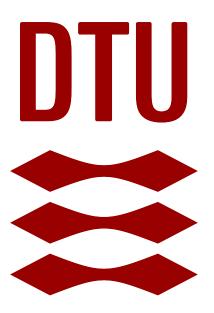
Danmarks Tekniske Universitet

Project 5 - 02526 Mathematical Modeling

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s174434 s174440 s184335

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1 Introduction

COVID-19 has caused devastating effects on people all over the world. As the death toll increases we see countries like the USA where more people have died from COVID-19 than in the Vietnam war [2]. One of greatest concerns in Denmark right now, is the capacity of the health system, especially for patients that need intensive care and ventilators [3]. To make estimates of the capacity needed, we will first use the SIR-model to model the number of infected people the coming year. Only a fraction of the infected would be hospitalized and even fewer need a ventilator, therefore we use demographic and epidemiological data to give an estimate of the needed ventilators within each region in Denmark.

All the models estimates are associated with uncertainty, however, given a scenario with too few ventilators, we will try to find the optimal distribution of ventilators formulated as a mixed integer linear problem. To get a perspective of the future the secondary wave is analyzed using a simplified PDE model.

2 Methodology

2.1 Classification

Based on the estimated probabilities for hospitalization shown in table 3 in the appendix, the number of hospital beds needed per 1000 infected can be determined. The sum of comorbidities in each age group S_i for 2014-2018, total hospitalizations H_{total} for 2014-2018, population in each age group N_i and total population N_{total} was extracted from INDP1 and FOLK1A in StatBank Danmark for the analysis.

To convert the data from INDP1 and FOLK1A age groups {0-4 years, 5-9 years, ..., 80-84 years, +85 years} to similar age groups as table 3 {0-9 years, 10-19 years, ..., 80-89 years, +90 years} the following equations were used:

$$S_{[80-89]} = S_{[80-84]} + S_{[85+]} \frac{N_{[85-89]}}{N_{[85-89]} + N_{[90+]}}, \quad S_{[90+]} = S_{[85+]} \frac{N_{[90+]}}{N_{[85-89]} + N_{[90+]}}$$
(1)

To determine the number of people that were hospitalized from a distribution of 1000 citizens, with and without comorbidities, we used two different assumptions given by:

Assumption 1 (pessimistic): We assume that the hospitalized people within a five year period is representative for the entire population, i.e. the percentage of hospitalized people with comorbidities is the same as the population. **Assumption 2** (optimistic): We assume that all people with comorbidities have been hospitalized within the last five years.

The number of beds needed based on assumption 1 across age groups $i \in \{1, 2, ..., 10\}$ was found using the following equations:

$$B_{comor,i} = 1000 \frac{S_i}{H_{total}} \tag{2}$$

$$B_{no-comor,i} = 1000 \left(\frac{N_i}{N_{total}} - \frac{S_i}{H_{total}} \right)$$
 (3)

Based on assumption 2, slightly different equations omitting H_{total} were used:

$$B_{comor,i} = 1000 \frac{S_i}{N_i} \frac{N_i}{N_{total}} = 1000 \frac{S_i}{N_{total}}$$

$$\tag{4}$$

$$B_{no-comor,i} = 1000 \left(1 - \frac{S_i}{N_i} \right) \frac{N_i}{N_{total}} = 1000 \left(\frac{N_i - S_i}{N_{total}} \right)$$
 (5)

The total number of beds required B_i per 1000 infected in an age group i is determined by:

$$B_{i} = \sum_{i=1}^{10} B_{comor,i} + B_{no-comor,i} \tag{6}$$

SIR model METHODOLOGY

The average age of hospitalization can be determined from beds required for each age group B_i , the average age of an age group A_i and the total number of beds $\sum_{i=1}^{10} B_i$.

Average age =
$$\frac{\sum_{i=1}^{10} B_i A_i}{\sum_{i=1}^{10} B_i}$$
 (7)

2.2 SIR model

We use a simple system of coupled differential equations to model the spread of COVID-19 - the SIR-model[6]:

$$\frac{\mathrm{d}S}{\mathrm{d}t} = -\frac{\beta SI}{N}, \qquad \frac{\mathrm{d}I}{\mathrm{d}t} = \frac{\beta SI}{N} - \gamma I, \qquad \frac{\mathrm{d}R}{\mathrm{d}t} = \gamma I \tag{8}$$

We have susceptible, S, infected, I, and recovered, R, individuals in a population of N individuals. The disease spread with the transmission rate, β , and infected recover with a rate γ . We can, therefore, see that we assume that all have people experience the same infection duration, i.e., $\frac{1}{2}$ days. In the bi-linear term $\frac{\beta SI}{N}$, we assume that the population is homogeneously distributed in space and all have the same contact patterns. Further assumptions include: no incubation period, no natural births or deaths (see [6][8] for further assumptions).

We can see that since R(t) = N - (I(t) + S(t)), we can simplify the system to only two equations. We could now make qualitative analysis of the systems dynamics in a (S, I) phase-plane. We will not cover this but only state the nullcline for $\frac{\mathrm{d}I}{\mathrm{d}t}$, e.i. when $\frac{\mathrm{d}I}{\mathrm{d}t}=0$, is interesting as it indicates the turning point for the epidemic: $0=\frac{\beta SI}{N}-\gamma I \qquad \Longrightarrow \qquad 1=\frac{\beta}{\gamma}\frac{S}{N}$

$$0 = \frac{\beta SI}{N} - \gamma I \qquad \Longrightarrow \qquad 1 = \frac{\beta}{\gamma} \frac{S}{N} \tag{9}$$

If we are in the beginning of an outbreak where we can assume $S(0) \approx N$, $I(0) = N - S(0) \approx 0$ and R(0) = 0, then we see that our RHS is exactly the $R_0 = \frac{\beta}{\gamma}$. It then follows from eq. 9 that we can use $R_0 > 1$ as a criterion to determine if an outbreak occurs - also often used in litterateur [1][8]. Further, in health policy & guidelines e.g. [3] R_0 can also be interpreted as the number of S that one I will infect before they recover. Since we start modelling with many infected cases, we will use the effective reproductive number with the same properties, $R_e = \frac{\beta}{\gamma} \frac{S(0)}{N}$.[8]

2.3 Mixed Integer Problem

We wish to allocate the ventilators in the best way possible. In order to do this, we want to model the need for and allocation of the ventilators as a mixed integer problem. There are some ambiguities when it comes to "the best possible allocation" since several things goes into this. Among these are: Minimizing total deficit of ventilator (i.e. number of people not treated), including some transportation time, minimizing the relative difference between the regions, and minimizing the amount of ventilators transported. To achieve this, we used the following setup: Sets

• W $\in \{1, 2 \dots 53\}$: Weeks, • R $\in \{1, 2 \dots 5\}$: Regions

Parameters

- $V_{w,r}$: Forecasted demand of ventilators in week w in region r
- V_a: Total ventilators available (1260)

Decision variables

- $D_{w,r} \geq 0$: Used number of ventilators in week w in region r
- $S_{w,r} \geq 0$: Storage of ventilators in week w in region r
- $B_{w,r} \in [0,1]$: Binary variable indicating if ventilators were sent in week w by region r

2.3.1Model 1

Objective function

We want to minimize the sum of uncovered patients in all regions.

Minimize
$$Z = \sum_{w=1}^{53} \sum_{r=1}^{5} V_{w,r} - D_{w,r}$$
 (10)

Constraints

For any week w the allocation of ventilators can not exceed 1260.

$$\sum_{r=1}^{5} D_{w,r} \le V_a, \quad \forall w \in W \tag{11}$$

The used number of ventilators should never exceed the forecasted number of ventilators $V_{w,r}$.

$$V_{w,r} - D_{w,r} \ge 0, \quad \forall w \in W, \quad \forall r \in R$$
 (12)

2.3.2Model 2 (transport constraints)

In order to model the include transportation time, we utilized the storage variable, $S_{w,r}$. We only allowed a region to use a ventilator that is in their current storage, and was in their storage 1 week ago too. This imitated a transportation time of 1 week, where a ventilator is said to be in the storage of region X as soon as it left region Y bound for region X. In turn we added the constraints:

$$S_{w,r} \ge D_{w,r}, \quad \forall w \in W, \quad \forall r \in R$$
 (13)

$$S_{w-1,r} \ge D_{w,r}, \quad \forall w \in W \setminus \{1\}, \quad \forall r \in R$$
 (14)

Model 3 (balance distribution) 2.3.3

In order to balance the relative deficit we used chained constraints not allowing each region to have better coverage than the neighboring region ± 1 person. This resulted in the following constraints:

$$\frac{V_{w,r} - D_{w,r}}{V_{w,r}} \le \frac{V_{w,r+1} - D_{w,r+1} + 1}{V_{w,r+1}}, \quad \forall w \in W, \quad \forall r \in R \setminus \{5\}
\frac{V_{w,5} - D_{w,5}}{V_{w,5}} \le \frac{V_{w,1} - D_{w,1} + 1}{V_{w,1}}, \quad \forall w \in W$$
(15)

$$\frac{V_{w,5} - D_{w,5}}{V_{w,5}} \le \frac{V_{w,1} - D_{w,1} + 1}{V_{w,1}}, \quad \forall w \in W$$
(16)

Model 4 (minimizing sent ventilators) 2.3.4

If we want to minimize the sum sent ventilators between the regions r. We do this utilizing the optimal value for deficit just found. We found that the minimal deficit of model 3 to be at some minimum \mathcal{D}_{min} , which means that we can therefore add a constraint that the deficit cannot be larger than this. Now we are free to change the objective to a minimization of the number of ventilators transported. We furthermore have to add some constraints to ensure $B_{w,r}$ is 1 when a region sends ventilators to another region, and 0 otherwise.

Minimize
$$Z = \sum_{w=1}^{52} \sum_{r=1}^{5} (S_{w,r} - S_{w+1,r}) \cdot B_{w,r}$$
 (17)
$$\sum_{w=1}^{53} \sum_{r=1}^{5} V_{w,r} - D_{w,r} \le \mathcal{D}_{min}$$
 (18)

$$\sum_{w=1}^{53} \sum_{r=1}^{5} V_{w,r} - D_{w,r} \le \mathcal{D}_{min} \tag{18}$$

$$S_{w,r} - S_{w+1,r} \le V_a \cdot B_{w,r}, \quad \forall w \in W \setminus \{53\}, \quad \forall r \in R$$

$$\tag{19}$$

$$S_{w,r} - S_{w+1,r} \ge -V_a \cdot (1 - B_{w,r}), \quad \forall w \in W \setminus \{53\}, \quad \forall r \in R$$

2.4 Modelling secondary waves

We here want to investigate how a wave of infection will spread across a finite spatial region - here represented in 1-D as a unit circle. The spatial interpretation of this region is quite abstract, though one picture it as something like a closed version of Pearl-Qatar in Doha where along the circle there is a local density of infected individuals, $\rho(\theta, t)$, at someplace for $\theta \in \{0, 2\pi\}$. The infected individuals move around with a local velocity of $u(\theta, t)[5]$:

$$u(\rho) = (1 - \rho)^{0.3} \tag{21}$$

This velocity we can also interpret as a some infection probability because, the more time an infected individual spend on a given spot, the more likely they are to infected susceptible individuals.

The flux of infected individuals at location ρ and time t is $q(\rho) = \rho(\theta, t)u(\theta, t)$. With this and the assumption that the population has almost attained herd immunity for some density ρ_0 , the conservation law for infected individuals takes the form as in equation 22. We will use this in the experiment section below.

$$\frac{\partial}{\partial t}\rho(\theta,t) + \frac{\partial}{\partial \theta}(\rho(\theta,t)u(\theta,t)) = 0 \tag{22}$$

3 Results

3.1 Hospitalized persons

The beds needed per 1000 infected are shown in table 1 for two given scenarios; (1) when equal infection rate is assumed and (2) when at-risk groups are isolated is assumed.

Table 1: Required beds per 1000 infected and average hospitalization age for assumption 1 & assumption 2.

	Beds r	reeded	Average hospitalization age						
	Equal infection	At-risk groups	Equal infection	At-risk groups					
	rate	isolated	rate	isolated					
Assumption 1	28	9	$64,\!67$	$45,\!31$					
Assumption 2	21	8	62,81	44,06					

Assumption 1 yielded a hospitalization percentage of 2,8% and assumption 2 yielded a hospitalization percentage of 2,0%. For the rest of the analysis the hospitalization rate 2,8% was used, as this produced the most interesting results for the SIR model and distribution of ventilators.

3.2 SIR-model

Using the parameters and data provided in [5], 360 days of the infection in the regions of Denmark have been simulated. All the regions will go through the epidemic and we find the lowest R_e , 1.26, in Nordjylland and the highest in Hovedstand, $R_e = 1.82$.

We have simulated using \mathbf{R} and the package $\mathbf{deSolve}[7]$ to numerically solve the ODEs - the simulation can be seen in appendix D). We can, however, limit our attention to figure 1 as we have predicted outbreaks in all regions and we are only concerned with the capacities of our health system. Therefore we are only interested in the number of infected at a given time. In figure 1 the infected individuals are scaled with the hospitalization rates calculated above and the probability of requiring a ventilator if hospitalized, 0.2. We can see that we require many ventilators, early and in a short interval in region Hovedstaden, whereas the demand for ventilators in Nordjylland is much later and more spread out. This is directly linked to the great and little value of the effective reproductive number, R_e . On a meta level this simple model provides very useful information about the outbreak and with only 5 spatial divisions, these estimates of ventilator requirements can be used to find solutions to some of our concerns. In the following these estimate are used to model how the regions should distribute their ventilators in the next year.

3.3 Distribution of ventilators

In figure 1 the distribution of ventilators for each model can be seen. From figure 1a to figure 1d it can be seen how the final model has a more even spread of ventilators, while still minimizing needed transport from region to region. Figure 1b & figure 1c show the intermediate steps to obtain model 4. The results and models used for this analysis, will be touched on in the discussion.

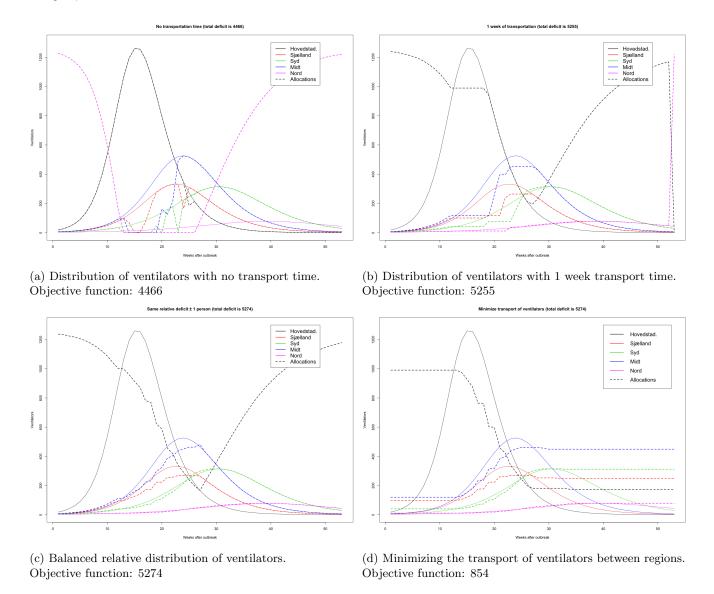


Figure 1: Ventilator allocation in different models

3.4 Perspective for the future

We now work with equation 22 and assume a constant herd immunity ρ_0 and with a tiny, localized increase in infected individuals, ρ_1 , at t = 0. We can now make a perturbation calculation to linearize (22) which correspond directly to the derivation for the traffic models p. 6, [4]. Here we have:

$$\frac{\partial}{\partial t}\rho_1 + c\frac{\partial}{\partial \theta}\rho_1 = 0 \tag{23}$$

where c is the derivative of the flux which we can determine using (21):

$$c \equiv q'(\rho_0) = u(\rho_0) + \rho_0 u'(\rho_0) = (1 - \rho_0)^{0.3} - 0.3\rho_0 (1 - \rho_0)^{-0.7} = \frac{1 - 1.3\rho_0}{(1 - \rho_0)^{7/10}}$$
(24)

Our tiny localized increase moves forward with velocity c which can be seen a traveling infection wave that moves along the characteristic lines: $\theta - ct = \theta_0$. We can now calculate the time it takes to travel the 2π space:

$$2\pi = q'(\rho_0) t \qquad \Longleftrightarrow \qquad t = \frac{2\pi}{\frac{1 - 1.3\rho_0}{(1 - \rho_0)^{7/10}}} = \frac{2\pi(1 - \rho_0)^{7/10}}{1 - 1.3\rho_0}$$
 (25)

We see that the local perturbation moves with the flow for positive c. We could interpret it as some of the infected begins to move faster. However, as a feature of these types of models, the infection can also move against the flow of infected individuals, i.e., $q'(\rho_c) < 0$. This directly corresponds to the point (ρ_c, q_{max}) in appendix H.1 where we he have $q'(\rho_c) < 0 \iff \rho_c = \frac{10}{13}$. We cannot map the value into a specific pragmatic context, as it is more a theoretical feature of the model used. The idea of this model is to include a spatial dimension of the spread using this PDE model which unfortunately requires many assumptions which makes the model less applicable. Below we will discuss alternative models that could be used to include some spacial dimensions for our problem.

4 Discussion

Throughout this project, we used several different models and all of them could be extended.

When estimating the hospitalization percentage, we had to make some assumptions. We are fully aware that some of the assumptions might be far fetched, e.g. assuming the hospitalized population is representative for the general population. However, we chose to work with the this assumption because it was the most pessimistic, and for this kind of analysis, it is better to be a bit too pessimistic rather than underestimate the impact of an epidemic.

In the SIR model we could extend it with natural death, heard immunity, and vaccination - when/if it is available. We could also make it stochastic to add some noise that also occur. Since countries are slowly opening again, one could make piece-wise parameters to mimic this behavior. A great extension could be to spatially represent each individual with an agent based model. Then we could also track down behavior as more people meet and test if prohibitions, like on Islands Brygge in Copenhagen, really are effective. This could also make the results more intuitive if we look at the second wave, as the modelling of secondary wave in 1-D is fairly abstract. This would of course add hugely to the computations and we could also quickly make it too complicated.

When modeling the distribution of respirators, the model could be improved by increasing the resolution. We assume that it takes 1 week to transport ventilators, while in reality this could be expected to be much faster. We chose to be strict regarding the relative deficit. This could be a thing to change in a real scenario, since we where able to obtain the same deficit as we be with no constraints (5255), if we allowed the same relative difference ± 8 people. We also looked into what would happen if we were able to isolate all with comorbidites and/or above 70 years old. We found that this would mean no ventilator deficit.

5 Conclusion

In this report we looked into the impact of COVID-19 with hospitalization probabilities, and infection rate as given. We found that we will see a outbreak lasting approximately 1 year with most infections after 114 days with approximately 300.000 people infected. Region Hovedstaden seems to be the suffering the most and seeing the steepest incline in infections. Furthermore, we will see a significant deficit in ventilators. When accounting for no large differences in relative deficit across the regions we found a minimal deficit of $5274 \ ventilators \cdot weeks$. This is based on a pessimistic approach as described throughout the report, however, even for at more optimistic approach we will still see a deficit.

The only instance where the Danish healthcare system is fully able to cope with the ventilator need, is when all people with comorbidites and/or above 70 years old are fully isolated.

6 References

References

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Appendices

A Contribution chart

Table 2: Contribution to each part of the report for each member of the group.

-	Classification	SIR model	MIP problem	Secondary waves
Introduction	ALL	ALL	ALL	ALL
Methodology	174440	184335	174434	174434
Results	174440	184335	174440	184335
Discussion	174434	184335	174440	184335
Conclusion	ALL	ALL	ALL	ALL

Classification: Collaboration was done primarily between s174434 and s174440, with help on the formulas from s184335.

SIR model: The whole group took part in this, with s184335 being the primary contributor in the report.

MIP problem: The models were set up and analyzed by s174440 and s174434 together. Plots generated by s174434 and scripts run by s174440. Text written in collaboration.

Secondary waves: The problem was discussed internally in the group, and s184335 was the primary solver.

B Excel

Exc	el																												
BEDS NEEDED IN EACH RANGE	GKOUP	0.749278033	707011820	1 105626403	1,103020403	1,959855/18	3,495094043	5,503832278	9,442910859	3,889980531	0,521804551	27,7188813	BEDS NEEDED IN	EACH RANGE	GROUP (NEW)	0,749278633	0,269355854	0,658442272	0,871491524	1,600725961	2,707404234	3,885216348	6,270086263	2,627611407	0,364646627	20,00425912		Sum of all hospital patients	in 2014-2018
COMOR	BED PROB	0,71	, , , , , , , , , , , , , , , , , , ,	0,00	0,40	6,53	7,78	9,94	15,94	11,98	7,23			COMOR	BED PROB	0,71	0,23	5,53	8,48	6,53	7,78	9,94	15,94	11,98	7,23				
NO COMOR	BED PROB	0,71	0.38	, C	c, o	6,0	1,28	1,7	2,53	2,84	2,27			NO COMOR	BED PROB	0,71	0,23	0,38	9'0	6′0	1,28	1,7	2,53	2,84	2,27				
WITH COMOR IN	8 11007E61E	0,1100/3043	5 270370373	6 76777573	0,4044/33/3	14,05442461	26,70004198	43,27994226	52,12995618	30,43058085	6,981113194		WITH COMOR IN	AGE GROUP	(NEW)	4,429168764	2,42101559	2,866852043	3,530454528	7,675565707	14,58173723	23,63654506	28,46981751	16,61910247	3,81260667				
NO COMOR IN	AGE GROUP	112 678215	120 1715133	111 /877749	111,401/149	115,7890878	110,7680294	70,6944716	44,79825471	8,605526236	0,751985336		NO COMOR IN	AGE GROUP	(NEW)	101,103033	114,6902252	131,5540406	114,421796	122,1679467	122,8863342	90,33786881	68,45839338	22,41700462	3,920491861				
	DIST 1000 INFECTED	117 1112408	13/ /208026	117 9522505	2053256,111	129,8435124	137,4680714	113,9744139	96,92821089	39,03610709	7,733098531																		
FRAC COMOR /	POP GROUP	0,07,0849298	0.039051811	0.057805869	0,034603603	0,108241254	0,194227225	0,379733844	0,537820266	0,779549579	0,902757564																		
HOSPITALIZATION	32FE01 8741	333331,8741		275087 5668	0000,100011	412901,7203	437147,7798	362438,0662	308231,226	124134,6254	24591,21466																		
	SUM COMOR 2014-2018	79071	16693	2055	20337	44693	84906	137630	165773	96769,09495	22199,90505																		
AGE GROUP	DISTRIBUTION	0,103332202	0.13/4/20893	0.117052251	0,11/932231	0,129843512	0,137468071	0,113974414	0,096928211	0,039036107	0,007733099				AGE CALC NEW	3,746393164	4,040337809	16,4610568	30,50220334	72,03266825	148,9072329	252,5390626	470,2564697	223,3469696	34,64142961		62,81031534		
	POP IN GROUP I	681911	782701	50,20,	000000	/56048	800444	663646	564390	227298	45028	5822763			AGE CALC AG	3,746393164	4,040337809	19,52856068	38,69692411	88,1935073	192,2301724	357,7490981	708,2183144	330,6483451	49,57143235		64,67155244		
	AGE	10-19 years	20-29 years	20.29 years	30-39 years	40-49 years	50-59 years	60-69 years	70-79 years	80-89 year	90+ year	II			4	5	15	25	35	45	55	65	75	85	95		Average Age:		

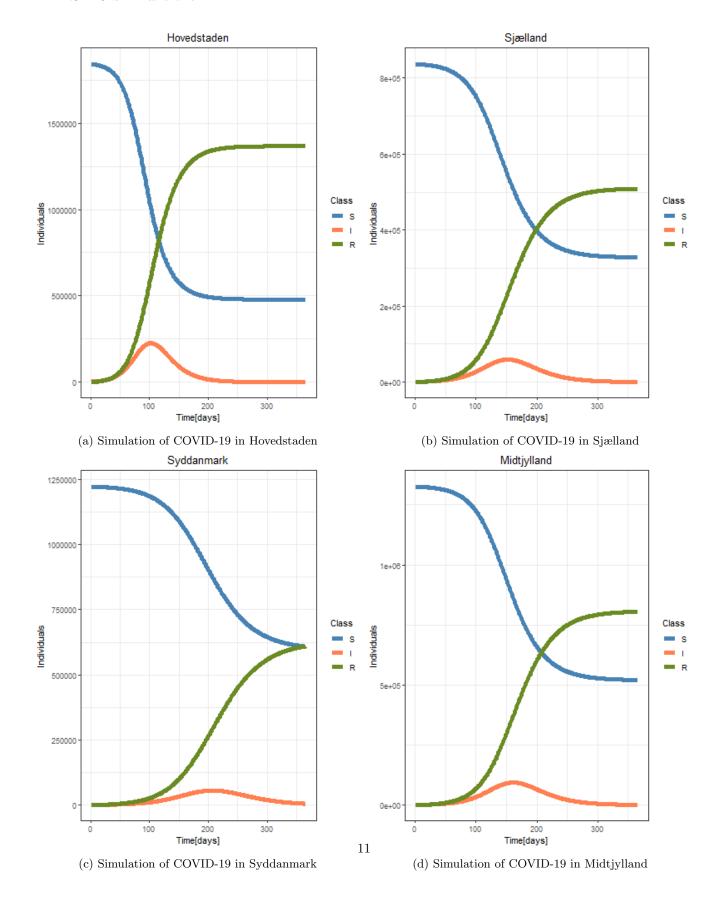
BEDS NEEDED IN	EACH KANGE	GROUP	0,749278633	0,269355854	0,781142427	1,105626403	1,959855718	3,495094043	5,503832278	9,442910859	3,889980531	0,521804551	27,7188813	BEDS NEEDED IN	FACH RANGE	GROUP (NEW)	0,900485014	0,33090871	0,627107139	0,717683103	1,379284135	1,973183683	1,926516437	0	0	0	7,855168222		Sum of all hospital	patients in 2014-2018	3179995
	COMOR	BED PROB	0,71	0,23	5,53	8,48	6,53	7,78	9,94	15,94	11,98	7,23			COMOR	BED PROB	0,71	0,23	5,53	8,48	6,53	7,78	9,94	15,94	11,98	7,23					
	NO COMOR	BED PROB	0,71	0,23	0,38	0,5	6′0	1,28	1,7	2,53	2,84	2,27			NOCOMOR	BED PROB	0,71	0,23	0,38	0,5	6'0	1,28	1,7	2,53	2,84	2,27					
	WITH COMOR IN	AGE GROUP	8,110075645	4,433025838	5,249379323	6,464475573	14,05442461	26,70004198	43,27994226	52,12995618	30,43058085	6,981113194		WITH COMOR IN	AGE GROUP	(NEW)	. 0	0	0	0	0	0	0	0	0	0					
	NO COMOR IN	AGE GROUP	97,42212616	112,678215	129,1715133	111,4877749	115,7890878	110,7680294	70,6944716	44,79825471	8,605526236	0,751985336		NO COMOR IN	AGE GROUP	(NEW)	126,8288753	143,8733521	165,0281945	143,5366206	153,2537928	154,1549752	113,3244963	0	0	0		1000,000307			
		DIST 1000 INFECTED	105,5322018	117,1112408	134,4208926	117,9522505	129,8435124	137,4680714	113,9744139	96,92821089	39,03610709	7,733098531																			
	FRAC COMOR /	POP GROUP	0,076849298	0,03785312	0,039051811	0,054805869	0,108241254	0,194227225	0,379733844	0,537820266	0,779549579	0,902757564																			
	HOSPITALIZATION	IN GROUP	335591,8741	372413,1603	427457,7664	375087,5668	412901,7203	437147,7798	362438,0662	308231,226	124134,6254	24591,21466																			
		SUM COMOR 2014-2018	25790	14097	16693	20557	44693	84906	137630	165773	96769,09495	22199,90505																			
	AGE GROUP	DISTRIBUTION	0,105532202	0,117111241	0,134420893	0,117952251	0,129843512	0,137468071	0,113974414	0,096928211	0,039036107	0,007733099				AGE CALC NEW	4,502425072	4,963630648	15,67767848	25,1189086	62,06778609	108,5251026	125,2235684	0	0	0		44,0575033			
		POP IN GROUP	614489	681911	782701	808989	756048	800444	663646	564390	227298	45028	5822763			AGE CALC A	93164	4,040337809	19,52856068	38,69692411	88,1935073	192,2301724	357,7490981	708,2183144	330,6483451	49,57143235		64,67155244			
		AGE	0-9 years	10-19 years	20-29 years	30-39 years	40-49 years	50-59 years	60-69 years	70-79 years	80-89 year	90+ year	II				2	15	25	35	45	55	9	75	85	95		Average Age:			

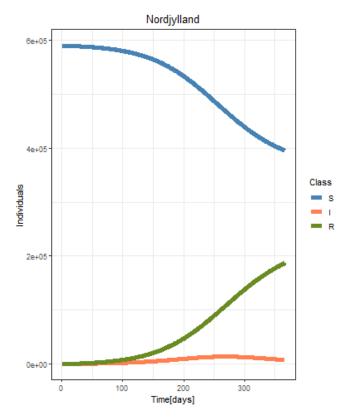
C Classification

Table 3: Probability in % of infection leading to hospitalisation for different age groups, with and without comorbidities. The comorbidities are hospitalisation due to: cancer, chronic lung disease, diabetes, haematological disease, and cardio-vascular diseases within the last 5 years. The numbers are under the assumption, that the real number of cases is 10 times higher than the reported

Age [y]	0 - 9	10 - 19	20 - 29	30 - 39	40 - 49	50 - 59	60 - 69	70 - 79	80 - 89	90 +
No comorbidities	0,71	0,23	0,38	0,50	0,90	1,28	1,70	2,53	2,84	2,27
With comorbidities	0,71	$0,\!23$	$5,\!53$	8,48	$6,\!53$	7,78	9,94	15,94	11,98	$7,\!23$

D SIR simulation





(e) Simulation of COVID-19 in Nordjylland

Figure 2: SIR simulation for one year ahead

Code for simulation made in R

```
# import relevatn packages
  library(deSolve)
3
  library(ggplot2)
   NRegion = 5
5
   # In the following we use:
7
   names = c("Hovedstaden", "Sj lland", "Syddanmark", "Midtjylland", "Nordjylland")
8
  #Initialize the parameters
10
11
  beta = c(0.13, 0.11, 0.1, 0.11, 0.09)
  gamma = rep(1/14, NRegion)
12
13 NPop = c(1846023, 837359, 1223105, 1326340, 589936)
14 NCase = c(3186, 825, 704, 933, 397)
15
   tvec = seq(0, 365, 1)
17
   beta/gamma*(NPop-NCase)/NPop
18
   # Initialize list to store result
19
20
   res = list()
^{21}
22
   # create function for the ode:
```

```
sir_model = function (t, x, p)
25
     with (as.list (c(x,p)),
26
             # define differential eqiations:
27
28
               dS = (-beta * S * I)/NPop
29
               dI = (beta * S * I)/NPop - (gamma * I)
30
               dR = (gamma * I)
31
32
              results = c (dS, dI, dR)
33
34
               list (results)
35
36
   }
37
38
39
   # for each region we simulate
40
   for (i in 1:NRegion) {
41
     # Define intial condition
42
     y0 <-c(S=NPop[i]-NCase[i], I=NCase[i],R=0)
43
44
     # store the result in a list
45
46
     res[[i]] <- ode(y0,tvec,sir_model,c(beta=beta[i],gamma=gamma[i],NPop=NPop[i]))</pre>
   }
47
48
49
   # make plots and save them
50
   for (i in 1:5) {
51
     png(file=paste(getwd(),"/", names[i],".png",sep=""),width=400,height = 400*1.2)
52
     print(ggplot(data.frame(res[[i]][,2:4]), aes(x=1:366)) +
       geom_line(aes(y=S,color="SteelBlue"),size=2) +
54
55
       geom_line(aes(y=I,color="Coral"),size=2) +
       geom_line(aes(y=R,color="Olivedrab4"),size=2) +
56
       scale_color_identity(name = "Class",
57
                             breaks=c("SteelBlue", "Coral", "Olivedrab4"),
                              labels = c("S", "I", "R"),
59
60
                              guide="legend") +
       labs(x="Time[days]", y="Individuals", title=names[i]) +
61
       theme_bw() +
62
63
       theme(plot.title = element_text(hjust = 0.5)))
     dev.off()
64
65
66
67
  # Vectors to store infeced:
69
70
   I <- matrix(NA, nrow=366, ncol=NRegion)</pre>
71
  #extract infected
72
  for(i in 1:NRegion){
73
74
     I[,i] <- res[[i]][,"I"]</pre>
75
76
  # define the hospitalized persons
  H \leftarrow data.frame(I*20.00425912/1000*0.2)
78
79
  # write to a txt file
81
  setwd("C:/Users/Nicolaj/OneDrive - Danmarks Tekniske Universitet/DTU mapper/4. ...
        semester/Matematiskmod/Exercises/COVID19")
  write.table(ceiling(H[seq(from=1, to=366, by=7),]), file="hosp.txt", sep = " ",row.names = ...
        F, col.names = F)
```

E MIP Problem

```
1 # Ceiled data of ventilator need
2 V = [
3 18 5 4 6 3
4 27 7 5 7 3
5 41 8 6 9 3
6 61 11 8 12 4
7 90 14 9 16 4
8 133 18 11 20 5
9 194 23 13 26 5
10 279 30 16 34 6
11 393 39 20 44 7
12 538 49 24 57 8
13 710 63 29 73 8
14 894 80 35 93 9
15 1065 100 42 118 11
16 1194 124 50 149 12
17 1260 152 60 185 13
18 1255 182 71 227 15
19 1187 214 84 274 17
20 1075 247 99 325 19
21 938 277 117 376 21
22 796 302 136 425 23
23 660 321 156 468 26
24 538 331 178 500 29
25 432 332 201 520 32
26 344 325 224 526 35
27 271 310 247 517 39
28 213 289 267 496 42
29 166 264 285 465 46
30 129 237 299 428 50
31 100 210 309 386 53
32 78 183 314 343 57
33 60 158 313 301 61
34 46 136 308 261 64
35 36 115 299 224 68
36 28 98 285 191 70
37 21 82 269 161 73
38 17 69 251 136 75
39 13 57 231 114 77
40 10 48 211 95 78
41 8 40 191 79 78
42 6 33 172 66 78
43 5 27 153 55 77
44 4 23 136 45 76
45 3 19 120 37 74
46 2 15 105 31 72
47 2 13 92 26 69
48 2 11 80 21 67
49 1 9 70 17 64
50 1 7 61 14 60
51 1 6 53 12 57
52 1 5 45 10 53
53 1 4 39 8 50
54 1 4 34 7 47
55 1 3 29 6 43
56 ]
```

F Julia Code, model 1-3

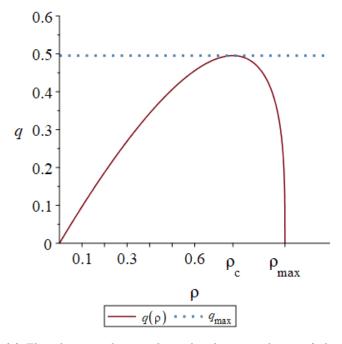
```
using Cbc, JuMP, SparseArrays, CSV, DataFrames
   # Ventilator need as hovedstad=1, sjlland=2 ... nord=5
   include("V.jl")
   function solveVenti(V)
        myModel = Model(with_optimizer(Cbc.Optimizer))
        # Ventilator in 5 regions (hovedstad, sjlland, syd, midt, nord)
9
10
        @variable(myModel, x[1:53,1:5] \ge 0, Int) # In use
        @variable(myModel, y[1:53,1:5] \geq 0, Int) # Total
11
12
13
        # Min deficit of ventilators
        @objective(myModel, Min, sum(sum(V[i,j] - x[i,j] \text{ for } j=1:5) \text{ for } i=1:53))
14
15
        @constraint(myModel, [i=1:53,j=1:5], x[i,j] \le y[i,j]) # max 1260 ventilators
16
        \texttt{@constraint} \, (\texttt{myModel, [i=2:53,j=1:5], x[i,j]} \, \leq \, y \, [\texttt{i-1,j]}) \, \, \# \, \, \texttt{one week of transportation time} \, \\ 
17
18
        @constraint(myModel, [i=1:53], sum(y[i,j] for j=1:5) == 1877) \# max 1260 ventilators
19
20
        @constraint(myModel, [i=1:53,j=1:5], V[i,j] - x[i,j] \ge 0) # Dont cover more than nessecary
21
        # Dont allow large difference in relative deficit
22
         \texttt{@constraint} \ (\texttt{myModel}, \ [\texttt{i=1:53}, \texttt{j=1:4}], \ (\texttt{V[i,j]} - \texttt{x[i,j]}) \ / \texttt{V[i,j]} \ \leq \ (\texttt{V[i,j+1]} - \texttt{x[i,j+1]} + \dots ) 
23
             1)/V[i,j+1]
24
         \texttt{@constraint(myModel, [i=1:53], (V[i,5] - x[i,5])/V[i,5]} \leq (V[i,1] - x[i,1] + 1)/V[i,1]) 
25
        optimize! (myModel)
27
28
        if termination_status(myModel) == MOI.OPTIMAL
29
             println("Objective value: \n", JuMP.objective_value(myModel))
             print("\n")
30
            println("Ventilator allocation: \n", round.(JuMP.value.(y)))
31
             print("\n")
32
33
             surplus = round.(JuMP.value.(x) - V)
             println("Ventilator surplus = \n", surplus)
34
             CSV.write("balanced1.csv", DataFrame(round.(JuMP.value.(y))))
35
36
             println("Optimize was not succesful. Return code: ", termination_status(myModel))
37
        end
38
39
   end
40
   solveVenti(V)
```

G Julia Code, model 4

```
13 #*********************
14 # Data
# (hovedstad, sjlland, syd, midt, nord)
16 include("V.jl")
17 R = length(V[1,:])
18 W = length(V[:,1])
19 START_STORAGE = [1000 65 65 65 65]
20
21 #*********************
22 # Model
23 myModel = Model(with_optimizer(Gurobi.Optimizer))
24
   # Ventilator in 5 regions (hovedstad, sjlland, syd, midt, nord)
26 @variable(myModel, x[1:53,1:5] \ge 0, Int) # In use
27 @variable(myModel, y[1:53,1:5] \ge 0, Int) # Total
28 @variable(myModel, bin[1:52,1:5], Bin) # 1 if a region sends in a given week, 0 otherwise
29
30
   # Min deficit of ventilators
31 @objective(myModel, Min, sum((y[i,j] - y[i+1,j])*bin[i,j] for i=1:52,j=1:5)) \# objective for min ...
       ventilators
  #@objective(myModel, Min, sum(sum(V[i,j] - x[i,j] \text{ for } j=1:5) \text{ for } i=1:53))
32
33
   # 1 week transportation time
35 @constraint(myModel, [i=1:53,j= 1:5], x[i,j] \le y[i,j]) # max 1260 ventilators
  \texttt{@constraint(myModel, [i=2:53,j=1:5], x[i,j] } \leq y[i-1,j]) \text{ \# one week of transportation time}
37
  Quantum (myModel, [i=1:53], sum(y[i,j]) for j=1:5) == 1260) # max 1260 ventilators
38
39
  @constraint(myModel, [i=1:53,j=1:5], V[i,j] - x[i,j] \ge 0) # Dont cover more than nessecary
40
41
  \texttt{@constraint(myModel, [i=1:53, j=1:4], (V[i,j] - x[i,j])/V[i,j] \leq (V[i,j+1] - x[i,j+1] + \dots)}
42
       1)/V[i,j+1])
43
   \texttt{@constraint(myModel, [i=1:53], (V[i,5] - x[i,5])/V[i,5] \leq (V[i,1] - x[i,1] + 1)/V[i,1] ) } 
44
  \texttt{@constraint(myModel, sum(sum(V[i,j] - x[i,j] for j=1:5) for i=1:53)} \leq 5274) \# \texttt{Max deficit} = 5255
46
   # Make sure send works correctly
47
48 @constraint(myModel, [i=1:52, j=1:5], y[i,j] - y[i+1,j] \leq 1260*bin[i,j])
49 @constraint(myModel, [i=1:52,j=1:5], y[i,j] - y[i+1,j] \geq -1260*(1-bin[i,j]))
50
51
  #*****************
52
53 # Solve
54  solution = optimize!(myModel)
55 println("Termination status: $(termination_status(myModel))")
56 #**********************
58 #******************
  if termination_status(myModel) == MOI.OPTIMAL
59
60
      println("Optimal objective value: $(objective_value(myModel))")
61
62
      println("No optimal solution available")
63 end
65 PATH = "C:/Users/Garsdal/Desktop/02526 Mathematical Modelling/Covid/minimize_send_x_v3.csv"
66 CSV.write(PATH, DataFrame(JuMP.value.(x)))
67 PATH = "C:/Users/Garsdal/Desktop/02526 Mathematical Modelling/Covid/minimize_send_y_v3.csv"
68 CSV.write(PATH, DataFrame(JuMP.value.(y)))
70 println("Successfull end of $(PROGRAM_FILE)")
```

H Perspective for the future

H.1 Flow-density relation



(a) Flow-density relation where the slope is velocity of the infection wave

Figure 3: Flow-Density relation