0:48)
      ),
    "death_diseases_blood"= c(
      sprintf("D%02d", 50:89)
      ),
    "death_endocrine_diseases"= c(
      "E"
    ),
    "death_mental_disorders"= c(
      "F"
      ),
```

Writing code — Diagnoses

```r
swereg::add_diagnoses(
  skeleton,
  diagnoses_and_operations,
  id_name = "lopnr",
  diags = list(
    "diag_gd_icd10_F64_0" = c("F640"),
    "diag_gd_icd10_F64_89" = c("F6489"),
    "diag_gd_icd10_F64_089" = c("F640", "F648", "F649"),
    "diag_gd_icd89_transsexual" = c("302[A-Z]", "302,31", "302,99"),

    "diag_psychiatric_not_gd" = c(
      "F", "!F640", "!F648", "!F649", # ICD10: F00-F99
      "29[0-9][A-Z]", "3[0-1][0-9][A-Z]", "!302[A-Z]", # ICD9: 290-319,
      "29[0-9],", "30[0-9],", "31[0-5],", "!302,31", "!302,99" # ICD8: 290-315
    ),

    "diag_intellectual_disability" = c(
      "F7", # ICD10
      "31[7-9][A-Z]",  # ICD9
      "31[0-5]," # ICD8
    ),
```

Writing code — Operations

```
swereg::add_operations(
  skeleton,
  diagnoses_and_operations,
  id_name = "lopnr",
  ops = list(
    "op_afab_mastectomy"= c(
      "HAC10",
      "HAC20",
      "HAC99",
      "HAC15"
    ),

    "op_afab_breast_reconst_and_other_breast_ops" = c(
      "HAD20",
      "HAD30",
      "HAD35",
      "HAD99",
      "HAE99"
    ),

    "op_afab_penis_test_prosth" = c(
      "KFH50",
      "KGV30",
      "KGW96",
      "KGH96"
    ),
```

Writing code — Prescriptions

```
swereg::add_rx(
  skeleton,
  lmed,
  id_name = "lopnr",
  rxs = list(
    "rx_hormones_pubblock"= c(
      "L02AE",
      "H01CA"
    ),
    "rx_hormones_testosterone" = c(
      "G03B"
    ),
    "rx_hormones_prog_estandro"= c(
      "G03C",
      "L02AA",
      "G03D",
      "L02AB",
      "G03H",
      "L02BB",
      "G04CB",
      "C03DA01"
    )
```

Future plans

Gather all of the definitions (cause of death, diagnoses, operations, prescriptions) and bundle them up in the swereg package.

'org' — Organizing projects

Three types of project material:

1. Data
    - Encrypted
    - Not stored on the cloud

2. Results
    - Immediately shared with collaborators (cloud?)
    - Results archived over time

3. Code
    - Version control
    - Publicly accessible
    - One sequential pipeline

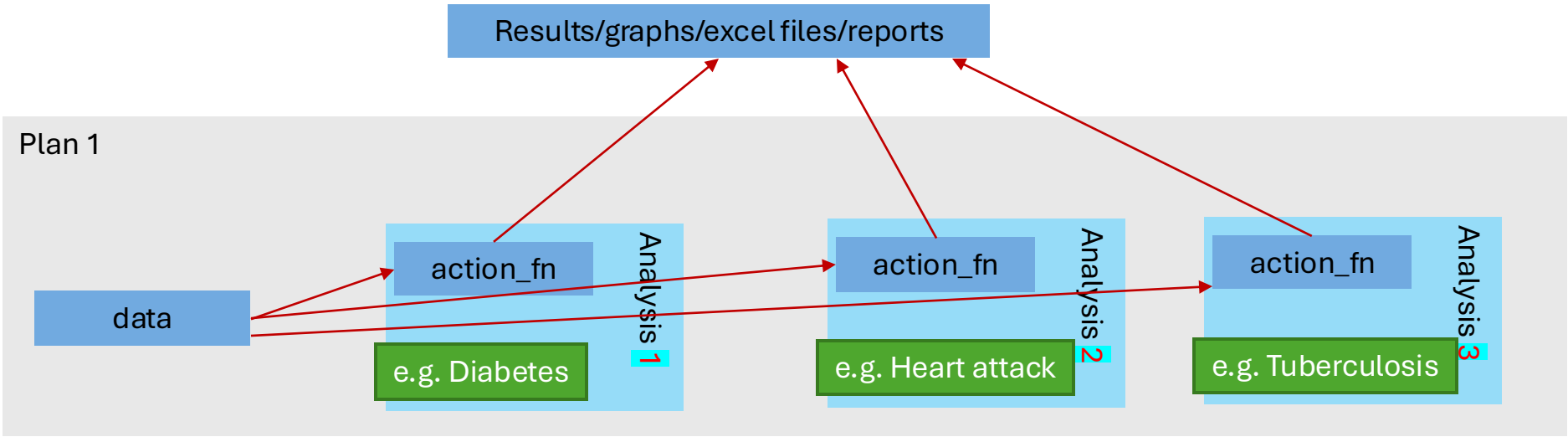
Additional problem:

- Will your code run on multiple computers?

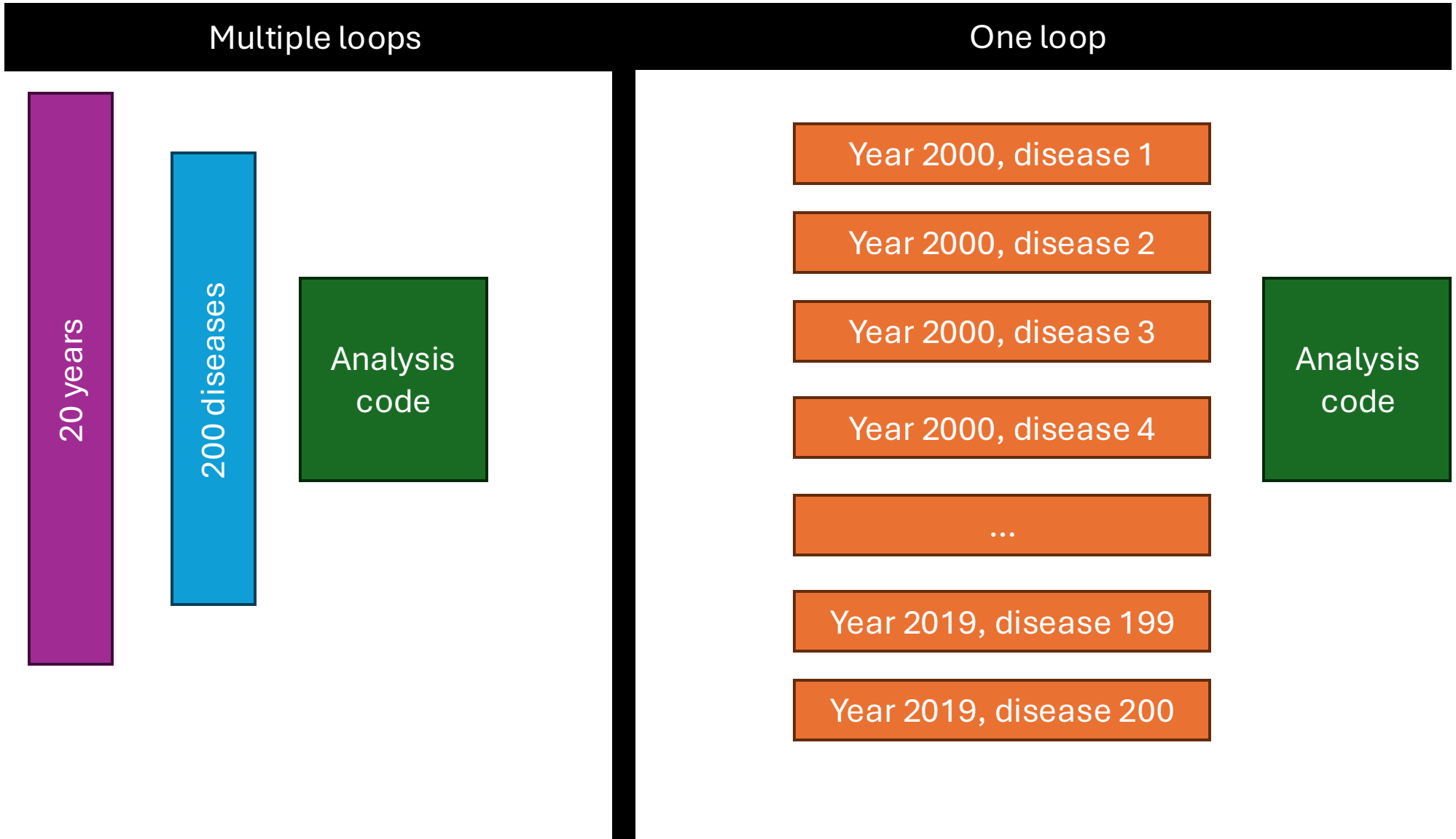
'org' — Organizing projects

Example

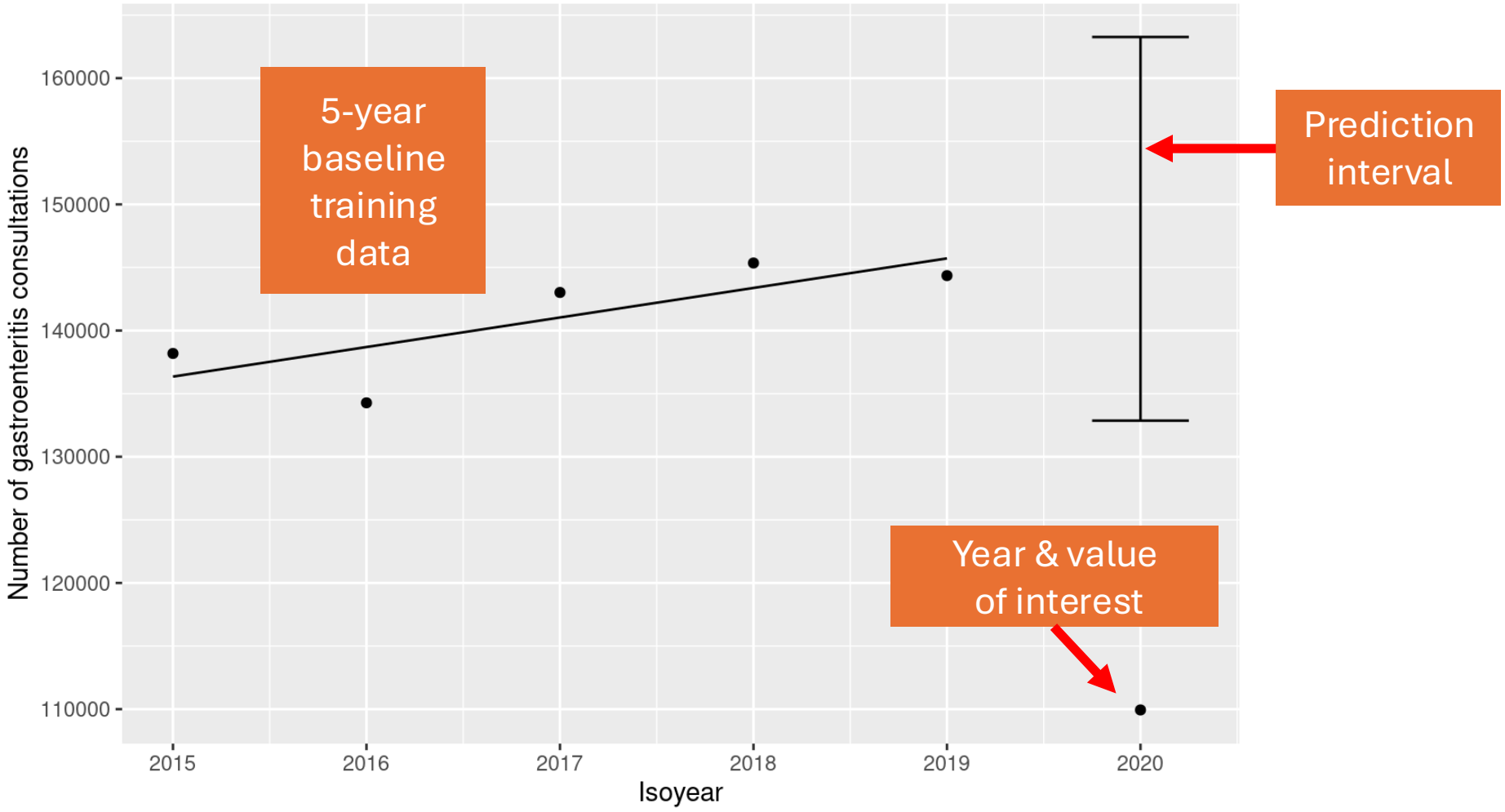
'plnr' — Organizing projects



'plnr' — Organizing projects



'plnr' — Organizing projects



'plnr' — Organizing projects

Argset: A named list containing a set of arguments

Analysis:

- 1 argset
- 1 action function that takes two arguments:
  - Data (named list)
  - Argset (named list)

Plan: Overarching "scheduler"

- 1 data pull
- 1 list of analyses

Mental model:

One (or more) datasets and we want to run multiple analyses.

Single-function plans:

One action function (e.g. make_figure) called multiple times with different argsets (e.g. year=2019, year=2020)

Multi-function plans:

Multiple action functions (e.g. figure_1, figure_2) called multiple times (maybe with/without different argsets)

'plnr' — Organizing projects

Example