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{r}amnog
Towards a common, open-source solution for programming AMNOG-style EU HTA analyses

OS10

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Views and opinions expressed are those of the speakers and not necessarily Novo Nordisk

Results

Happy users

3 submissions

- 50% reduction in time spent – with MVP
- Ad hoc interface with SAS for modelling

First project. Equivalent to 3400 CSR summaries. 90% done by chef.

What is HTA?

REGULATORY

Do benefits outweigh risks?

Can we use the treatment?

Is quality acceptable?

HTA

Is it good value?

… for whom?

Should we use the treatment?

Is it better than what we currently have?

So - what is AMNOG?

Arzneimittelmarkt-Neuordnungsgesetz
.. or just AMNOG

Pharmaceuticals Market Reorganisation Act

Benefit assessment of drugs to the German market

EU HTA and JCA

- Largely influenced by AMNOG.
- For all EU members.
- In effect from 2025/28/30

What about EU HTA Joint Clinical Assessment (JCA)?

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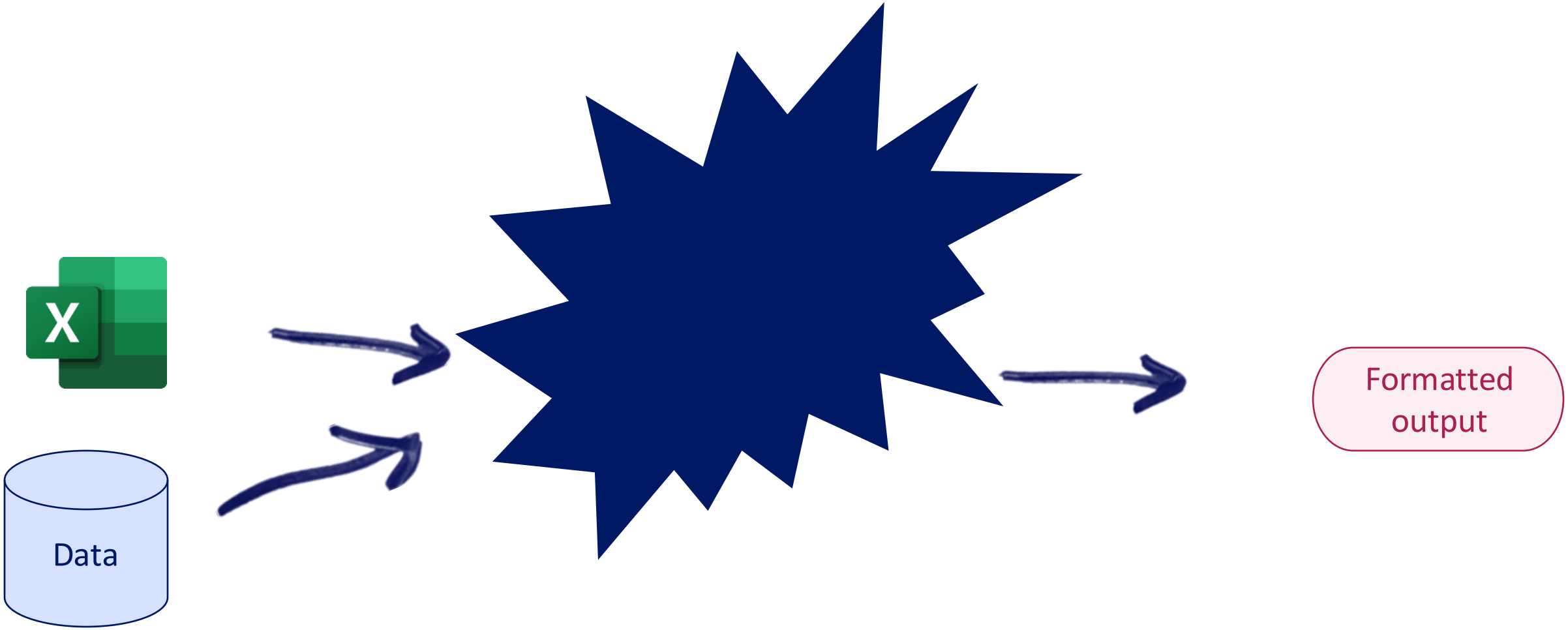
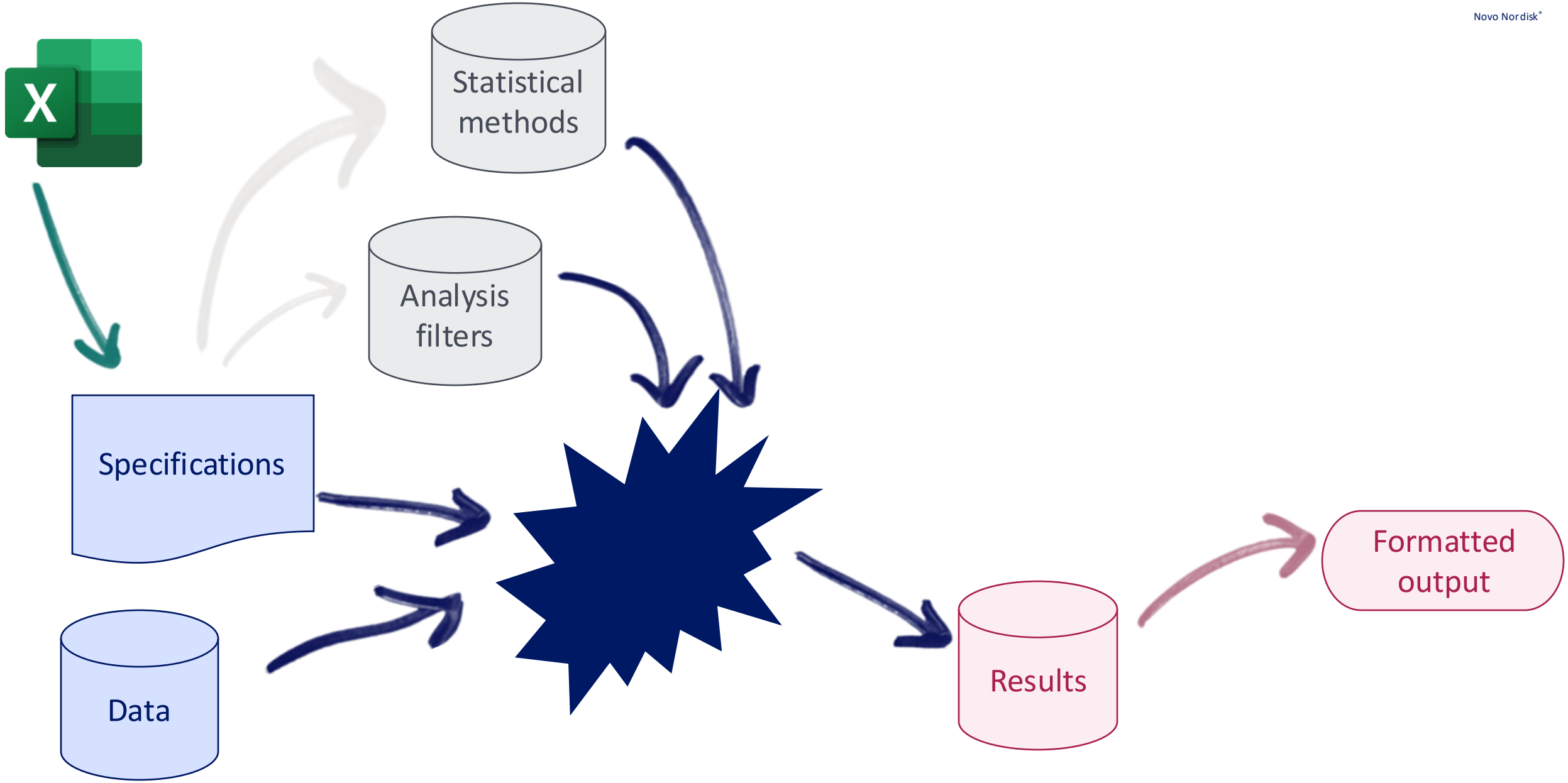
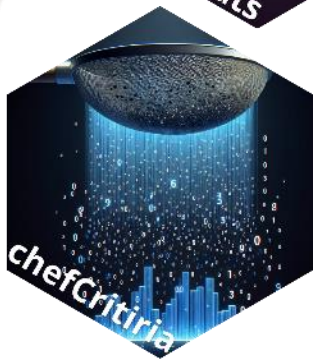

Data
Formatted output


Statistical methods
Analysis filters
Specifications
Data
Results
Formatted output



Specifications

Data

Results

Formatted output

Hey – I'd like No. subjects, No. AEs, No. subjects with event, RR between arms, OR between arms, p-value

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9 endpoints

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9 endpoints

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		Xanomeline High Dose			Placebo			Xanomeline High Dose vs. Placebo		
Subgroup	Category	N	n	%	N	n	%	RR	OR	p-value
Total		XXX	XXX	X.X	XXX	XXX	X.X	X.XX	X.XX	0.XXXX

Hey – I'd like No. subjects, No. AEs, No. subjects with event, RR between arms, OR between arms, p-value

Now stratify by sex, age group, race

9 endpoints

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72 endpoints

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Now do the same but also for each severity level

216 endpoints

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9 endpoints

Now stratify by sex, age group, race

72 endpoints

Now do the same but also for each severity level

216 endpoints

Just kidding! I meant each **cross** of severity level & System Organ Class

>4000 endpoints!

Oh, and do, say, ~150 different variants of this…

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…but only when certain conditions in your data are met

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No. subjects, No. AEs, No. subjects with event, RR between arms, OR between arms, p-value

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chef::mk_endpoint_str(
  data_prepare = mk_adlb,
  treatment_var = "TRT01A",
  treatment_refval = "High Dose",
  pop_var = "SAFFL",
  pop_value = "Y",
  stat_by_strata_by_trt = list(
    chefStats::n_subj,
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No. subjects, No. AEs, No. subjects with event, RR between arms, OR between arms, p-value stratified by sex, age group, race for each **cross** of severity & SOC

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  stratify_by = list(c("SEX", "AGEGR", "RACE")),
  group_by = list(list(AESOC = c(),
                       AESEV = c())))
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treatment_var = "TRT01A",
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group_by = list(list(AVISIT = c())),
stratify_by = list(c("AGEGR2")),
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chefStats::mean_value,
var = "VALUE_BASELINE"
),
"sd: VALUE_BASELINE" = c(
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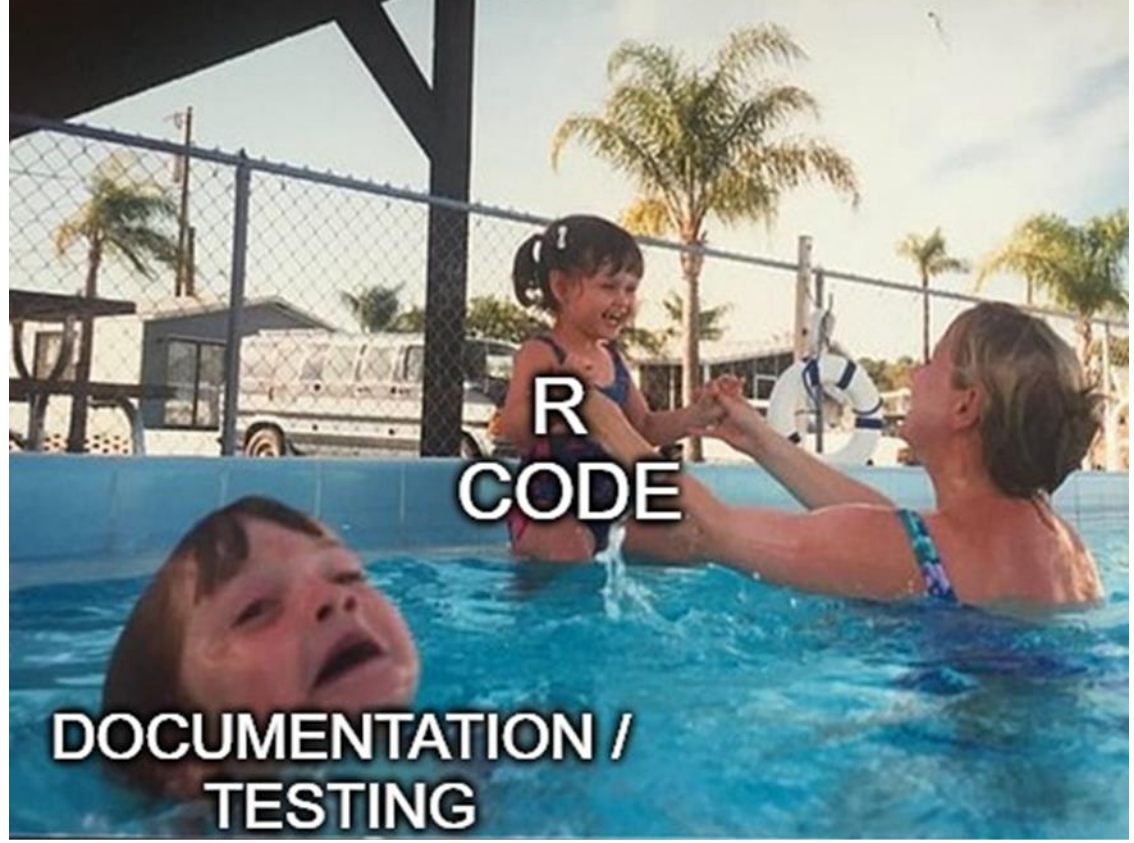
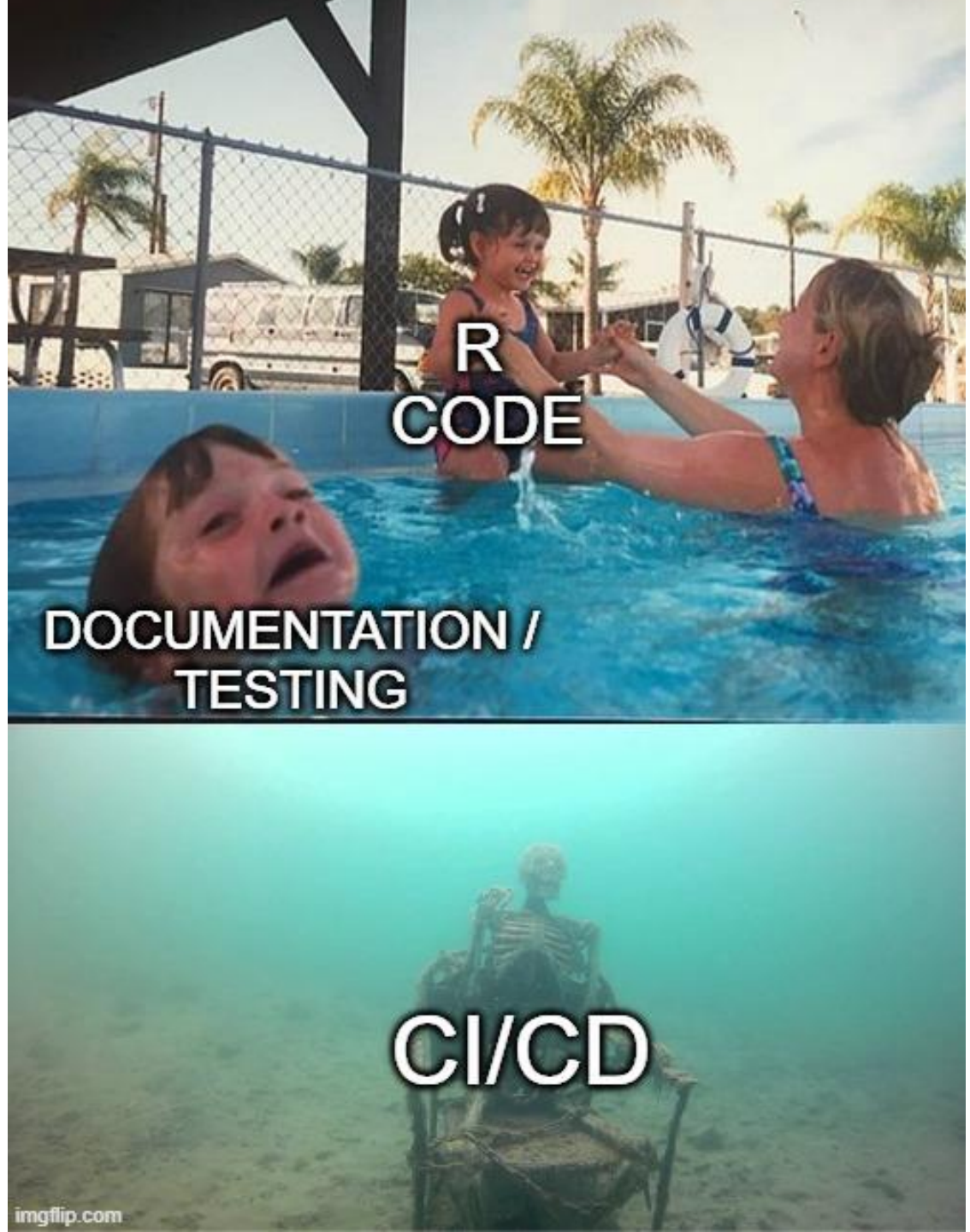
https://github.com/ropensci/targets


R
CODE


R
CODE
DOCUMENTATION /
TESTING


R
CODE
DOCUMENTATION /
TESTING
CI/CD
imgflip.com

Open source

Why?

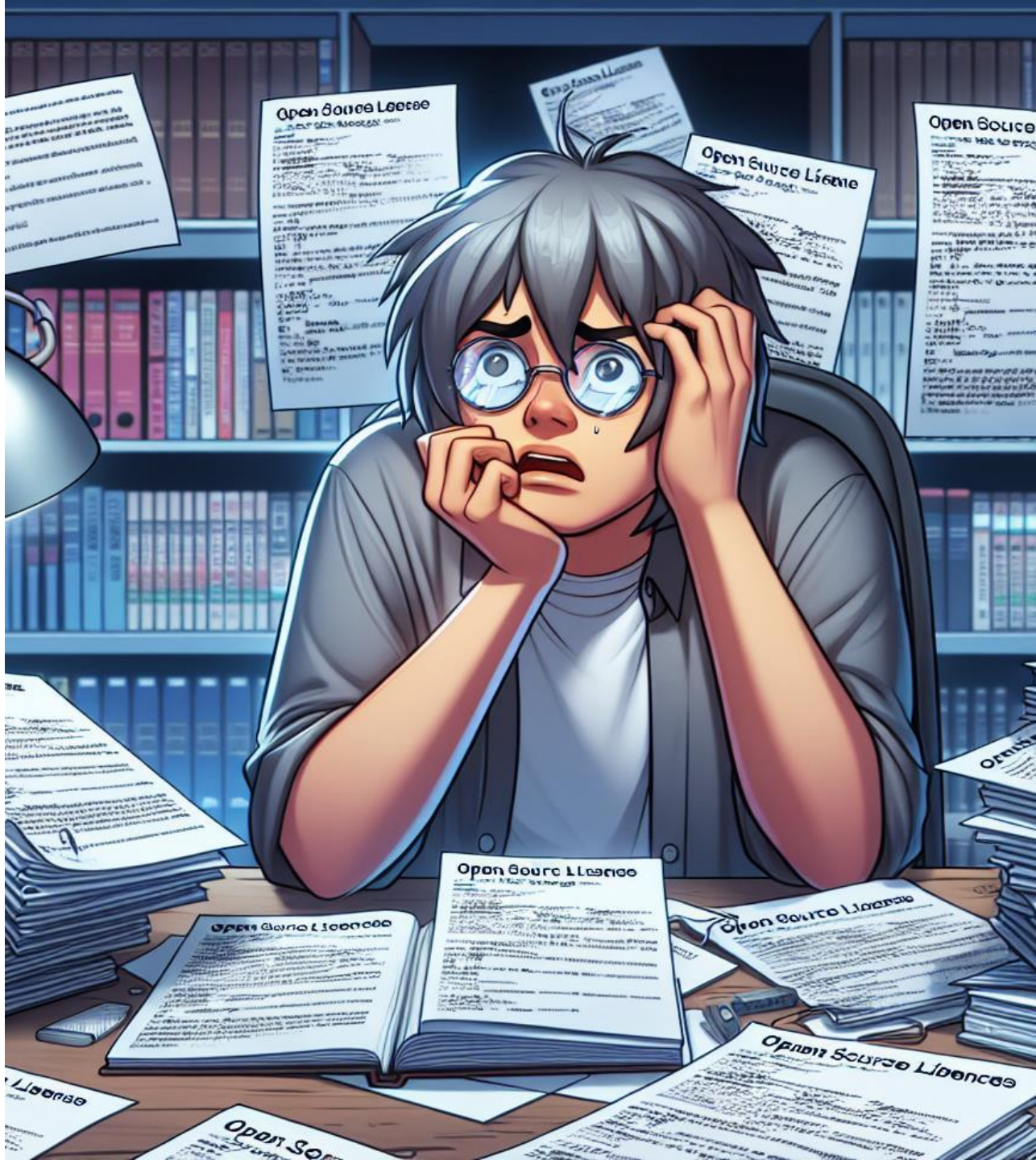
Collaboration!

- Broader perspective
- Broader skill set
- More resources
- More users
- Better quality

How did we do it?

Value

License



Visibility

Accessibility

Collaboration

What we should have done..

What we did

Value

License

Visibility

Accessibility

Collaboration

What we did

Value

License

Visibility

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Collaboration

What we should have done

Collaboration

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License

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What we should have done

Collaboration

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Visibility

HTA-R workstream

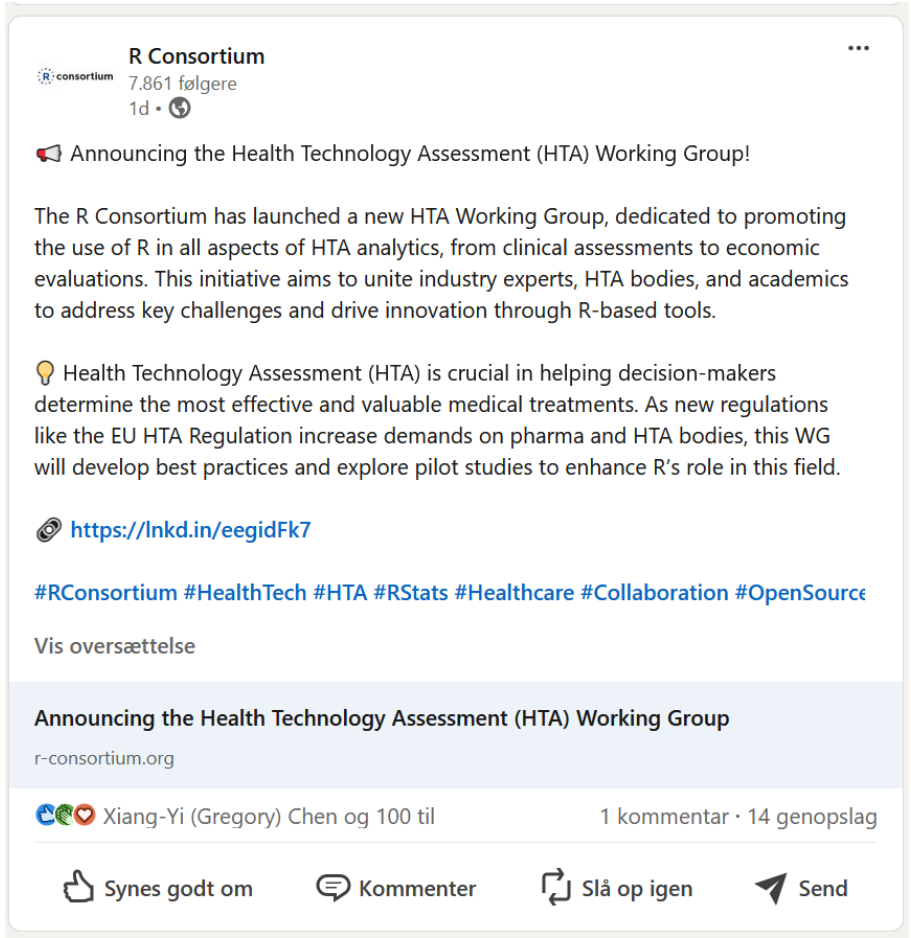
Lead: Gregory Chen (MSD)

Objective: This workstream of the SWE WG unites voluntary statistical software engineers that are experienced in HTA (Health Technology Assessment) or highly-interested in this area. The team aims to develop open-source R tools of good quality in the right formats (R packages, apps, user guides) that are useful to both manufacturers and payers, to support crucial analytic topics in HTA dossier submission across various countries, particularly the topics with unmet needs in R implementation and/or related to EUnetHTA.

The workstream also works within a broader group of business and methodological SMEs in HTA and Market Access space of our pharma industry, to ensure this open-source HTA pipeline of R tools is relevant over time and the tools can be adopted easily by business and payers.

Find more details in our GitHub organization: link.

First Name	Last Name	Affiliation
Cedric	Revil	MSD
Christian Haargaard	Olsen	Novo Nordisk
Christos	Kokaliaris	Roche
Chrysostomos	Kalyvas	MSD
Claudia	Carlucci	Daiichi Sankyo
Gregory	Chen	MSD
Isaac	Gravestock	Roche
Issac	Gravestock	Roche
Keovilay	Chanthavinout	Roche
Matthew	Phelps	Novo Nordisk
Michael	Seo	Roche
Miranta	Antoniou	Roche
Nicolai Skov	Johnsen	Novo Nordisk
Rossella	Belleli	Roche
Sergei	Krivtov	Daiichi Sankyo
Simon	Clancy	Novo Nordisk
Thomas	Maltesen	Novo Nordisk

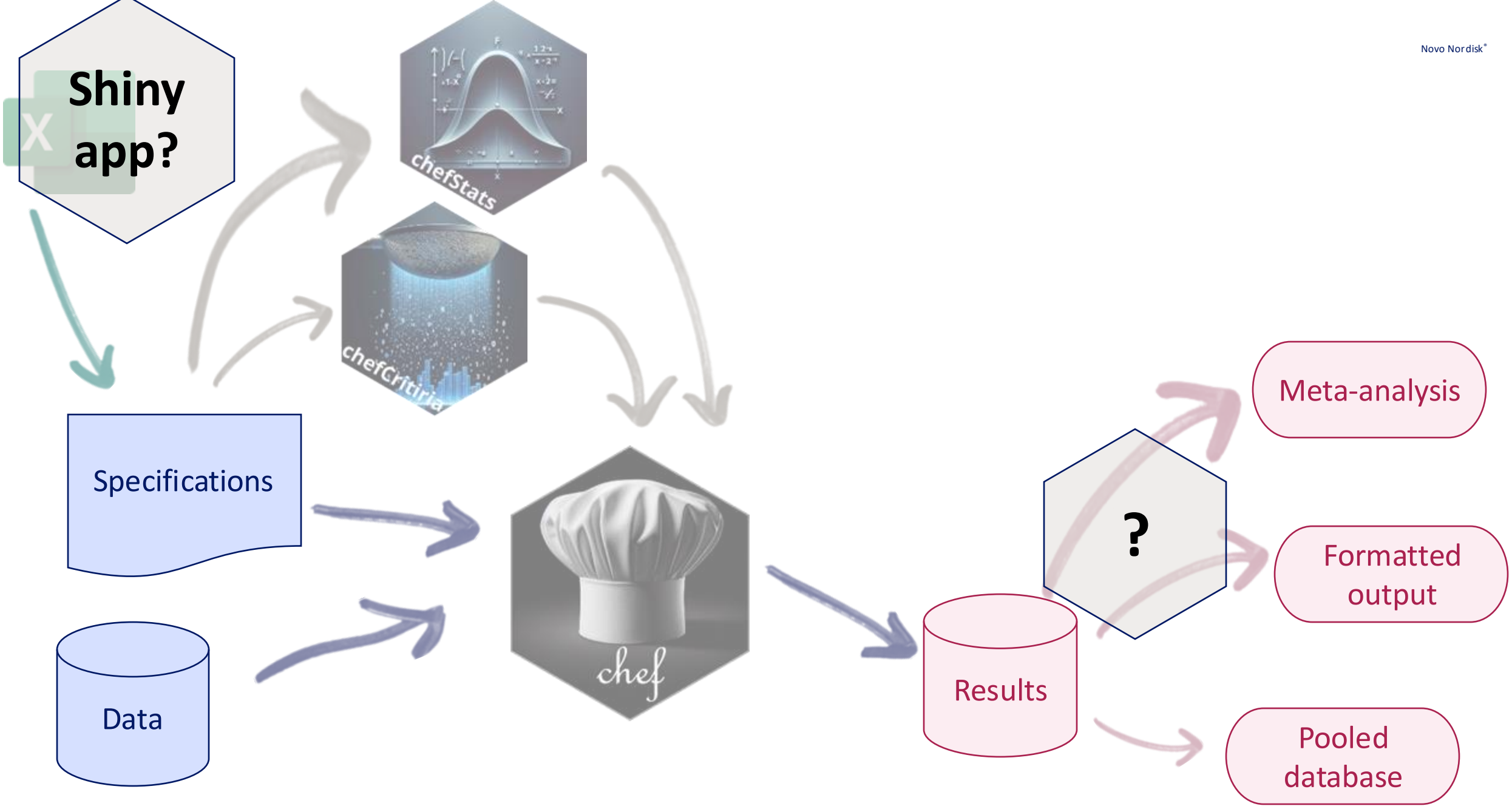


Summary

- Efficient tool for amnog style analysis
- Open source has a huge potential
- Collaboration is hard to get off the ground

Questions ?

https://hta-pharma.github.io/ramnog/


Shiny app?
chefStats
chefCriteria
Specifications
Data
chef
Results
?
Meta-analysis
Formatted output
Pooled database