

Supplementary Table 1: Equations and initial values for dynamic compartmental transmission models

Compartment	Equation
ON-CAMPUS	
Susceptible (S_1)	$dS_1(t) = -S_1 \times \sum_{j=1}^2 \{\beta_{1j} \times (I_{j1} + I_{j2}) / N_j\}$
Exposed (E_1)	$dE_1(t) = S_1 \times \sum_{j=1}^2 \{\beta_{1j} \times (I_{j1} + I_{j2}) / N_j\} - \sigma \times E_1$
Asymptomatic/not-detected (I_{11})	$dI_{11}(t) = (1 - \alpha) \times \sigma \times E_1 - \phi \times I_{11}$
Symptomatic/detected (I_{12})	$dI_{12}(t) = \alpha \times \sigma \times E_1 - \gamma \times I_{12}$
Isolation (H_1)	$dH_1(t) = \gamma \times I_{12} - \rho \times H_1$
Recovered (R_1)	$dR_1(t) = \phi \times I_{11} + \rho \times H_1$
OFF-CAMPUS	
Susceptible (S_2)	$dS_2(t) = -S_2 \times \sum_{j=1}^2 \beta_{2j} \times (I_{j1} + I_{j2}) / N_j$
Exposed (E_2)	$dE_2(t) = S_2 \times \sum_{j=1}^2 \beta_{2j} \times (I_{j1} + I_{j2}) / N_j - \sigma \times E_2$
Asymptomatic/not-detected (I_{21})	$dI_{21}(t) = (1 - \alpha) \times \sigma \times E_2 - \phi \times I_{21}$
Symptomatic/detected (I_{22})	$dI_{22}(t) = \alpha \times \sigma \times E_2 - \gamma \times I_{22}$
Isolation (H_2)	$dH_2(t) = \gamma \times I_{22} - \rho \times H_2$
Recovered (R_2)	$dR_2(t) = \phi \times I_{21} + \rho \times H_2$

Model assumes an on-campus population of $N_1 = 7,500$ and off-campus population of $N_2 = 17,500$, with a 2% active infection rate at semester start. S_j , E_j , I_{1i} , I_{2i} , H_j , and R_j indicate the number of students in each compartment at time t for population i ($i=1$ indicates on-campus, $i=2$ indicates off-campus). Infectious individuals return to campus through compartment I_{1i} . Pre-arrival testing with one NAT test, assuming 90% test sensitivity, yields $I_{1i} = (N_i - R_i) \cdot 0.02 \cdot (1 - 0.90)$. Pre-arrival testing with two NAT tests, assuming 90% sensitivity for each test, yields $I_{1i} = (N_i - R_i) \cdot 0.02 \cdot (1 - 0.90)^2$. This model is an extension of the Metapopulation SEIR model introduced in equations (8)-(10) of Lloyd and Jansen (2004),¹ and uses the cross-coupling transmission matrix described in Section 3.1.1.

1. Lloyd AL, Jansen VAA. Spatiotemporal dynamics of epidemics: synchrony in metapopulation models. *Mathematical Biosciences*. 2004;188(1):1-16. doi:10.1016/j.mbs.2003.09.003