



extRpolateS: A Shiny-Based Interactive Platform for Time-to-Event Data Modeling in Health Technology Assessments

R for HTA workshop 2025


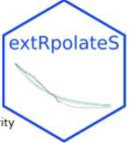
Máté Szilcz, PhD

Postdoc @ Karolinska Institutet, Sweden
CEO & Founder of Viti Science

Agenda

extRpolateS – HTA Survival Analysis Platform

- Purpose-built platform for robust survival extrapolation for HTA
- Caters to novices & advanced users
- Standardised, yet flexible
- Cloud-based R-Shiny web app with high security (Auth0, AWS S3 data storage, MS Azure deployment)



1. Introduction


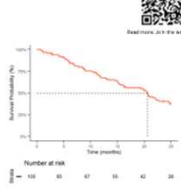
Background

Clinical trials often have limited follow-up time

Trials are primarily designed for regulatory approval

Median follow-up times between 24–60 months for many pivotal studies


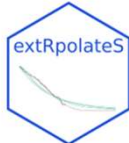
For HTA estimating long-term survival differences between treatment options are crucial



2. Background

extRpolateS – HTA Survival Analysis Platform

- Streamlines the analysis
- Accelerates timelines
- HTA modelling ready
- Enables self-sufficiency
- Repository of data



3. Demo

Discussion – questions & suggestions?

✉ mate.szilcz@vitiscience.se

 <https://www.linkedin.com/in/mateszilcz/>



4. Discussion

extRpolateS – HTA Survival Analysis Platform



Read more. Join the waitlist!



Purpose-built platform for robust survival extrapolation for HTA



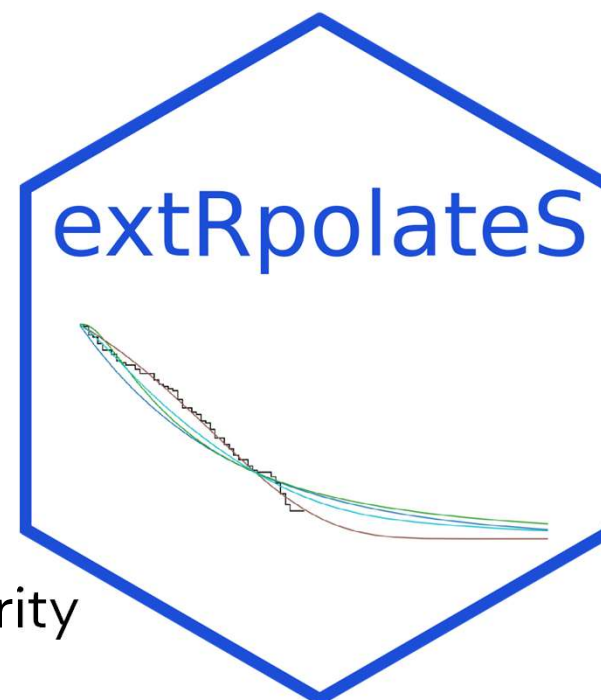
Caters to novices & advanced users



Standardised, yet flexible



Cloud-based R-Shiny web app with high security
(AuthO, AWS S3 data storage, MS Azure deployment)



Background



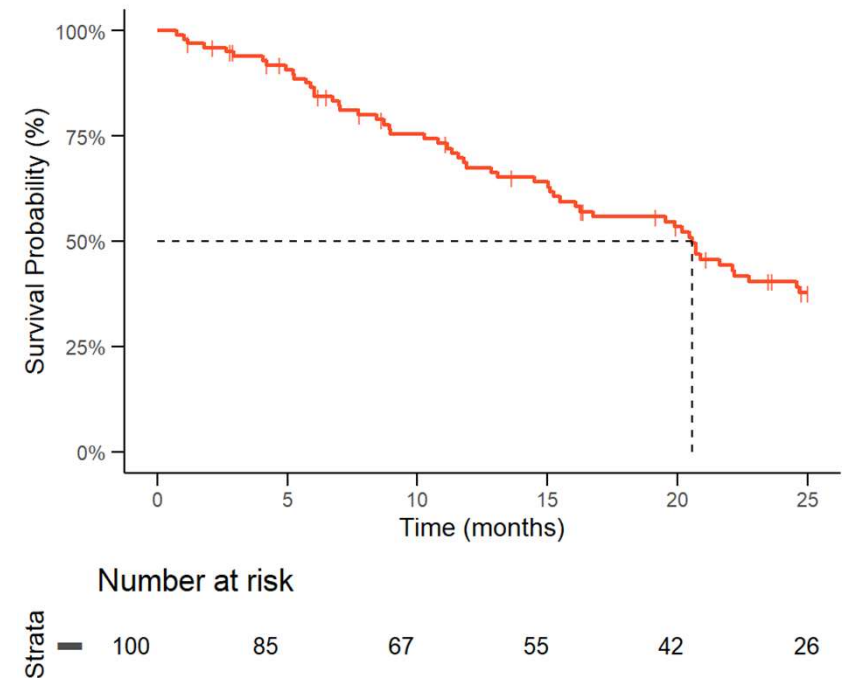
Read more. Join the waitlist!

Clinical trials often have limited follow-up time

Trials are primarily designed **for regulatory approval**

Median follow-up times between **24–60 months** for many pivotal studies

For HTA estimating **long-term survival differences** between treatment options are crucial

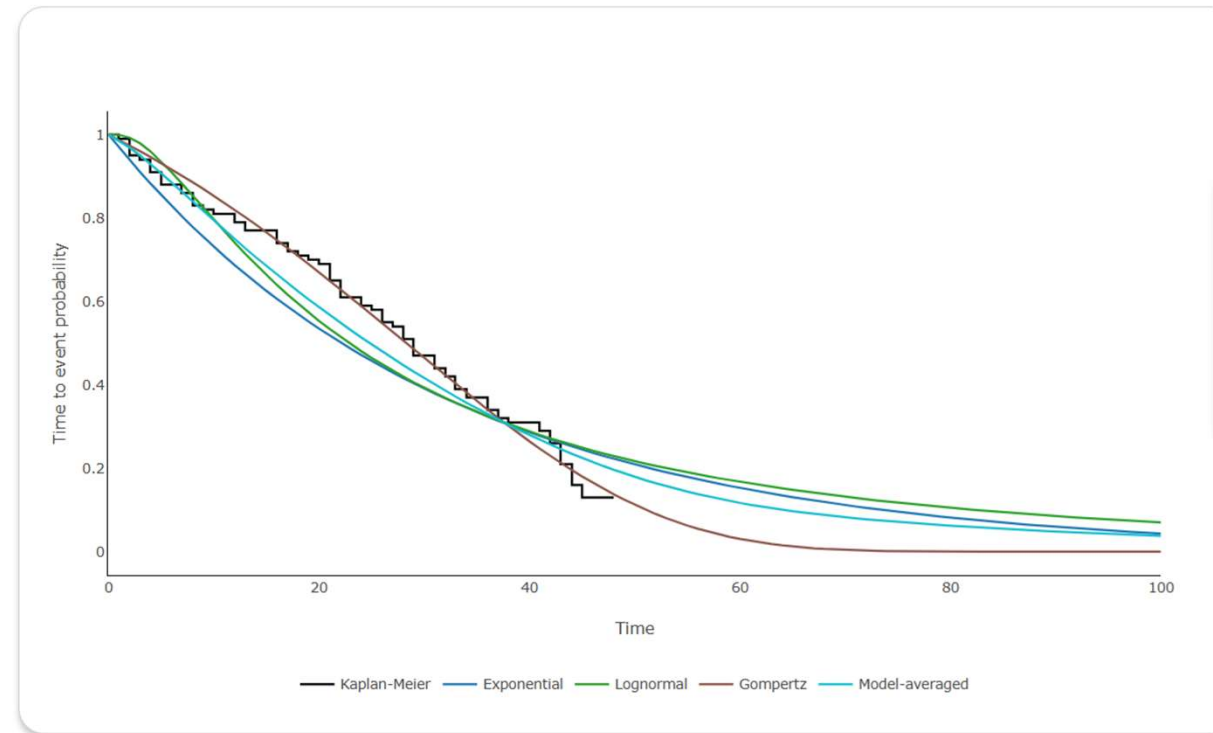


Extrapolation bridges the gap



Read more. Join the waitlist!

HTA require lifetime horizon

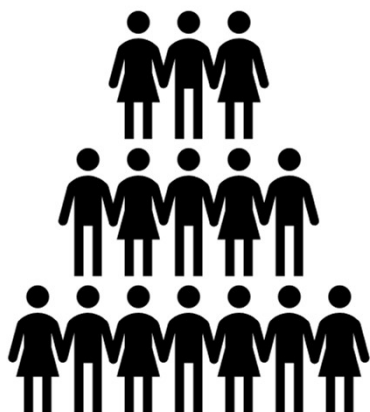


Current way of extrapolating survival

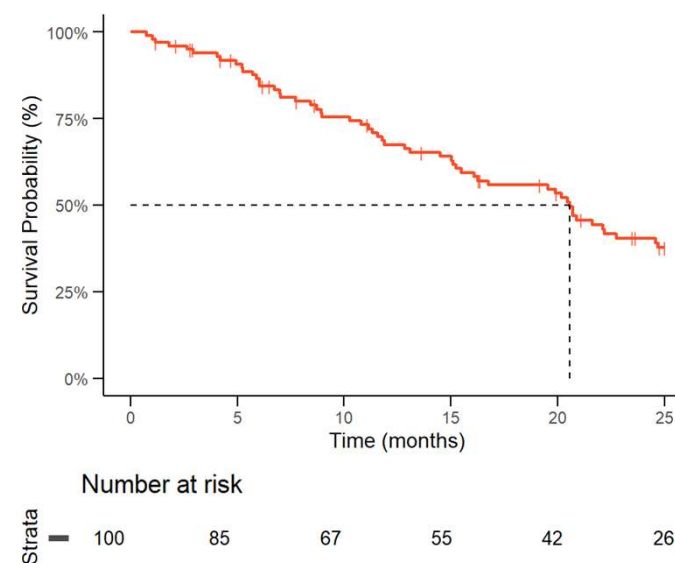


Read more. Join the waitlist!

Individual patient level data (IPD)



Reconstructed IPD from Kaplan-Meier (KM) plots



When IPD is available



Read more. Join the waitlist!



Do the analysis in R (or your choice of software, but it should really be R)



Several R packages are available for the different modeling options (e.g. survHE)



Needs highly specialised programming knowledge

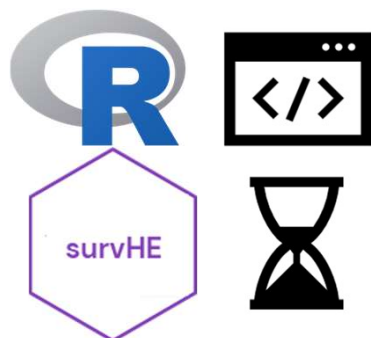


Time consuming

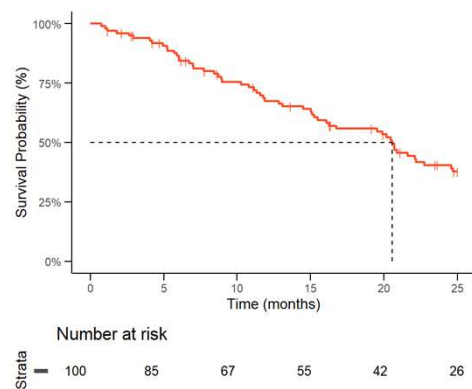
When IPD is NOT available



Read more. Join the waitlist!



Same steps as before



BUT first we need to

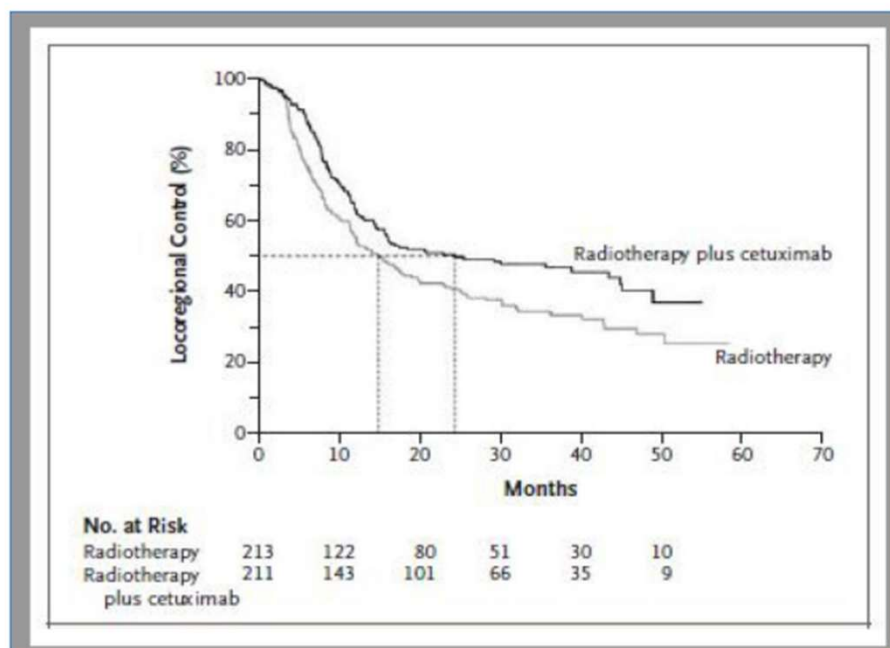
Reconstructed IPD from published KM curve

When IPD is NOT available

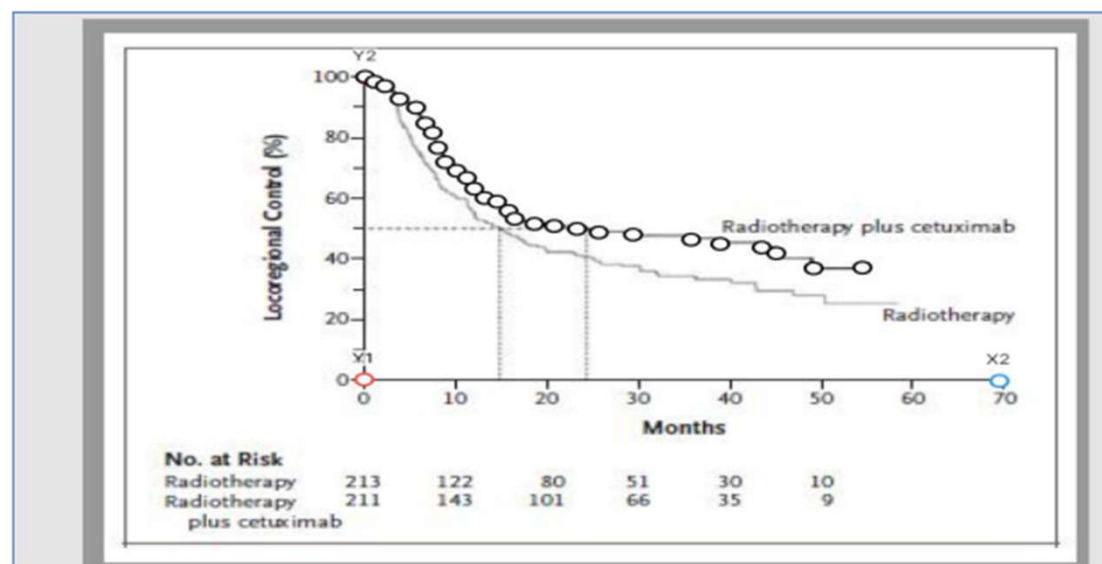


Read more. Join the waitlist!

Reconstruct IPD from published KM curve



Display 1. Published KM Curve (Guyot 2012)



Source: PharmaSUG 2024 – Paper RW-125

When IPD is NOT available



Read more. Join the waitlist!

Reconstruct IPD from published KM curve

	A	B	C		A	B	C	D
1	Coordinate	Time	Proportion		nrisk	trisk	lower	upper
2	1	0	1		331	0	1	3
3	2	0.595812	0.993397		323	2	4	6
4	3	1.167244	0.993397		314	4	7	11
5	4	2.25816	0.993397		303	6	12	18
6	5	2.959463	0.981056		285	8	19	24
7	6	3.712714	0.972829		268	10	25	30
8	7	4.439991	0.972829		250	12	31	35
9	8	4.621811	0.960489		199	14	36	40
10	9	5.11532	0.960489		168	16	41	46
11	10	5.60883	0.952261		116	18	47	53
12	11	5.7387	0.948148		81	20	54	57
13	12	6.414028	0.944034		51	22	58	59
14	13	6.595848	0.931694		26	24	60	62
15	14	6.621823	0.923467		9	26	63	63
16	15	7.245203	0.911126					

```

Code IPD from KM DB04 - Copy.R* x Code IPD from KM DB04.R* x
Source on Save Run
11 ###FUNCTION INPUTS
12 path<-"H:/New Folder/"
13 digisurvfile<-"data initials study2 figA arm1 time1.txt" #Input survival times from graph readi
14 nriskfile<-"nrisk study2 figA arm1 time1.txt" #Input reported number at risk
15 KMdatafile<-"KMdata study3 figA arm1 time1 ne.txt" #Output file events and cens
16 KMdataIPDfile<-"KMdataIPD study3 figA arm1 time1 ne.txt" #Output file for IPD
17 tot.events<-NA #tot.events = total no. of events reported. If not reported, then tot.events="NA
18 arm.id<- 1 #arm indicator
19 ###END FUNCTION INPUTS
20
21 #Read in survival times read by digizeit
22 surv_times <- read.csv("Test_plot_1.csv")
23 digizeit<- data.matrix(surv_times)
24 digizeit[1,2]=0
25 t.s<-digizeit[,2]
26 S<-digizeit[,3]
27
28 #Read in published numbers at risk, n.risk, at time, t.risk, lower and upper
29 # indexes for time interval
30 nrisk trisk <- read_excel("Test_nrisk trisk.xlsx")
  
```

extRpolateS – HTA Survival Analysis Platform



Read more. Join the waitlist!

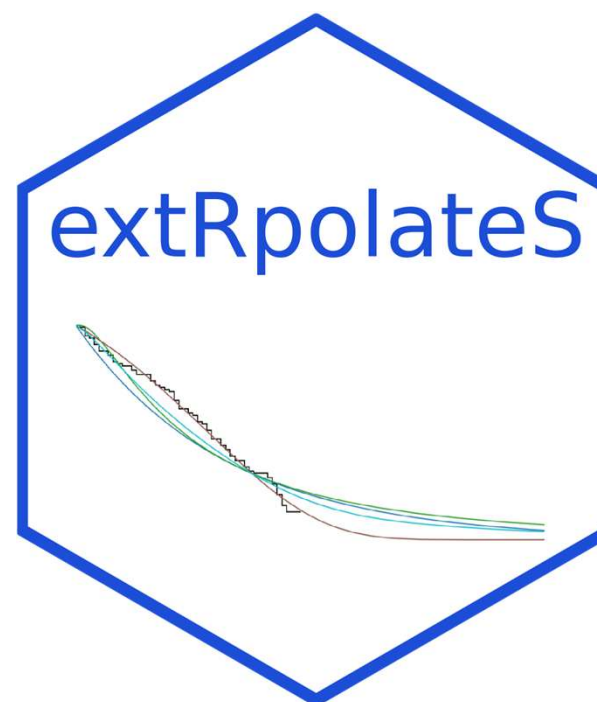
»»» Streamlines the analysis

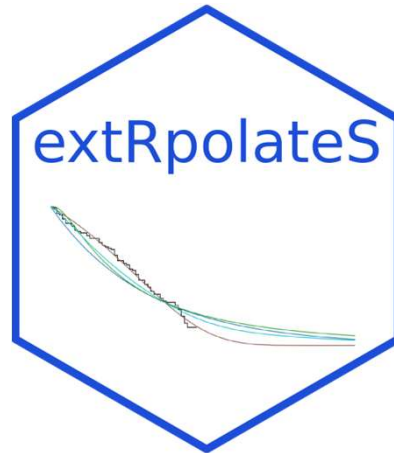
⚡ Accelerates timelines

📋 HTA modelling ready

👤 Enables self-sufficiency

🗄️ Repository of data





Read more. Join the waitlist!

Demo

<https://extrpolates.app.vitiscience.se/>

Upcoming features



Read more. Join the waitlist!



Import your extrapolated survival curves directly into a template-driven PSM



Probabilistic survival curves



SaaS or Enterprise deployment



Suggestions are welcomed!



Read more. Join the waitlist!

Discussion – questions & suggestions?



mate.szilcz@vitiscience.se



<https://www.linkedin.com/in/mateszilcz/>



Scan for LinkedIn!

Thank you