

## Cohort Breakdown

A summary of the initial states and disease progression outcomes and how they change, depending on the maximum initial amount of Ee allowed (exclusion group), time at which outcome is determined, and type of sampling distribution.

Numbers in parentheses are the number of sets that leave the state and enter the state at the end of the simulation for initial condition (IC) and ending state (ES), respectively.

	Log-uniform, 200h			Log-uniform, 2h	Log-normal
Initial condition criteria:	Ee(0)<75%	Ee(0)<50%	Ee(0)<25%	Ee(0)<50%	Ee(0)<50%
Total number of sets that reached steady-state:	24798	22432	23517	22432	33256
Healthy IC:	16833 (635)	16833 (635)	16833 (635)	16833 (14260)	21403 (37)
Health ES:	16198 (0)	16198 (0)	16198 (0)	2573 (0)	21373 (7)
Moderate damage IC:	5382 (572)	5382 (572)	4697 (265)	5382 (3387)	10892 (155)
Moderate damage ES:	5105 (295)	5104 (294)	4726 (294)	10116 (8121)	10771 (34)
Moderate damage IC:	2583 (1)	2217 (0)	1987 (0)	2217 (0)	961 (0)
Moderate damage ES:	3495 (913)	3130 (913)	2593 (606)	11743 (9526)	1112 (151)

## Top Correlations

The parameters that have the highest correlation with parameters and other predictors, for each exclusion group and disease progression group.

	Log-uniform			Log-uniform, 2h	Log-normal
Criteria:	Ee(0)<75%	Ee(0)<50%	Ee(0)<25%	Ee(0)<50%	Ee(0)<50%
	kmne, Eh ratio 0.5h			kmne, Eh ratio 0.5h	kmne, Eh ratio 0.5h
Healthy	0.1	0.1	0.1	0.24	0.06
Moderate damage	0.66	0.66	0.66	0.43	0.47
Severe damage	0.55	0.87	0.86	0.73	0.67
	br, Eh ratio 0.5h			br, Eh ratio 0.5h	br, Eh ratio 0.5h
Healthy	0.29	0.29	0.29	-0.04	0.19
Moderate damage	0.42	0.42	0.43	0.27	0.23
Severe damage	0.05	0.18	0.22	0.32	0.22
	sm, max M2			sm, max M2	sm, max M2
Healthy	0.32	0.32	0.32	0.28	0.48
Moderate damage	0.31	0.31	0.31	0.32	0.51
Severe damage	0.4	0.29	0.3	0.32	0.52

# Significance Testing

Parameters and other predictors that show a statistically significant difference (p-value<0.05) between all three disease progression groups, using Kruskal-Wallis and Wilcoxon tests.

	Log-uniform			Log-uniform, 2h	Log-normal
Criteria:	Ee(0)<75%	Ee(0)<50%	Ee(0)<25%	Ee(0)<50%	Ee(0)<50%
Significant predictors:	kmne	kmne	kmne	kep	kmne
	xmne	xmne	xmne	br	xmne
	M2% at 10h	M2% at 10h	br	Eh ratio at 0.5h	Eh ratio at 2h
	min M2	min M2	M2% at 10h	Eh ratio at 2h	mup
	M1 peak time	br	ken	Eh ratio at 6h	ken
	Eh ratio at 2h	Eh ratio at 2h	min M2	min M1	kep
	min M1	M1 peak time	min M1	ken	M1 peak ratio
	kep	kep	Eh ratio at 2h	sn	br
	br	min M1	M1 peak ratio	max M1	M1 peak time
	M1 peak ratio	M1 peak ratio	kep	min M1%	min M1%
	Eh ratio at 0.5h	Eh ratio at 0.5h	Eh ratio at 0.5h	kan	M2 peak time
	mup	mup	kem1	max M1%	kem1
	kem1	kem1	bp	kem1	sn
	kpe			M1 peak time	M2% at 10h
				kam1	ainf
				muna	
				max M2%	
				kn	
				mup	
				min M2%	
				ainf	
				sm	
				M2% at 10h	
				muab	
				kpm1	
				kmne	
				bp	
				knn	
				xm0ab	
				mum1b	

# Random Forest Decision Tree

Ten highest average importance values, as determined by 1000 random forests.

	Log-uniform, 200h				Log-uniform, 2h		Log-normal
Criteria:	Ee(0)<75%	Ee(0)<50%	Ee(0)<25%		Ee(0)<50%		Ee(0)<50%
Top ten, in order:	kmne	kmne	kmne		Eh ratio at 2h		kmne
	Eh ratio at 6h	Eh ratio at 6h	Eh ratio at 6h		Eh ratio at 0.5h		xmne
	Eh ratio at 2h	xmne	xmne		Eh ratio at 6h		Eh ratio at 2h
	xmne	Eh ratio at 2h	Eh ratio at 2h		kmne		Eh ratio at 0.5h
	min M1	min M1	Eh ratio at 0.5h		br		Eh ratio at 6h
	Eh ratio at 0.5h	Eh ratio at 0.5h	min M1		kep		mup
	min M2	min M2	min M2		xmne		min M1
	M2% at 10h	M2% at 10h	M2% at 10h		min M1		ken
	br	br	br		ken		min M1%
	ken	ken	ken		sn		kep