

Unlocking Discrete Event Simulation Modelling in R using **WARDEN**



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June 6th 2025

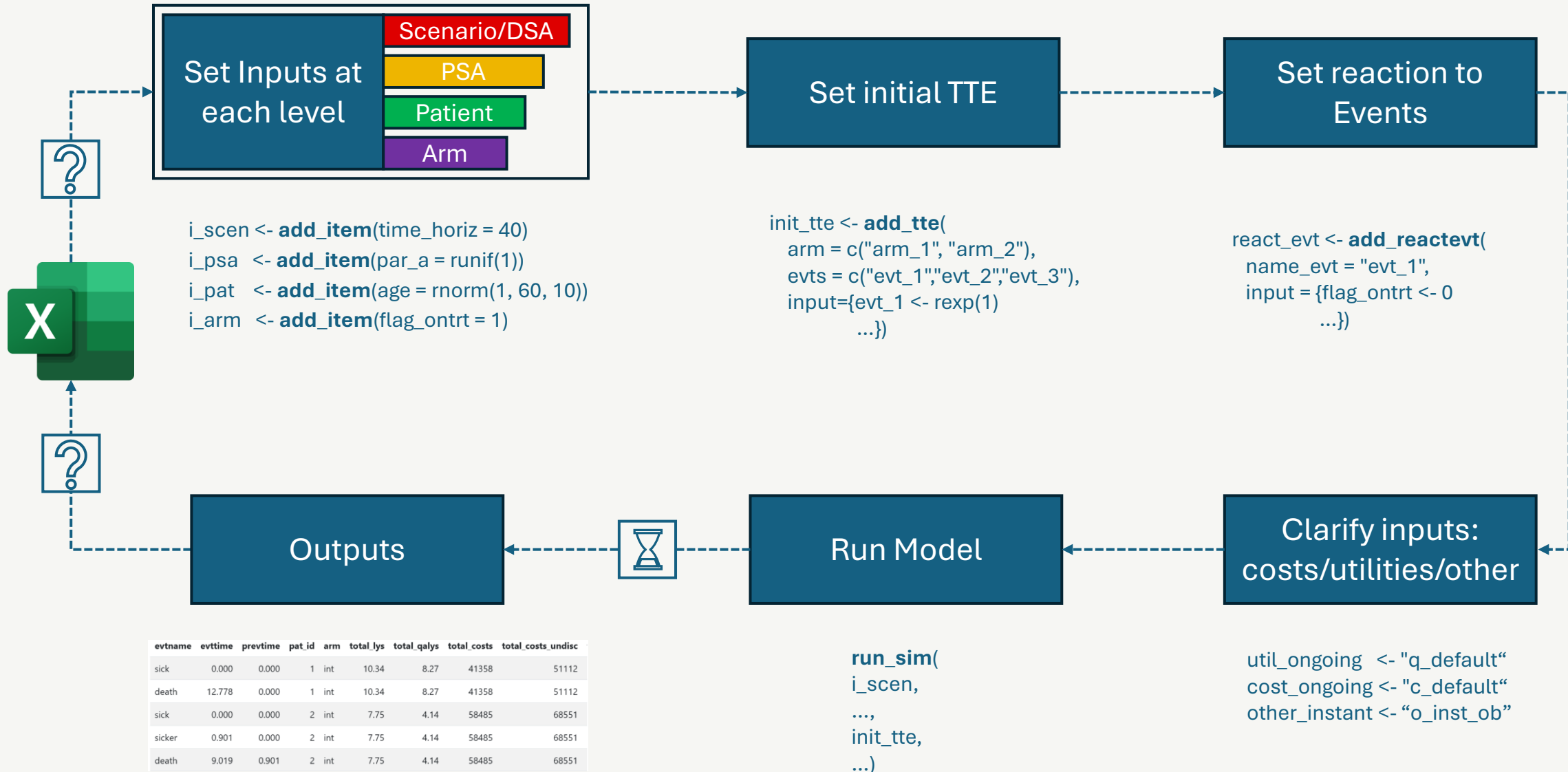
Why WARDEN?

- DES and R are increasingly relevant for HTA submissions, however existing packages
 - Have non-HE focus
 - May require knowledge of C++
 - Require major work to use in HTA submissions
- WARDEN: DES without resource constraints - R package (CRAN)
 - Evolved over Roche, Evidera and AbbVie thanks to the support for **open source and copyleft** license
 - HE focus (comparison of interventions, QALYs, LYs, Costs...)
 - **HTA submission ready** (full toolset: PSA, OWSA, scenarios...)
 - “Beginner” friendly (no C++), grammar tidyverse style (pipes)
 - Focus on **flexibility** and **transparency**



How to work with WARDEN?

Nested Loops and Delayed Execution



QR code to WARDEN website

Advantages

- Massive improvement over descem (presented in 2021)
 - **2-3x faster**
 - New analyses (**deterministic/probabilistic**): **base case, scenarios, OWSA**
 - Numerous **helper functions** (automatic input handling, profile replication, reaction summary...)
 - **Statistical functions** for DES (conditional quantiles, luck adjustment...)
 - **Debug mode** with **log** file (even on error)
 - Fully **documented** with many examples
 - Improved outputs
 - Option: **aggregation** levels: full IPD, IPD but aggregating events, only summary
 - Option: evolution of cohort **outputs over time**



Showcase

How to handle deterministic/PSA/OWSA/Scenarios in a single function?

parameter_name	base	distribution	a	b	n	dsa_min	dsa_max	scenario_1	scenario_2	psa_indicators	indicators
age	60	rnorm	60	12	1	40	80	45	65	1	1
util.sick	0.5	rbeta_mse	0.5	0.1	1	0.3	0.7	0.3	0.7	1	1
cost.sick	3000	rgamma_mse	3000	600	1	1000	5000	1000	5000	1	0

- Once model is written, user should only interact with **run_sim()** to change analysis type
- **pick_val_v()** automatically obtains the right values and iterates as needed over all type of analyses
- Accepts **vector parameters** (e.g., multivariate normal) and **multiple parameters covaried** (e.g., in DSA)

```
add_item(  
  pick_val_v(  
    base      = l_inputs[["base"]],  
    psa       = pick_psa(  
      l_inputs[["distribution"]],  
      l_inputs[["n"]],  
      l_inputs[["a"]],  
      l_inputs[["b"]]  
    ),  
    sens      = l_inputs[["sensitivity_used"]],  
    psa_ind   = psa_bool,   
    sens_ind  = sensitivity_bool,   
    indicator = l_inputs[["indicators"]],  
    indicator_psa = l_inputs[["psa_indicators"]],  
    names_out = l_inputs[["parameter_name"]]  
  )  
)
```

```
run_sim(  
  ...,  
  sensitivity_names = c("dsa_min", "dsa_max"),  
  psa_bool = TRUE,  
  sensitivity_bool = TRUE  
)
```

sensitivity_bool = FALSE

```
$age  
[1] 40  
$util.sick  
[1] 0.3  
$cost.sick  
[1] 3121.052
```

```
$age  
[1] 73.86918  
$util.sick  
[1] 0.4571762  
$cost.sick  
[1] 2954.461
```



Showcase

How to summarize all interactions in reactions?

- If the model is complex, event reactions can become hard to read
 - Summarizing all items/events interactions by event, with definitions and whether they are conditional can be useful
- **extract_from_reactions()** summarizes all interactions using **abstract syntax trees** for easy inspection/debugging/documentation

```
evt_react_list2 <-  
  add_reactevt(name_evt = "sick",  
    input = {  
      modify_item(list(a=1+5/3))  
      assign("w", 5 + 3 / 6 )  
      x[5] <- 18  
  
      for(i in 1:5){  
        assign(paste0("x_",i),5+3)  
      }  
  
      if(j == TRUE){  
        y[["w"]] <- 612-31+3  
      }  
  
      modify_event(list(b=25))  
    }) %>%  
  add_reactevt(name_evt = "sicker",  
    input = {  
      q_default <- 0  
      c_default <- 0  
      new_event(list(b=curtime + 0.01))  
    })  
results <- extract_from_reactions(evt_react_list2)
```

event	name	type	conditional_flag	definition
sick	a	item	FALSE	1 + 5/3
sick	W	item	FALSE	5 + 3/6
sick	x[5]	item	FALSE	18
sick	paste0("x_", i)	item	FALSE	5 + 3
sick	y[["w"]]	item	TRUE	612 - 31 + 3
sick	b	event	FALSE	25
sicker	q_default	item	FALSE	0
sicker	c_default	item	FALSE	0
sicker	b	event	FALSE	curtime + 0.01



Conclusion

- WARDEN **massively expands** upon previous package and **provides necessary tools** for HE modelling
- WARDEN: **CRAN** package for **DES ready for HTA submissions**
 - Focus on **transparency, flexibility, and being easy to use**
 - New version with improvements coming to CRAN in ~ 2 weeks.
- **Future development: resource constraints**, efficiency improvements, other features (as needed)
- Your **feedback** would be welcome!



Q&A



Appendix

Appendix - Showcase

Luck Adjustment

- Patient draws survival from **Weibull(3,50)** with “**luck**” (random draw number) **0.37** → Time to event = 38.65 (**qweibull(0.37, 3, 50)**)
 - At **time 10**, patient has an event and switches to **Weibull(3,4)** (worsens TTE).
 - At **time 25**, patient has another event and switches to **Weibull(3, 66.67)** (improves TTE).
 - What would be the final time to event of this patient?
 - We cannot draw directly from the last Weibull (TTE = 51.54), as the patient spent most of the time on another parametrization. Solution: adjust the patients’ “luck”.
- Use of **luck_adj()** function facilitates this computation

```
# Parameter goes from 0.02 at time 10 to 0.025 to 0.015 at time 25,  
# Starting luck is 0.37  
new_luck <- luck_adj(prevsurv = 1 - pweibull(q=10,3,1/0.02),  
                    cursurv = 1 - pweibull(q=10,3,1/0.025),  
                    luck = 0.37,  
                    condq = FALSE) #time 10 change  
#new luck is 0.3748  
  
new_luck <- luck_adj(prevsurv = 1 - pweibull(q=25,3,1/0.025),  
                    cursurv = 1 - pweibull(q=25,3,1/0.015),  
                    luck = new_luck,  
                    condq = FALSE) #time 25 change  
#new luck is 0.2429  
  
qweibull(new_luck, 3, 1/0.015) #final TTE  
#final TTE is 43.52338
```

