

# Answers to Exercises

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**Exercise 1.** Given in slides. For general  $n$  (1 index case and  $n - 1$  susceptibles) we for example have

$$P(i \rightarrow 1 \rightarrow 2 \rightarrow 0) = \binom{n-1}{1} p^1 (1-p)^{n-2} \times \binom{n-2}{2} p^2 (1-p)^{n-4} \times \binom{n-4}{0} (1-(1-p)^2)^0 ((1-p)^2)^{n-4}.$$

Table 1: **Exercise 2.** The final size  $\tau_*$  (in case of major outbreak) as a function of  $R_0$ .

$R_0$	$\tau_*$
0.8	0
1.5	0.583
3	0.940
6	0.997

Table 2: **Exercise 3.** The final size  $\tau_*$  (in case of major outbreak) as a function of  $R_0$ , and  $P(\text{major outbreak})$  for deterministic infectious periods (called Reed-Frost model) and exponentially distributed infectious periods (called General Stochastic Epidemic model).

$R_0$	$\tau_*$	$P_{R-F}(\text{major})$	$P_{GSE}(\text{major})$
0.8	0	0	0
1.5	0.583	0.583	0.33
3	0.940	0.940	0.66
6	0.997	0.997	0.83

Table 3: **Exercise 4+5.** Final fraction infected among initial susceptibles ( $\tau_*$ ), and among all individuals ( $\tau_{all}$ ) as a function of  $R_0$  when 50% were vaccinated prior to outbreak.

$R_0$	$\tau_*$	$\tau_{all}$
0.8	0	0
1.5	0	0
3	0.583	0.391
6	0.940	0.470

**Exercise 6.** Diseases having  $R_0 < 1$  will not result in many getting infected, and hence they have not been discovered and investigated by humans (there are probably loads of them).

Table 4: **Exercise 7.** Expected number of infectives the first 4 weeks.

week $t$	$E(I(t))$
1	1
2	$e^{2.8} \approx 16$
3	$e^{5.6} \approx 250$
4	$e^{8.4} \approx 4000$

Table 5: **Exercise 8.** The critical vaccination coverage  $v_c$  as a function of  $R_0$ .

$R_0$	$v_c$
0.8	0
1.5	0.33
3	0.67
5	0.82

Table 6: **Exercise 9.** The fraction susceptible at endemicity  $\tilde{s}$  as a function of  $R_0$

$R_0$	$\tilde{s}$
0.8	1
1.5	0.67
3	0.33
6	0.17

**Exercise 10.**  $\tilde{i} = \frac{1/50}{75} = \frac{1}{3750} \approx 0.00027$ .

**Exercise 11+12.** For Iceland with  $n \approx 250\,000$ ,  $n\tilde{i} \approx 67$  and for England and Wales with  $n \approx 60\,000\,000$ ,  $n\tilde{i} \approx 60\,000$ . Since there are seasonal variations (beside stochastic variations) the disease will probably rather quickly go extinct in Iceland, whereas it will remain endemic in England. This is also what happened for measles in Iceland (extinction and later re-introduction from outside) and UK (endemic) before vaccination programs were initiated.

**Exercise 13.** 95% confidence interval for  $p$ :

$$\hat{p} \pm \lambda_{\alpha/2} \sqrt{\hat{p}(1-\hat{p})/n} = 0.27 \pm 1.96 \sqrt{0.27 * 0.73/100} = 0.27 \pm 0.09.$$

**Exercise 14.**  $\hat{R}_0 = \frac{-\ln(1-\tilde{\tau})}{\tilde{i} \text{ilder} \tau} = \frac{-\ln 0.8}{0.2} = 1.12$ .

**Exercise 15.**  $\tilde{\tau} = 0.4$ ,  $1-r = 0.5$ , so  $\hat{R}_0 = \frac{-\ln 0.6}{0.5 * 0.4} = 2.55$ . A very big difference! (So initial immunity very important to take into account!).

**Exercise 16.**

$$\hat{v}_c = \frac{1}{0.9} \left( 1 - \frac{(1-r)\tilde{\tau}}{-\ln(1-\tilde{T})} \right) = \frac{1}{0.9} \left( 1 - \frac{0.2}{-\ln 0.6} \right) = 68\%.$$

**Exercise 17.**  $\hat{\rho} = \frac{\ln(121/7)}{2} = 1.42$  (per week)

**Exercise 18.**  $\hat{v}_c = \frac{1}{E}(1-\hat{s}) = \frac{1}{0.95}(1-(1/15)) = 98\%$ . With  $E = 0.9$  we get  $\hat{v}_c = 104\%$  which is impossible meaning that herd immunity cannot be achieved.

**Exercise 19-20** don't exist

**Exercise 21.**  $\frac{\beta_{ij}}{n} \pi_j n \nu = \beta_{ij} \pi_j \nu$ .

**Exercise 22.**  $\alpha_i$  is the "infectivity" of type  $i$  and  $\gamma_j$  is the "susceptibility" of type  $j$ .

**Exercise 23.**  $\alpha_1 = 1$ ,  $\alpha_2 = 2$ ,  $\gamma_1 = 1$  and  $\gamma_2 = 2$ . So  $R_0 = (1+4)/2 = 2.5$ . The naive guess would be to compute the expected number a type-1 individual infects and the corresponding for type-2 individuals. Since the two types are equally frequent one would then take the average of these two means. Let's do this. A type one individual infects on average  $\alpha_1 \beta_1 \nu \pi_1 = 0.5$  type one individuals and  $\alpha_1 \beta_2 \nu \pi_1 = 1$  type-2 individuals, so in total 1.5 individuals. The corresponding total for a type-2 infected is 3. The mean of these two values is  $(1.5 + 3)/2 = 2.25$  which is different from the  $R_0 = 2.5$  above. So what is wrong with the naive estimate? In the beginning there will be more type-2 infected than type-1 infected, so there will be more infecting 3 on average than 1.5 on average.

**Exercise 24.** For all set-ups,  $p = 0.25$  and  $E(D) = 3$ . Recall that  $R_0 = p(E(D) + (V(D) - E(D))/E(D))$ .

Table 7: The basic reproduction number  $R_0$  for a network model for different values of standard deviation of the degree distribution  $\sqrt{V(D)}$

$\sqrt{V(D)}$	$V(D)$	$R_0$	$v_c = 1 - 1/R_0$
0	0	0.5	0
1	1	0.9	0
3	9	1.25	0.2
10	100	9	0.88

**Exercise 25.** The point estimate of  $R_0$  and  $v_c$  are independent of the coefficient of variation of the infectious period  $r$ . The are  $\hat{R}_0 = 1.25$  and  $\hat{v}_c = 20\%$ . The standard errors depend on  $r$ . When  $r = 0$  (Reed-Frost) we get  $s.e.(\hat{R}_0) = 0.08$  and  $s.e.(\hat{v}_c) = 0.05$ . When  $r = 1$  (for example the General Stochastic Epidemic) the corresponding standard errors become 0.11 and 0.07 respectively.

**Exercise 26.** The point estimates are unchanged but all standard errors shrink by a fact  $1/\sqrt{10} \approx 0.32$ .