Appendix A

COVID-19 Agent-based Model: Overview, Design Concepts, Details Description

Purpose

This model is designed to explore questions around the effects of various class schedules on the potential spread of COVID-19 in an undergraduate student population. The world view for the model is a “social space” representation where the distance between student agents is intended to represent the closeness of social relationships (e.g., friendships, shared timetable cohort).

Entities, States, and Variables

The model contains two kinds of entities: student agents and link agents. Student agents represent students in a specific timetabling cohort. Link agents represent connections between students during a shared activity. For example, students in a laboratory section are connected together based on their laboratory groups. At the beginning of each simulation run, student agents are placed randomly in the environment to represent random social connectedness in the student population.

An example of the simulation interface is show in Figure A.1. Student agents are represented by “person” shapes; link agents are represented by lines. At the beginning of each simulation run, student agents are placed randomly in the environment to represent random social connectedness in the student population. It should be noted that the worldview shown in Figure 1 “wraps” vertically and horizontally: i.e., students at the top edge of the view are co-located with students at the bottom edge of the view and students at the left edge of the view are co-located with students at the right edge of the view.

Student agents are initialized in two respects: (1) timetabling, and (2) health. Each timetabling option specifies a set of timetabling cohorts, which are groups of students who share the same course components (e.g., tutorial sections, laboratory sections). These timetabling cohorts result in a form of emergent behaviour, as student agents cluster together based on their shared timetabling cohort and the closeness of personal relationships with other students. Student interaction occurs within these timetable cohort clusters whenever a course component is active.

Appendix 1, as supplied by the authors. Appendix to: Brennan RW, Nelson N, Paul R. Estimating the effect of timetabling decisions on the spread of SARS-CoV-2 in medium-to-large engineering schools in Canada: an agent-based modelling study. *CMAJ Open* 2021. doi:10.9778/cmajo.2020280.

The distance between students (i.e., the closeness of their personal relationships) are assigned randomly at the start of each simulation run and are assumed to be constant over the run (i.e., the 12.7 week term). The timetabling cohorts are established at the start of each simulation run by dividing the students evenly between the cohorts and assigning students to each cohort based on their proximity to each other. The assumption here is that "close relationships" are primarily related to students sharing the same classes; however, the random placement of students in the simulation world view results in some relationships to be closer than others (e.g., through friendships and shared interests) and opportunities for cross cohort interactions (e.g., in hallways between classes).

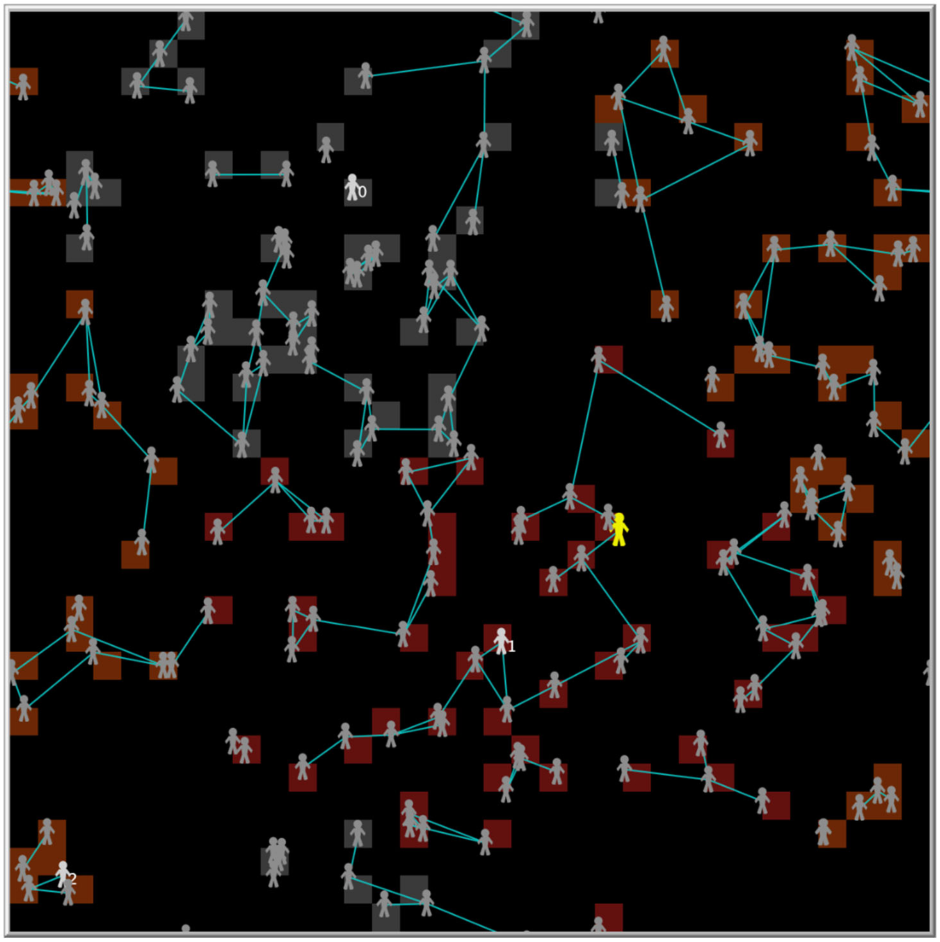

Figure A.1: The agent-based model simulation interface in Netlogo 6.1.1[8]

Given that links are activated when the end node students are involved in a shared activity, the link agent state variables relate to the student timetable. These state variables are link-activity (the activity associated with the link) and link-timetable (the timetable that the link is associated with).

Each of the timetabling options follow a single, 12.7-week term of classes for a typical medium to large undergraduate engineering cohort (typically, 100 to 200 students). The choice of 12.7 weeks is based on the minimum required number of contact hours (accreditation units) specified by the Canadian Engineering Accreditation Board[3]. Although undergraduate academic terms are nominally longer (typically 15 weeks), they include a term break and an exam period; the 12.7 weeks used in this model corresponds to the average length of the classroom portion of the academic term (i.e., lectures, tutorials, and laboratories). All students were registered in the same five courses; each course involves three hours of lectures per week and two hours of tutorial or laboratory per week ("tutorial/laboratory" section). As is common for most Canadian universities, the lectures were timetabled as either three 50-minute sections (Monday, Wednesday, Friday) with 10-minute class changes, or two 75-minute sections (Tuesday, Thursday) per week with 15-minute class changes. Tutorial/laboratories were timetabled as single 110-minute sections per week with 10-minute class changes. All of the timetabling scenarios were structured to fall within a Monday to Friday, 8:00-18:00 window, resulting in a maximum of three weekly laboratory/tutorial sections per course, and a maximum of six bi-weekly laboratory/tutorial sections per course. Lecture sections were timetabled as either in-person, or online, resulting in a total of twelve timetabling scenarios. Further details on the timetabling scenarios are provided in Appendix B.

The model's "health related" variables (Table 1) are based on extant epidemiology and transmission models[10-17]. The COVID-19 parameter estimates shown in Table 1 were incorporated into the model as global variables, shown in Table A.1, that define the transmission model for the experiments.

Table A.1. COVID-19 transmission model parameters used in the agent-based model. The "model" column indicates whether a sampled value or a fixed value is used in the model. For the sampled parameters, the standard deviations were derived from the He et al.[10] meta-analysis (shown as "meta" in the table) or by calculating the standard deviation (SD) from the reported 95% confidence intervals and sample size (N). All samples are taken from the Gaussian distribution with distribution parameters α and λ.

Parameter	**Mean and 95% CI**	**N**	**SD**	α	λ	**Model**
Incubation Period (days)	5.08 (4.77-5.39)	meta	0.18	796.49	156.79	Sampled
Latent Period (days)	2.50	-	-	-	-	Fixed
Time to Isolation, symptoms-based (days)	4.60 (4.10-5.00)	292	3.91	1.39	0.30	Sampled
Time to Isolation, contact-based (days)	1.90 (1.10-2.70)	87	3.75	0.26	0.13	Sampled
Recovery Time (days)	20.80 (20.10-1.50)	391	7.04	8.73	0.42	Sampled
Asymptomatic Infection Rate (%)	46.00 (18.40-73.60)	meta	14.10	10.64	0.23	Sampled

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Parameter	**Mean and 95% CI**	**N**	**SD**	**α**	**λ**	**Model**
Attack Rate (%)	6.10 (3.00-12.10)	114	24.52	0.06	0.01	Sampled
Secondary Attack Rate (%)	4.00	-	-	-	-	Fixed
Outside Transmission (cases/100,000/week)	153	-	-	-	-	Fixed
Test Duration (days)	2	-	-	-	-	Fixed
Isolation Period (days)	14	-	-	-	-	Fixed
Vaccine Effectiveness for 1 dose (%)	30.70	-	-	-	-	Fixed
Vaccine Effectiveness for 2 doses (%)	79.60	-	-	-	-	Fixed
Initial Seeding (number of students)	1	-	-	-	-	Fixed

The *spatial scale* for the model is a "social space" representation where the distance between student agents is intended to represent the closeness of social relationships (e.g., friendships, shared timetable cohort). The world view wraps both vertically and horizontally, which allows student agent clusters at the "edges" of the world view to find close student agents within their cluster.

The *temporal scale* is: 1 tick equals 1 minute.

- 0:00 Sunday = 0 ticks
- 24:00 Sunday = 1440 ticks

The model is designed to roll the timetable over once the last activity has finished. Typical timetable lengths are 1 week (labs every week) or 2 week (labs every second week). This feature allows the timetable to be simulated for an entire term without having to explicitly create a 12 or 13 week timetable.

Process Overview and Scheduling

Once the student agents and student timetables are initialized (see "Initialization"), the model advances forward in ticks (i.e., minute-by-minute). After each tick, the timetables are first checked to see if any change in state is required (i.e., if a new activity such as students entering or leaving a hallway or a class is scheduled). If a timetabling state change is identified, the student agents in the timetabling cohort either form links (entering the activity) or dissolve links (leaving the activity).

Whenever a state change occurs, the *spread-virus* procedure is invoked. This procedure asks all infectious student agents (asymptomatic and symptomatic) to spread the virus amongst students whom they are in contact with (i.e., linked to). This check is done, student-by-student based on the symptomatic virus spread chance and asymptomatic virus spread chance.

The virus-spread procedure is also invoked by the *contact-frequency* global user interface variable. This variable allows the user to set the time between student-student contacts during an activity. This allows the duration of the activity influence the virus spread chance: i.e., activities with longer durations would have a higher chance of virus spread.

The model allows the user to select between two forms of surveillance: *symptom-based* and *contact-based*. For symptom-based surveillance, only symptomatic students are isolated. For contact-based surveillance, the symptomatic student isolates along with this student's contacts as follows:

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- all students who were in contact with the symptomatic student isolate; a user interface variable, *tracing-depth*, is used to determine how many activities back the symptomatic student looks to identify contacts; *tracing-depth* is a nested list of the student's most recent contacts; each sub-list in tracing-depth contains the list of students that student was in contact with during the student's last activity

Student agent health state variables are updated based on the following transmission model.
If *symptom-based surveillance* is used, the following transmission model is followed (student agent colour updates are shown in brackets):

1. susceptible (grey)
2. exposed for the incubation period (yellow)
3. presentation: symptomatic (violet) or asymptomatic (red) based on *asymptomatic infection rate*; if *asymptomatic* go to 5 (i.e., student does not isolate)
4. individual student isolated (colour is unchanged; shape changes to "house")
5. recovered (green)

If *contact-based surveillance* is used:

1. susceptible (grey)
2. exposed for the incubation period (yellow)
3. presentation: symptomatic (violet) or asymptomatic (red) based on *asymptomatic infection rate*
4. isolated (colour is unchanged; shape changes to "house")
5. recovered (green)

At the end of the incubation period, student agents spread the virus (based on the virus spread chance) until isolated or recovered. If contact-based surveillance is used, all students in the contacts cohort are isolated at the time to isolation of the first symptomatic student; they remain in isolation for the *isolation-period* (a user interface input); any students that remain symptomatic or asymptomatic at the end of the isolation period remain in isolation while all other students move out of isolation (this assumes that the isolated cohort is tested prior to leaving isolation). If symptom-based surveillance is used, only symptomatic students are isolated (based on the time to isolation).

The model also provides the option for daily testing of students by selecting the number of tests per day (*tests-per-day*). The *tests-per-day* are divided equally among the timetabling cohorts (e.g., if there are 3 timetabling cohorts, and *tests-per-day* = 18, 6 students from each timetabling cohort will be tested each day). The test procedure is as follows:

1. Every class day (Monday - Friday) at 7:00 am, a group of students from each timetabling cohort is tested. The group is selected from students with the lowest *last-test* time (i.e., time of the student's last COVID-19 test); any ties for lowest *last-test* time are broken using random selection.
2. The *test-duration* is based on the Government of Alberta “COVID-19 Q&A” of 2 days: “from swab collection to test result takes less than two days; it takes about one day for the lab to receive the swab; at the lab, it takes about 13 hours for the result”[15].
3. If a tested student is *symptomatic* or *asymptomatic* the student is isolated as soon as the positive test result is received, or as soon as the student self-isolates in the case of *symptomatic* infection (whichever occurs first).

Once the student agents’ health state variables have been updated, the simulation time is checked relative to the timetable and student agent / link agent states are updated based on the next timetabled activity.

Design Concepts

The *basic principle* addressed by this model is *class timetabling and its effect on the potential spread of an infectious disease (COVID-19)*. In order to reduce the risk of disease transmission, post-secondary institutions are considering a mixture of online and in-person class components (i.e., a “class component” is a timetabled component of the class such as a lecture, tutorial, or laboratory). This model is designed to explore a wide range of timetabling options that could be used for a single cohort of post-secondary students (e.g., a first-year engineering cohort).

Each timetabling option specifies a set of timetabling cohorts: i.e., groups of students who share the same course components (e.g., tutorial sections, laboratory sections). These timetabling cohorts result in a form of *emergent* behaviour, as student agents cluster together based on their shared timetabling cohort and the closeness of personal relationships with other students. Student *interaction* occurs within these timetable cohort clusters whenever a course component is active. Given that the model is concerned primarily with disease transmission, the interactions amount to determining if the virus has spread from an infected student to a susceptible student during an active course component. The timetable determines the frequency of these interactions (i.e., when each course component is active). As well, the user can specify the node degree (number of links between students within a cluster) to influence the number of potential interactions during each active course component (e.g., size of student groups, seating arrangement, etc.). A histogram and monitor output have been provided on the user interface to provide information on the number of student contacts.

Stochasticity plays a big role in this model given the nature of our current understanding of the COVID-19 transmission model and the general variability of disease transmission and progression. This COVID-19 transmission model is based on extant meta-analyses[10-17]: transmission model parameters are initialized as global variables (mean and standard deviation).

We sampled from the Gamma distribution to initialize individual student agent variables and use the discrete Binomial distribution for the chance of virus spread between student agents. Given that the model is concerned primarily with disease transmission, the interactions amount to determining if the virus has spread from an infected student to a susceptible student during an active course component. The timetable determines the frequency of these interactions (i.e., when each course component is active).

The probability of virus spread is based on the non-household secondary attack rate (SAR)[12]. It is generally agreed that the virus spread probability from asymptomatic cases is considerably lower than that from symptomatic cases given that COVID-19 appears to be spread through respiratory droplets. For both cases, the virus spread chance is modelled using the Bernoulli distribution.

As noted previously, one of the factors that influences student clustering is the closeness of personal relationships between students. These relationships are initialized in the model by randomly placing students within the "social space". The intention is to mimic varying degrees of interrelationships between students that would influence factors such as seating arrangements, group formation, walking together to/from class, etc.

In order to test the hypothesis that the choice of class timetable will influence the spread of COVID-19, a series of experiments can be run with various timetabling options. The current student cohort is intended to represent a "typical" cohort: i.e., 5 courses with lectures, tutorial, labs; 180 students.

Initialization

Student agents are initialized in two respects: (1) timetabling cohorts, and (2) health. From a timetabling cohort perspective, the model first creates one "seed" student agent per timetabling cohort. These "seed" student agents are assigned to each of the timetables and are located randomly in the model's world view. Next, the remaining student agents are created, then are clustered around each of the "seed" student agents. For the clustering process, the *n* - 1 student agents nearest each of the "seed" student agents (*n* = number of students in the "seed" student agent's timetabling cohort) are assigned the "seed" student agent's timetable number. The idea is that students within the same timetabling cohort will, by necessity, have closer social connections.

From a health perspective, student agents are all initialized to be susceptible (other than the student agents identified by the initial-outbreak-size). The global virus transmission parameters are initialized using the COVID-parameters.txt file. When individual student agents are infected, these global variables are used to sample individual COVID-19 parameters for student agents.
The model is also initialized with an "outside of class" exposure probability that is based on the incidence rate[14].

Given the stochastic nature of the simulation, we ran multiple replications of the ABM for each test scenario. Each replication represents one 12.7-week term, and as such, the model can be viewed as a terminating system: i.e., each simulation run has a fixed starting condition and an event defining the natural end of the simulation. For simulations of terminating systems, we can assume that observations

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across replications are statistically independent (i.e., a different random seed is used for each run) and all observations are normally distributed (i.e., by the Central Limit Theorem). To determine the number of replications, *n*, for each experiment, we used our key output measure, number of students infected, and performed an initial experiment of 500 replications to estimate the coefficient of variation. For the experiments reported in the next section, we targeted a 95% confidence interval with a width of 5%.

Validation

The purpose of this model is to compare alternative timetabling and intervention strategies for undergraduate engineering programs in response to potential COVID-19 virus transmission. As such, the model is not intended to make specific predictions concerning the number of exposures, but instead it is intended to show the relative impact of alternative strategies.

Given that there have been only very limited returns to the classroom at most undergraduate engineering programs in Canada since March 2020 (i.e., a small number of laboratory sessions at or below the provincial capacity limits) and that data is not available on COVID-19 virus transmission at these reduced capacities or at regular operating capacities, we are unable to make comparisons between the model and the real classroom environment. However, to determine if the model is consistent with the purpose of this study, we performed test to investigate its operational validity. More specifically, we performed tests to determine if the model generates behavioural data characteristic of the real system's behavioural data.

We began by testing the model's underlying susceptible-infectious-recovered (SIR) framework. As noted by Ng et al.[7], we expect that the number of susceptible (S) will decrease monotonically from its initial value to its final value while the number of recovered (R) will increases monotonically until it reaches a limiting value (R_∞). When plotted, the typical dynamics of both the S and R curves should have two distinct periods where the decrease or increase is exponentially slow or fast respectively. The typical dynamics of the number of infected (I) first increases exponentially then reaches a maximum then decreases to 0.

To test our model's behaviour, we ran a set of experiments with in-person lectures and tutorials/laboratories and no interventions. The intention was to run the scenario with the most

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opportunities for virus spread (i.e., a large cohort with many opportunities for interactions) that would replicate a classic susceptible-infected-recovered outbreak. The result of this set of experiments is shown in Figure A.2. As can be seen in this figure, the model's behaviour is consistent with the SIR model described by Ng et al.[7], showing the characteristic curves of the SIR model described previously.

To test for reasonableness, we performed both consistency checks (multiple runs of our experiments with different random number seeds) and degeneracy tests (removing features of the model and determining if the output reflects their removal). As well, we performed continuity test on parameters that were reported with considerable uncertainty in the literature. Table A.2 shows three of these tests of asymptomatic infection rate, incident rate (outside transmissions), and tracing depth. Asymptomatic infection rate was chosen for this analysis given the high variability in the estimate reported by He et al.[10]. Similarly, outside transmission number has a high variability: at the time of writing, this parameter varies from 2.7 per 100,000 population in Newfoundland and Labrador to 194.5 per 100,000 in Alberta; we use the national number of 153 per 100,000 population for our experiments. Tracing depth represents the maximum number of contacts that student remembers having most recent contact with for the purpose of contact tracing. We set this value at 10 contacts in the simulations; however, we recognize that cannot recall contacts with 100% accuracy.

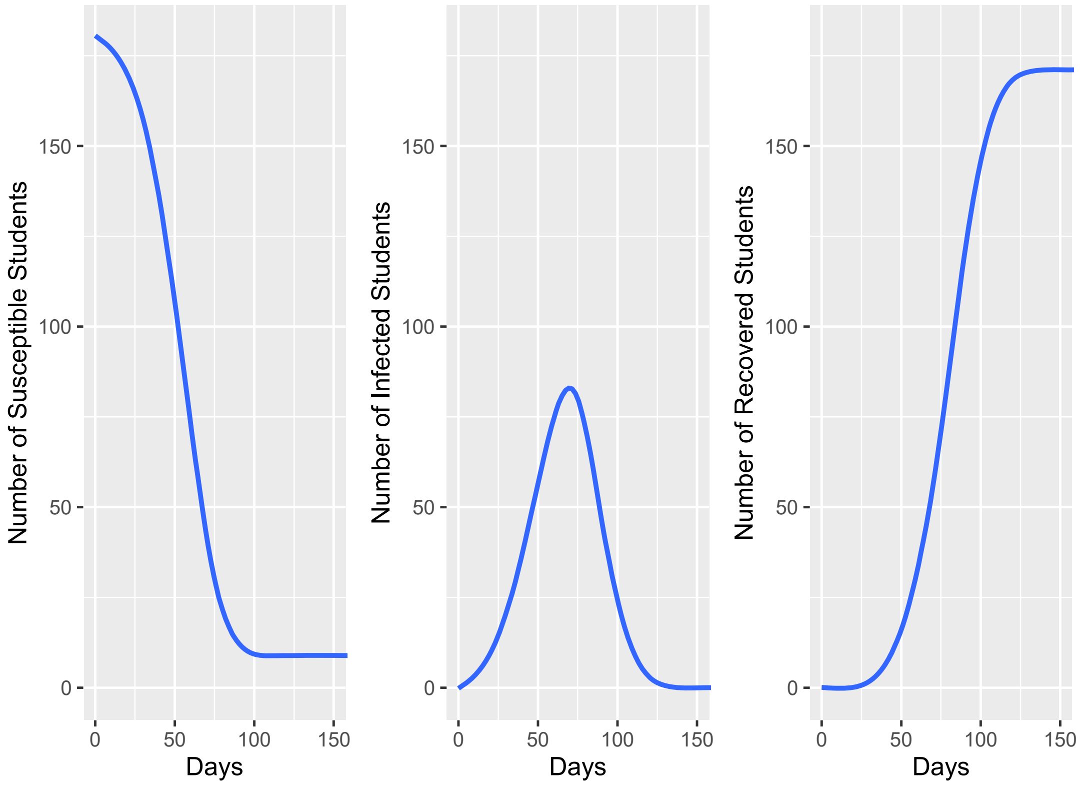

Figure A.2: SIR test with a single-cohort student population over 150 days with the worst-case timetable (i.e., 1x180, in-person lectures, weekly tutorial/laboratory sections). The line of best fit and 95% confidence region for number of students susceptible, infected, and recovered is shown.

Table A.2. Sensitivity tests with a single-cohort student population with the worst-case timetable (i.e., 1x180, in-person lectures, weekly tutorial/laboratory sections).

Parameter	**Standard Value**	**[Minimum, step, maximum value]**	**Regression Statistics**	
			Slope	**R^2**
Asymptomatic infection rate	46%	[15%, 10%, 75%]	0.1519	0.0142
Outside transmission / 100,000	153	[0, 50, 300]	0.286	0.4301
Tracing Depth	10	[2, 2, 10]	-1.513	0.7336

As can be seen in Table A.2, the model appears to have little sensitivity to the asymptomatic infection rate; however, the model is relatively sensitive to incident rate. As expected, the model does show some sensitivity to the tracing depth: i.e., as tracing depth increases, the number of infections slightly decreases. However, the key difference occurs when comparing the results without contact tracing and with contact tracing. Without contact tracing, we observe a mean of 136.71 students infected with 95% CI [130.24 – 143.17] compared to a mean of 42.19 students infected with 95% CI [38.84 – 45.53] at a tracing depth of 2 and a mean of 28.98 students infected with 95% CI [26.62 – 31.34] for a tracing depth of 10.

Appendix B
Timetabling

The experiments with the ABM are designed to simulate a single, 12.7-week term of classes for a typical medium to large undergraduate engineering cohort (typically, 100 to 200 students). All students are registered in the same five courses; each course involves three hours of lectures per week and two hours of tutorial or laboratory per week ("tutorial/laboratory" section). As is common for most Canadian higher education institutions, the lectures are timetabled as either three 50-minute sections (Monday, Wednesday, Friday) or two 75-minute sections (Tuesday, Thursday) per week, and tutorial/laboratories are timetabled as single 110-minute sections per week.

All of the timetabling scenarios are structured to fall within a Monday to Friday, 8:00-18:00 window, resulting in a maximum of three weekly laboratory/tutorial sections per course, and a maximum of six bi-weekly laboratory/tutorial sections per course. The three base timetabling scenarios are shown in Figures B.1, B.2, and B.3.

The convention used for each figure is <course number>-<section number>: e.g., "C1-L01" represents lecture section 1 of course 1; "C1-B01" represents tutorial/laboratory section 1 of course 1. The tutorial/laboratory section numbering in each figure (B01-B03) corresponds to the weekly timetables. For the bi-weekly timetables, the number of tutorial/laboratory sections are doubled for each course: i.e., one section attends during the specified timeslot on odd weeks while a second section attends during even weeks. This results in six possible timetables: three weekly + three bi-weekly. For the simulation experiments, we also consider in-person and online lectures, resulting in twelve timetables.

As noted, the course components are timetabled as 50 minute, 75 minute, and 110 minute blocks. The grey blocks shown in Figures A.1 to A.3 represent hallway transitions between classes of 10 minutes, 15 minutes, and 10 minutes respectively. It is assumed that students leave the campus when there is a long

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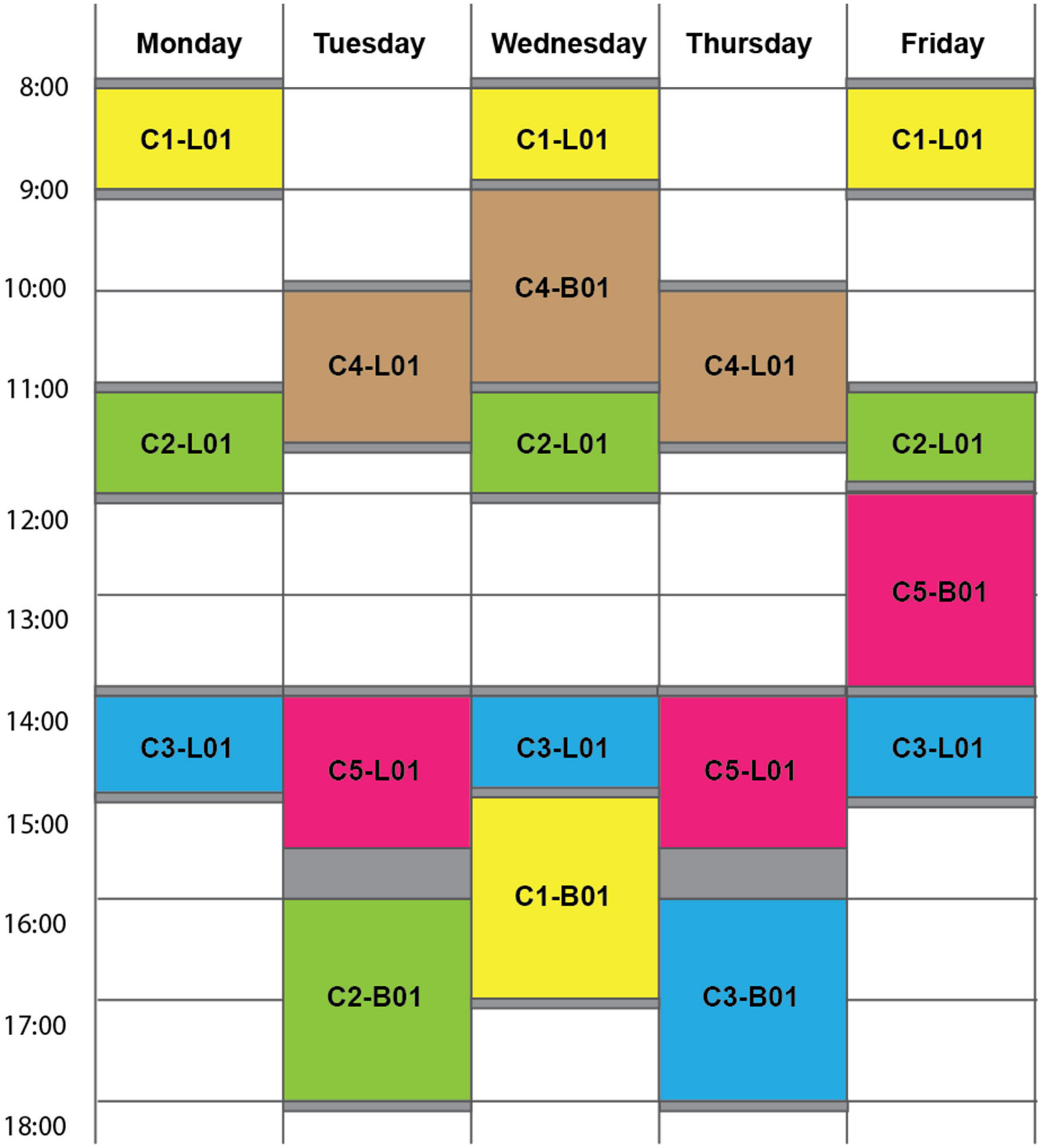
break between classes; however, in cases when there is 30 minutes or less between classes, students remain in the hallway for the entire transition time (e.g., the transition between “C5-L01” and “C2-B01”).



	Monday	Tuesday	Wednesday	Thursday	Friday
8:00	C1-L01		C1-L01		C1-L01
9:00			C4-B01		
10:00		C4-L01		C4-L01	
11:00	C2-L01		C2-L01		C2-L01
12:00					C5-B01
13:00					
14:00	C3-L01	C5-L01	C3-L01	C5-L01	C3-L01
15:00			C1-B01		
16:00		C2-B01		C3-B01	
17:00					
18:00					

Figure B.1: Base timetabling scenario with one tutorial/laboratory section per week

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Figure B.2: Base timetabling scenario with two tutorial/laboratory section per week

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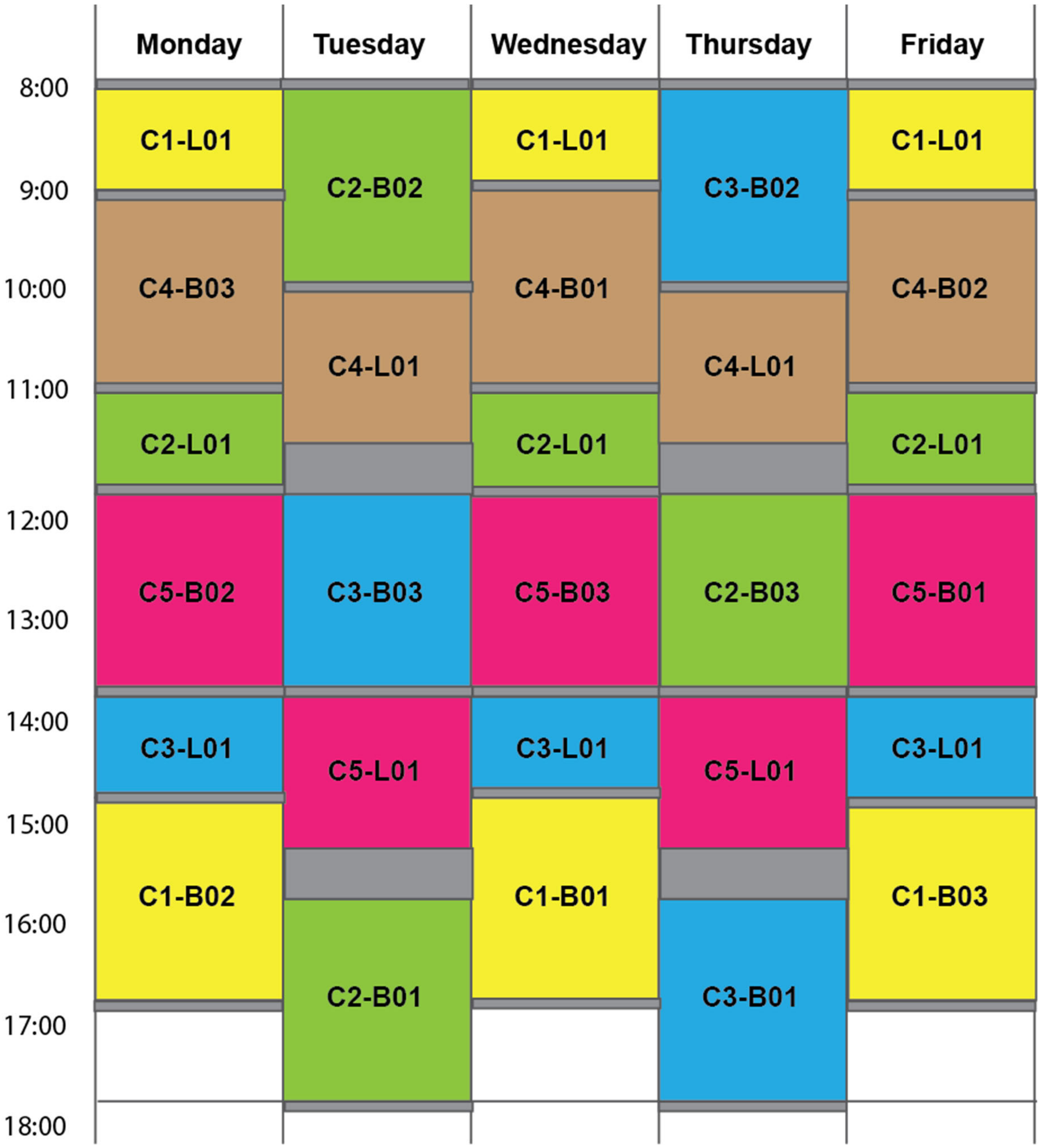

Figure B.3: Base timetabling scenario with three tutorial/laboratory sections per week

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