Duration of antibiotic treatment on resistance emergence in hospital setting

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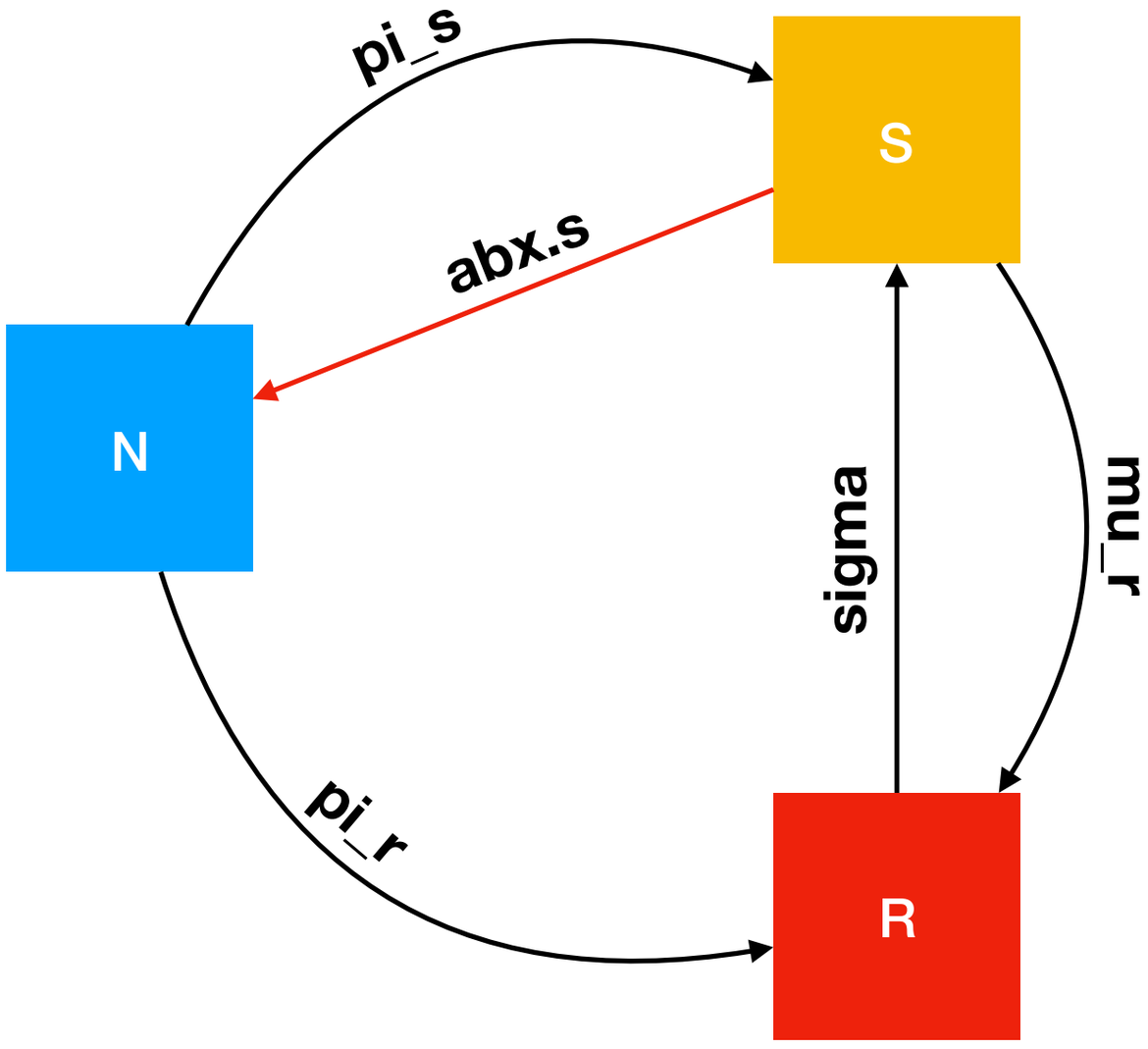
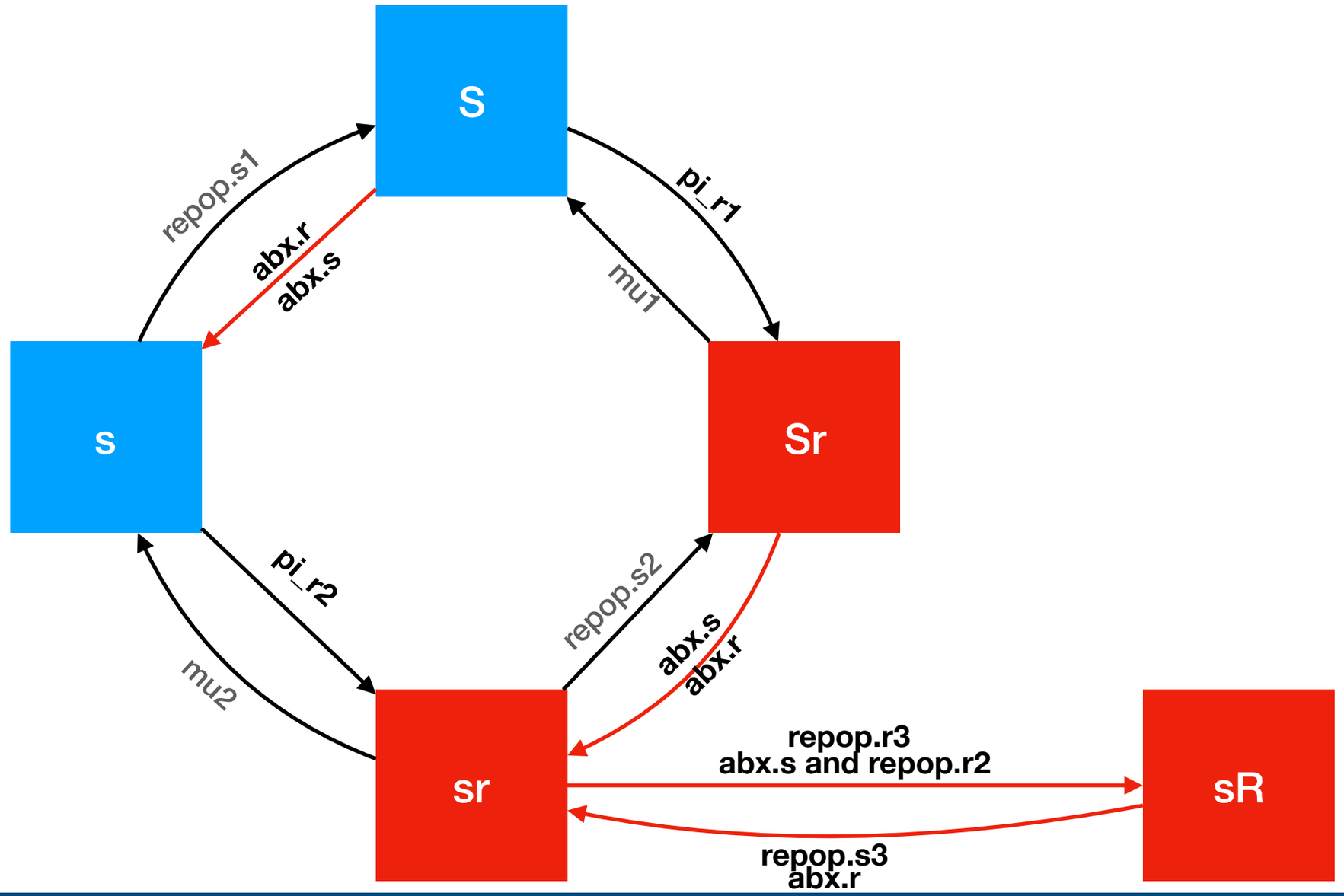
Model 1



Parameters	
abx.s	probability of clearing S to become N
pi_s	probability of regrowth of S
pi_r	probability of being transmitted R
sigma	probability of being decolonised
mu_r	probability of being transmitted R

Model 2



Parameters	
p.s	probability of being prescribed narrow spectrum antibiotic
p.r	probability of being prescribed broad spectrum antibiotic
pi_r1	probability of being transmitted r to S (S—> Sr)
pi_r2	probability of being transmitted r to s (s—>sr)
repop.s1	probability of regrowth of S (s—>S)
repop.s2	probability of regrowth of S (sr—>Sr)
repop.s3	probability of transmission of r to S (s—> Sr)
repop.r2	probability of transmission of r to S (s—> Sr)

Parameters	
repop.r3	probability of regrowth of s (sR—> sr)
abx.s	probability of clearing S to become s
abs.r	probability of clearing R to become r
mu1	probability of being decolonised to S (Sr—> S)
mu2	probability of being decolonised to S (sr—> s)
bif	bacterial interference factor (pi_r2 = pi_r1 * bif)
bif1	bacterial interference factor 1 (repop.r3=repop.r2*bif1)

	S	s	Sr	sr	sR
S	- (abx.r or abx.s + pi_r1)	abx.r or abx.s	pi_r1	0	0
s	repop.s1	- (repop.s1 + pi_r2)	0	pi_r2	0
Sr	mu1	0	- (abx.r or abx.s + mu1)	abx.r or abx.s	0
sr	0	mu2	repop.s2	-(repop.s2 +repop.r3 or abx.s and repop.r2)	repop.r3 or abx.s and repop.r2
sR	0	0	0	repop.s3 or abx.r	- (repop.s3 or abx.r)

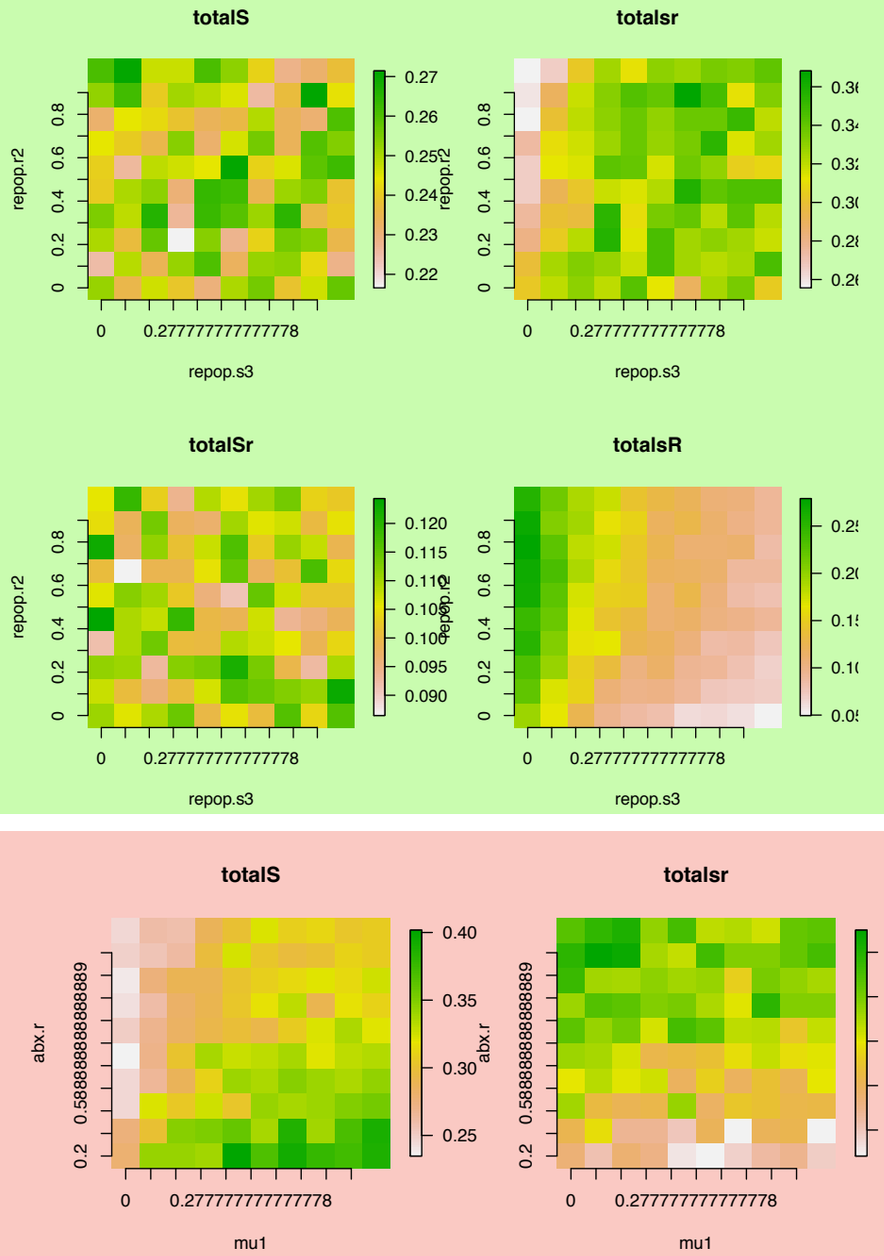
Model 2 exploration

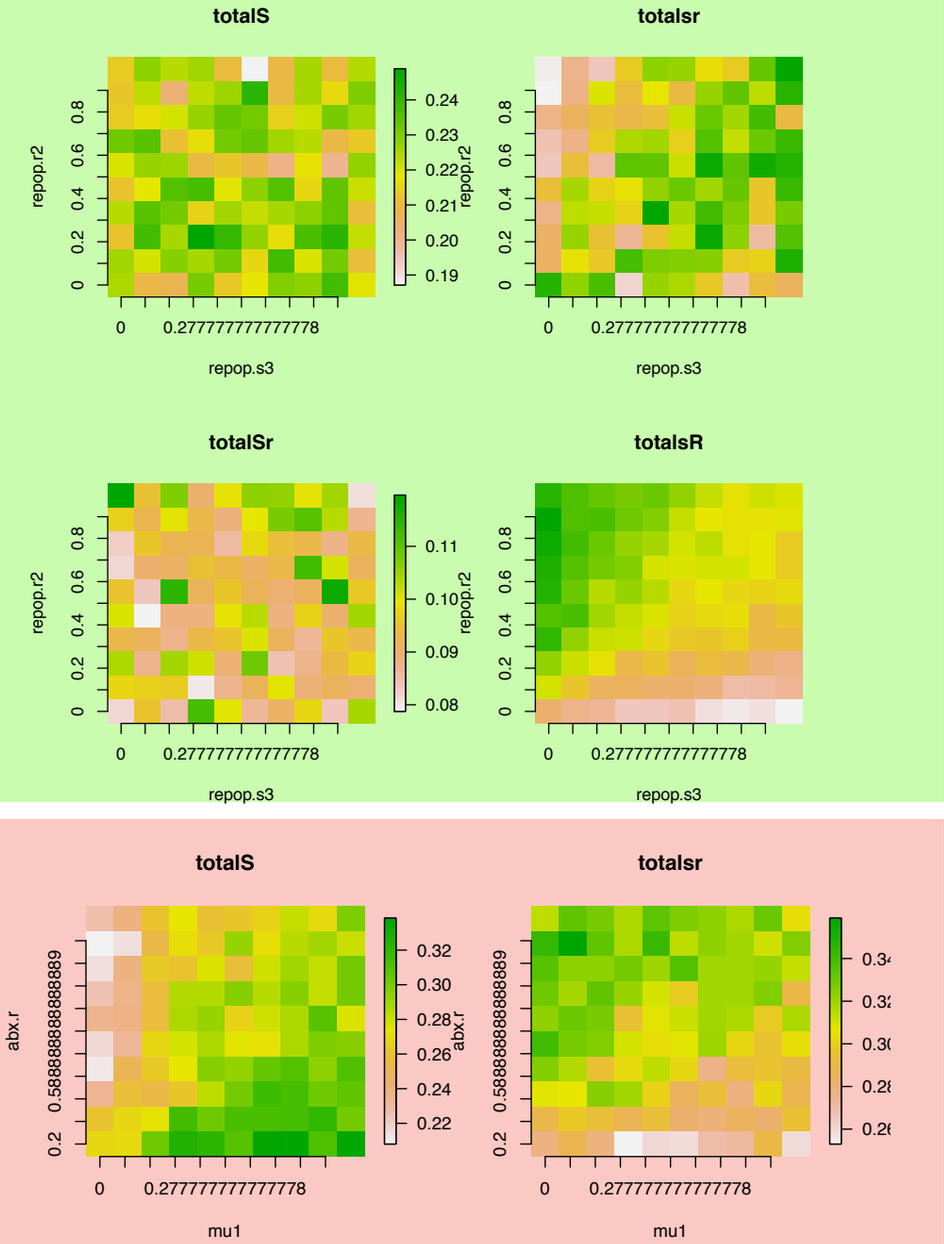
Parameters		Values explored	Baseline value
p.s	probability of being prescribed narrow spectrum antibiotic	0.1-0.9	0.4
p.r	probability of being prescribed broad spectrum antibiotic	0.01-0.05	0.05
abx.s	probability of clearing S to become s	0.2-0.9	0.5
abx.r	probability of clearing R to become r	0.2-0.9	0.5
pi_r1	probability of being transmitted r to S (S—> Sr)	0.003-0.5	0.003
pi_r2	probability of being transmitted r to s (s—>sr)		depends on bif
repop.s1	probability of regrowth of S (s—>S)		0
repop.s2	probability of regrowth of S (sr—>Sr)		0
repop.s3	probability of transmission of r to S (s—> Sr)	0-0.5	0.05
repop.r2	probability of transmission of r to S (s—> Sr)	0-0.9	0.5
repop.r3	probability of regrowth of s (sR—> sr)		depends on bif1
mu1	probability of being decolonised to S (Sr—> S)	0-0.5	0
mu2	probability of being decolonised to S (sr—> s)		0
bif	bacterial interference factor (pi_r2 = pi_r1 * bif)	1-500	20
bif1	bacterial interference factor 1 (repop.r3=repop.r2*bif1)	0-1	0.2
n.bed	number of beds		20
mean.max.los	mean of length of stay (normal distribution)		20
n.days	number of days of observation		100
prob_StartBact	probability of initial carriage		S = 0.5, Sr = 0.2, sR=0.1, sr=0.05
mean_dur	mean duration of antibiotics (normal distribution)		4 vs 14

Model 2 exploration

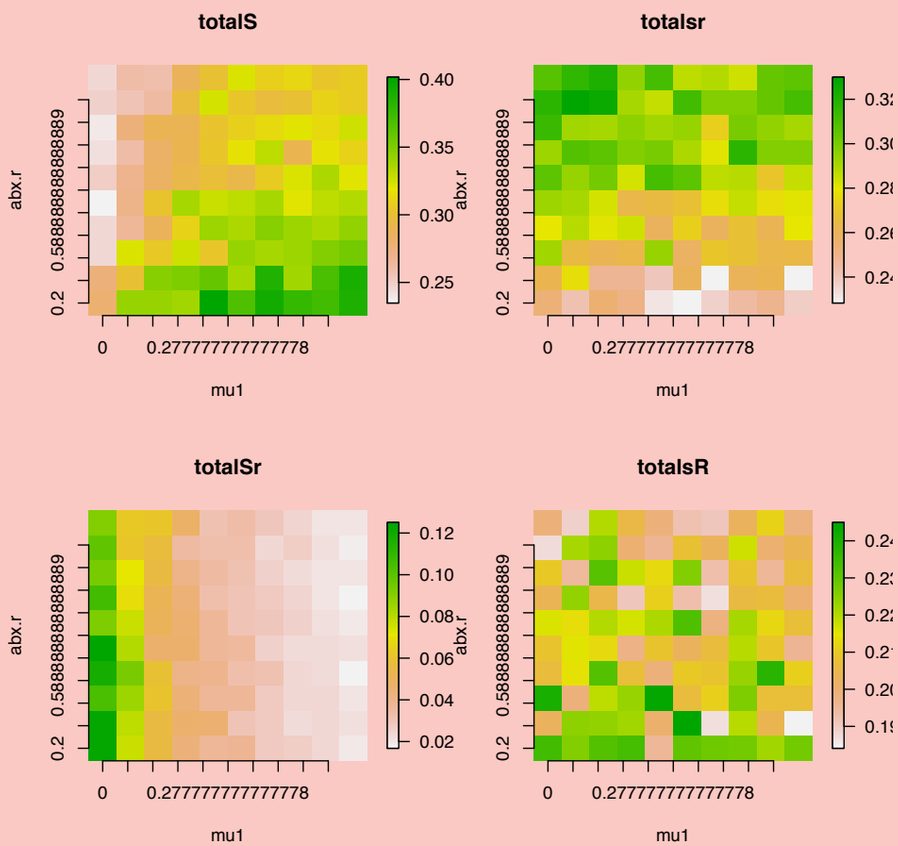
Pairs of parameters explored to determine the effect of each parameter on resistance

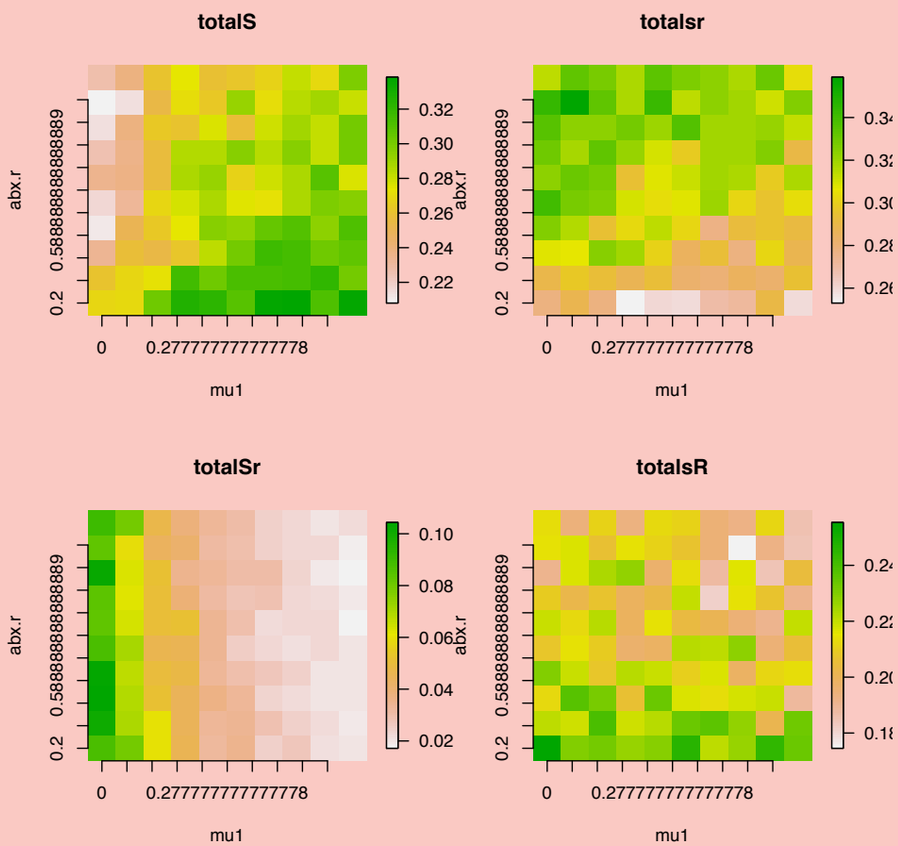
repo.r2 vs repo.s3





abx.r vs mu1

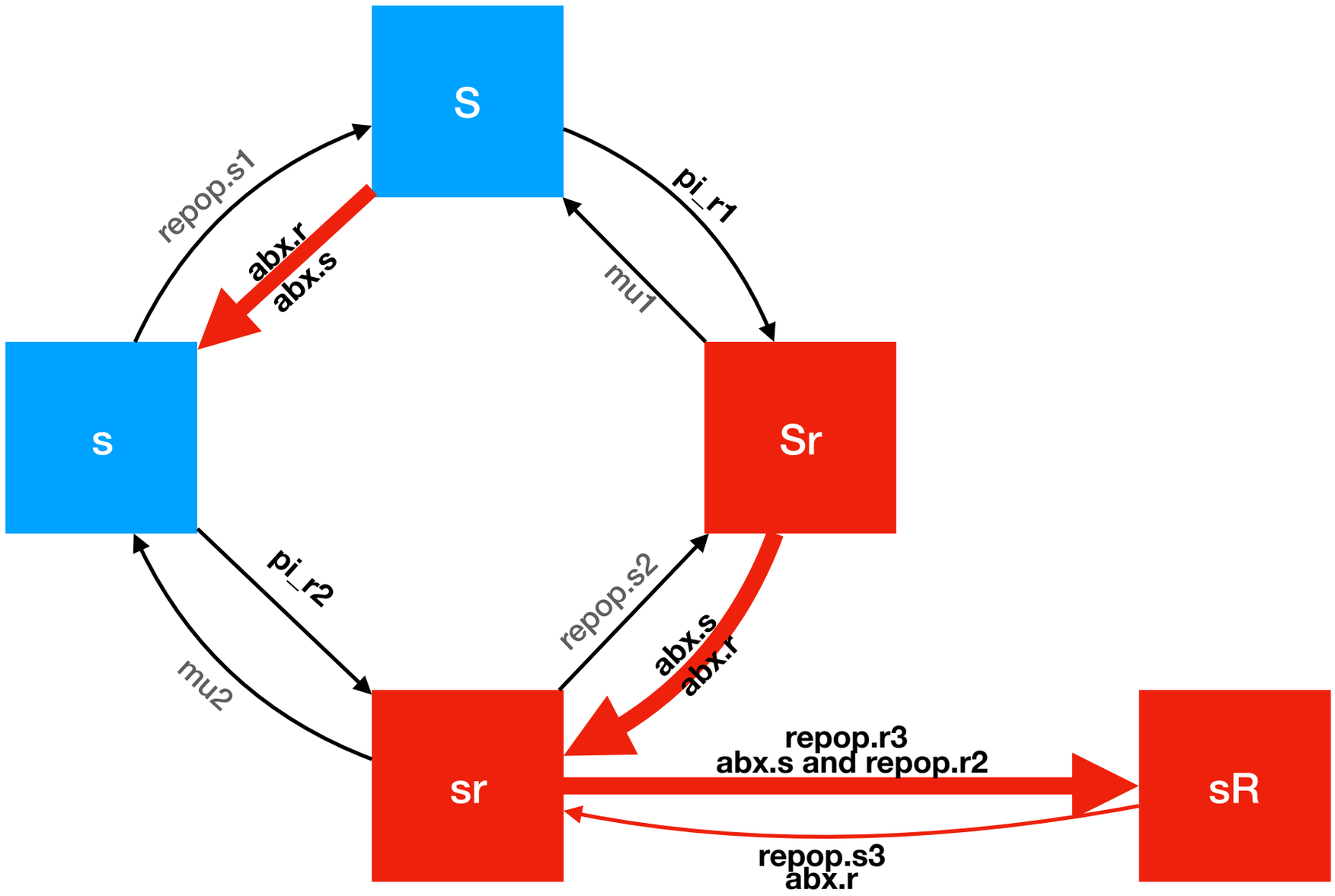




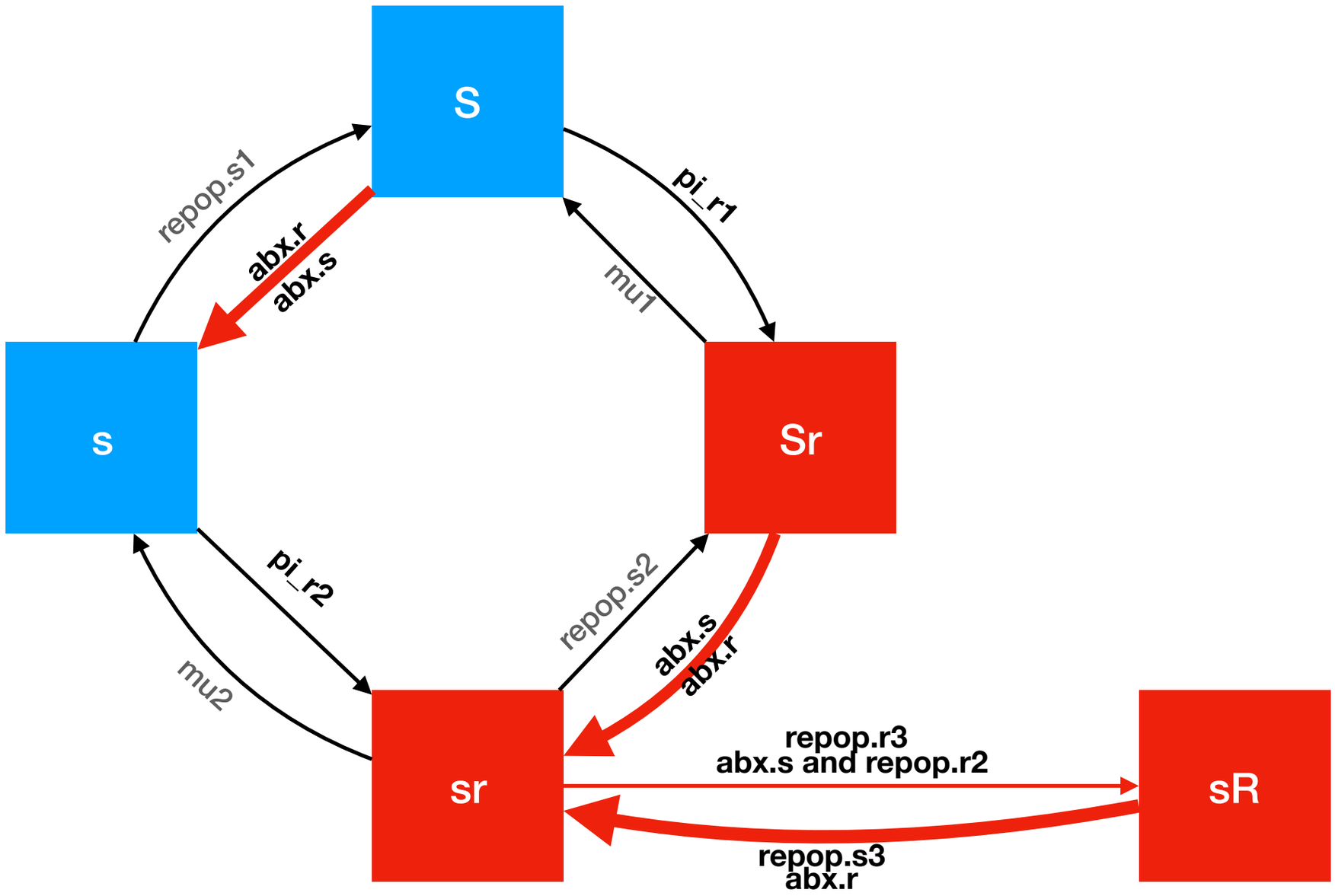
Model 2 exploration

Parameters		Values explored	Baseline value	Increase resistance
p.s	probability of being prescribed narrow spectrum antibiotic	0.1-0.9	0.4	increasing
p.r	probability of being prescribed broad spectrum antibiotic	0.01-0.05	0.05	decreasing
abx.s	probability of clearing S to become s	0.2-0.9	0.5	None
abx.r	probability of clearing R to become r	0.2-0.9	0.5	None
pi_r1	probability of being transmitted r to S (S—> Sr)	0.003-0.5	0.003	None
pi_r2	probability of being transmitted r to s (s—>sr)	depends on bif		
repop.s1	probability of regrowth of S (s—>S)		0	
repop.s2	probability of regrowth of S (sr—>Sr)		0	
repop.s3	probability of transmission of r to S (s—> Sr)	0-0.5	0.05	decreasing
repop.r2	probability of transmission of r to S (s—> Sr)	0-0.9	0.5	increasing
repop.r3	probability of regrowth of s (sR—> sr)	depends on bif1		
mu1	probability of being decolonised to S (Sr—> S)	0-0.5	0	None
mu2	probability of being decolonised to S (sr—> s)		0	
bif	bacterial interference factor (pi_r2 = pi_r1 * bif)	1-500	20	increasing
bif1	bacterial interference factor 1 (repop.r3=repop.r2*bif1)	0-1	0.2	increasing
n.bed	number of beds		20	
mean.max.los	mean of length of stay (normal distribution)		20	
n.days	number of days of observation		100	
prob_StartBact	probability of initial carriage		S = 0.5, Sr = 0.2, sR=0.1, sr=0.05	
mean_dur	mean duration of antibiotics (normal distribution)		4 vs 14	

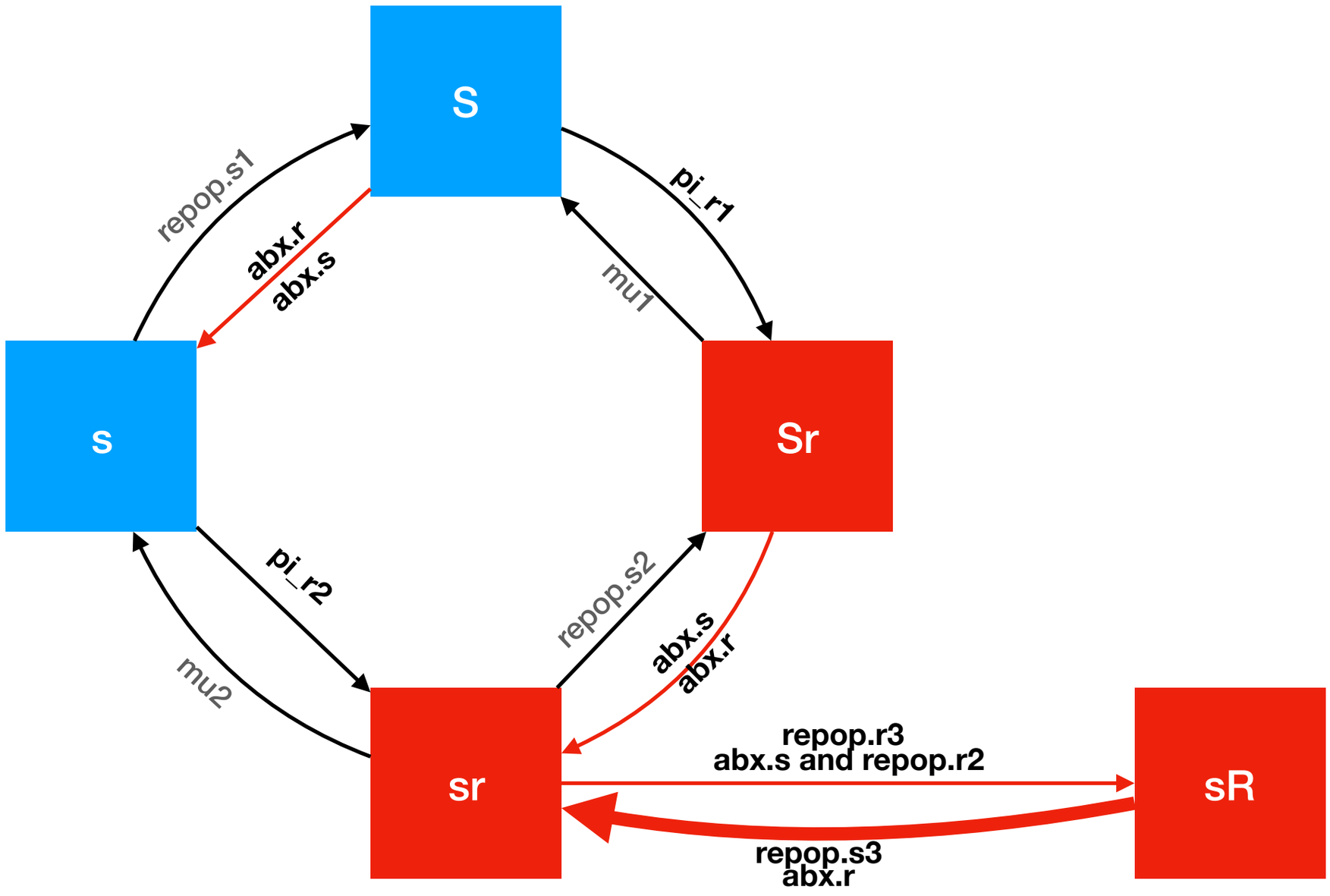
Increasing p.s



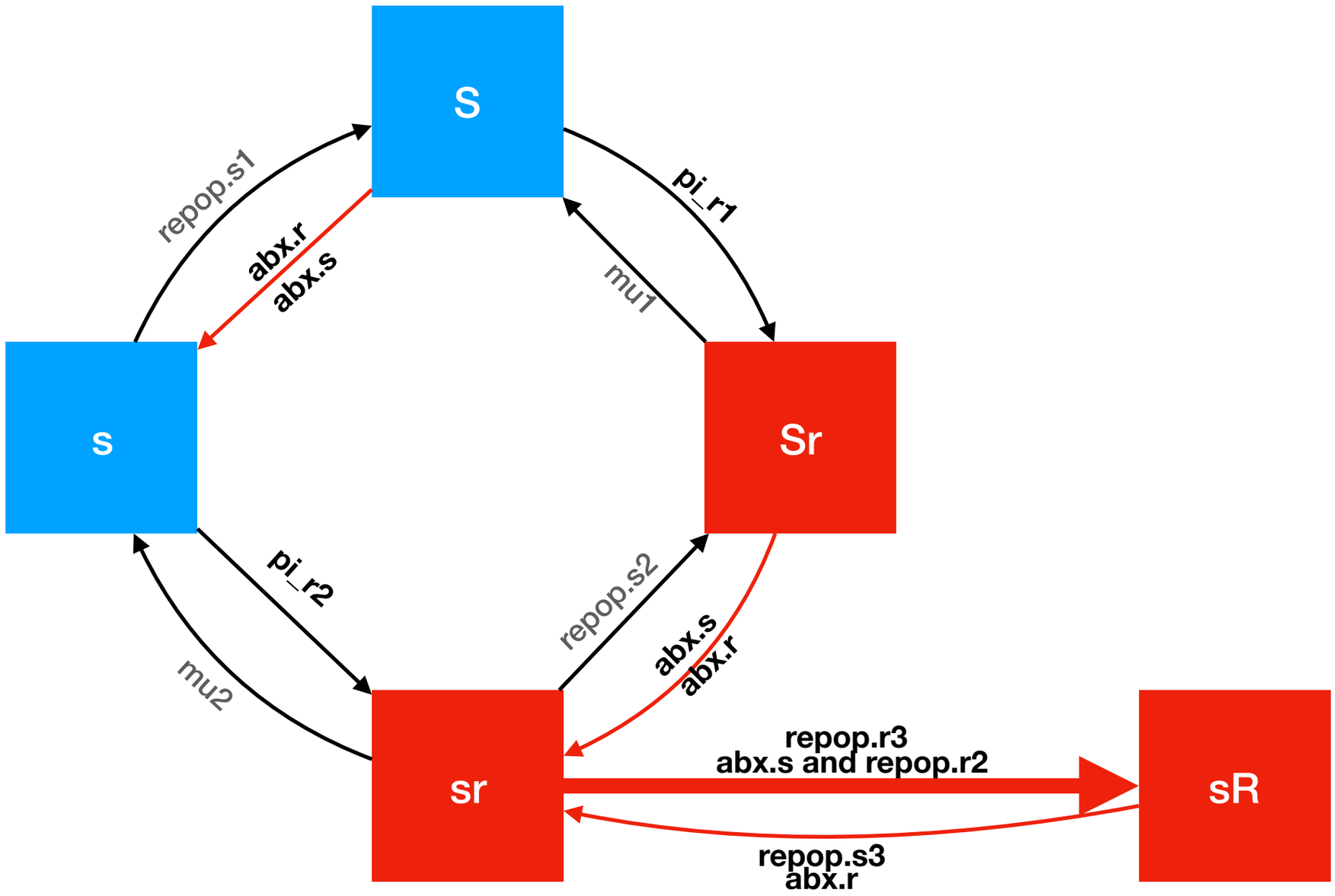
Increasing p.r
(p.r<<p.s)



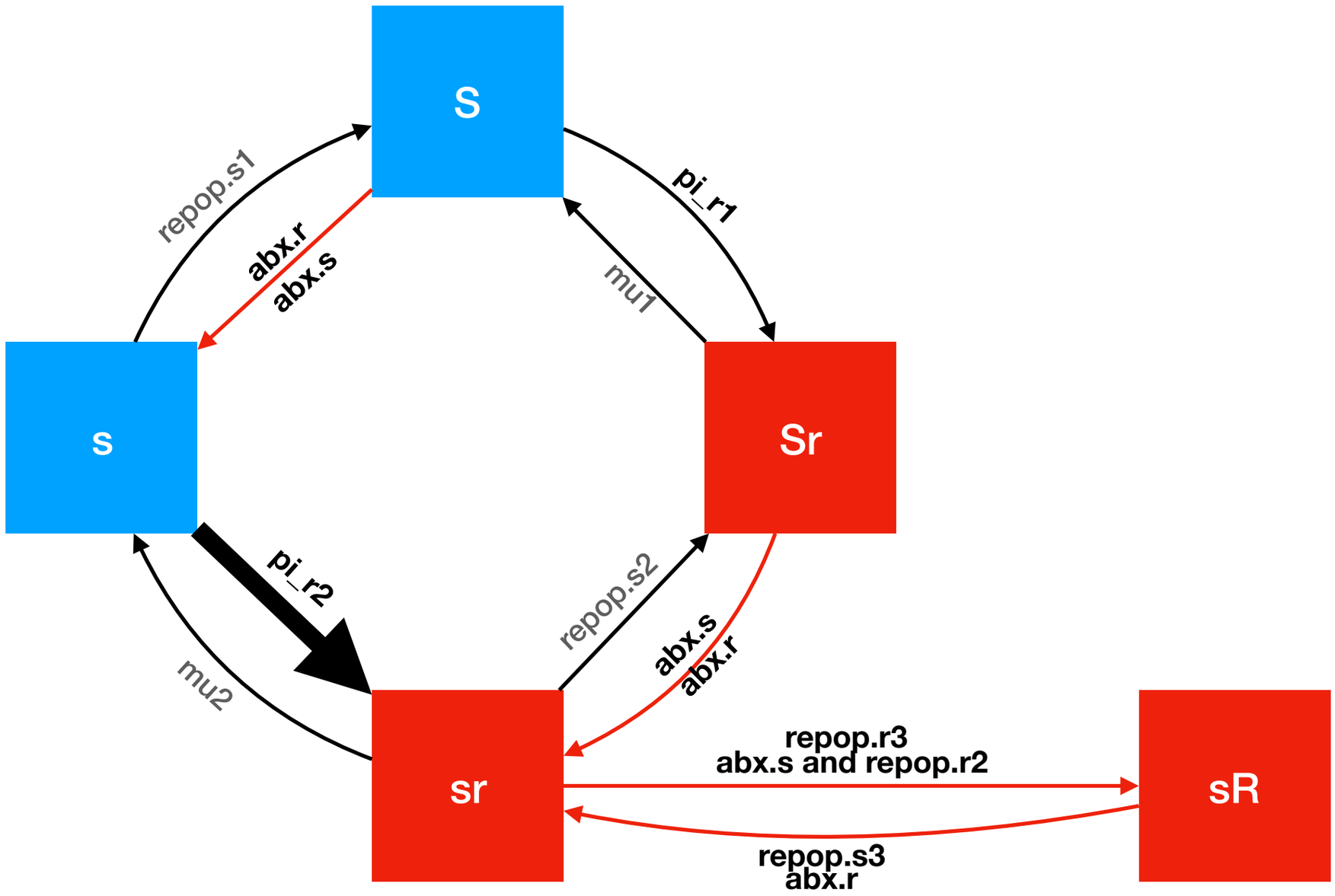
Increasing repop.s3



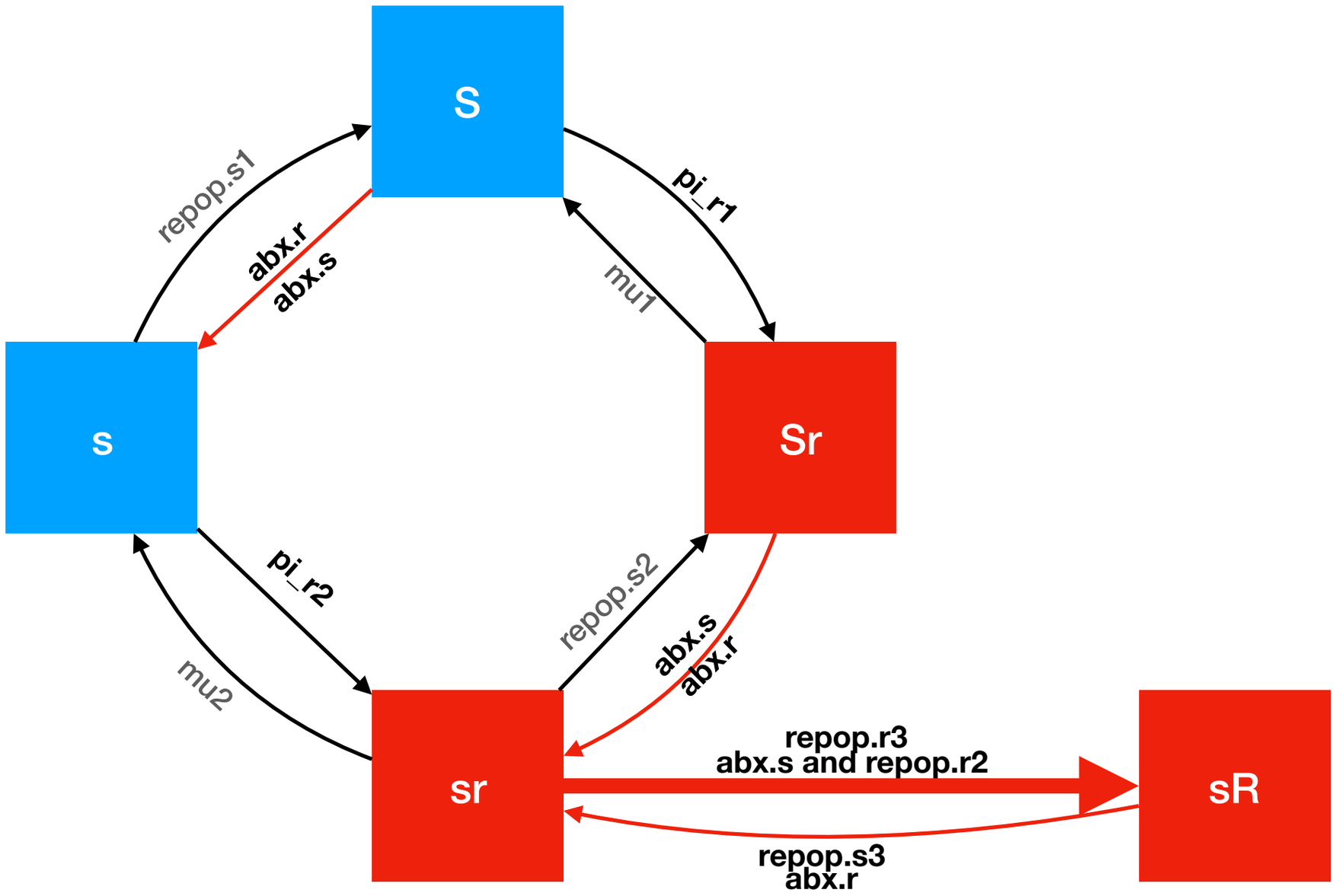
Increasing repop.r2

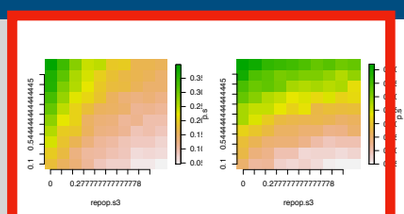
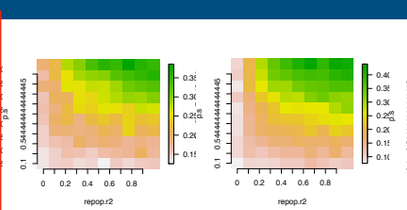
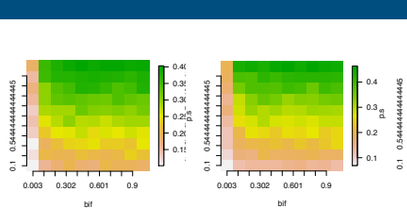
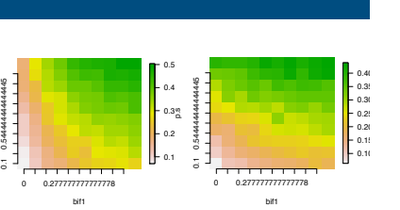
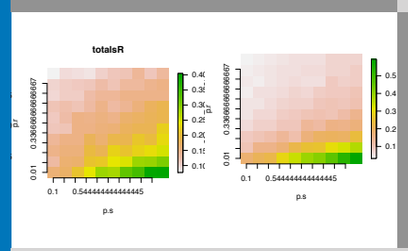
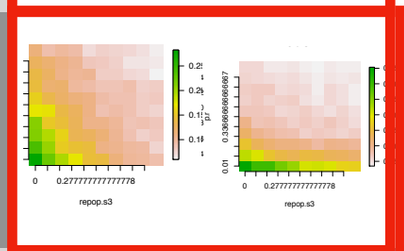
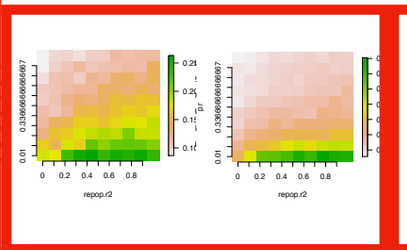
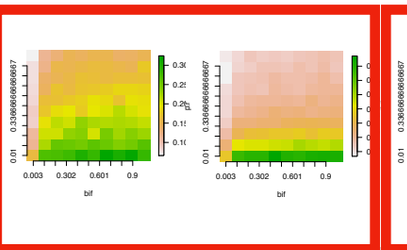
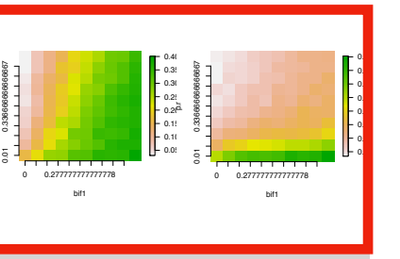
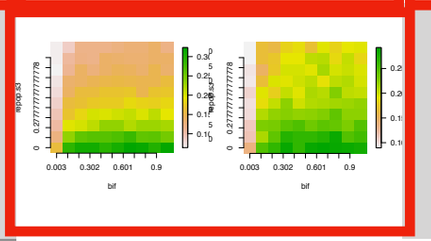
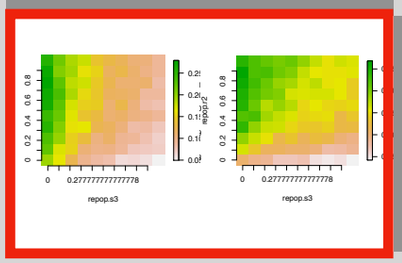
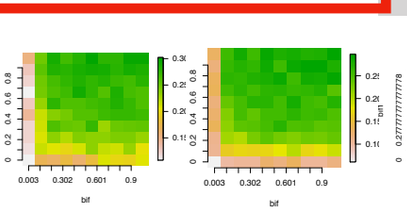
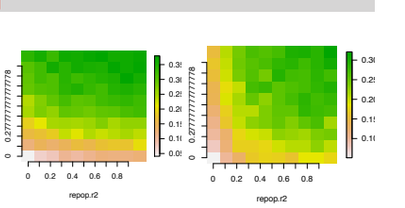
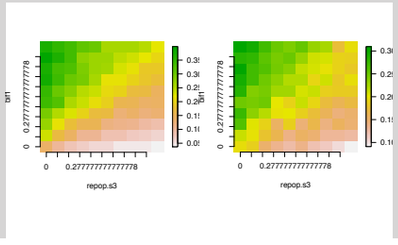
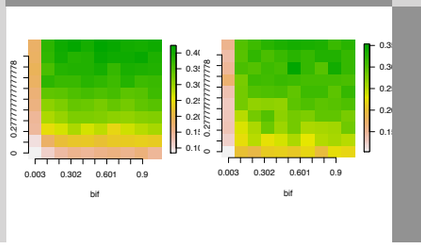


Increasing bif



Increasing bif1



	p.s		p.r		repop.s3		repop.r2		bif		bif1	
	Short	Long	Short	Long	Short	Long	Short	Long	Short	Long	Short	Long
p.s												
p.r												
repop.s3												
repop.r2												
bif												
bif1												

Model 3

- Within host model
- Gut bacterial population is made up of S, R, E (empty)

	Population growth	Antibiotic against S	Antibiotic against R	Transmission	Random death
$\frac{dNs}{dt}$	$r(N_s + N_r)(1 - (N_s + N_r)/K)$	$-\gamma_s N_s$	$-\gamma_r N_s$	$+m_r p_r$	$-\beta$
$\frac{dNr}{dt}$	$r(N_s + N_r)(1 - (N_s + N_r)/K)$	$+\varepsilon N_r$	$-\gamma_r N_r$		$-\beta$