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COVID Symptoms, Symptom Clusters, and Predictors for Becoming a Long-Hauler Looking for Clarity in the Haze of the Pandemic

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Abstract
Post-acute sequelae of SARS-CoV-2 (PASC) is defined as persistent symptoms after apparent recovery from acute COVID-19 infection, also known as COVID-19 long-haul. We performed a retrospective review of electronic health records (EHR) from the University of California COVID Research Data Set (UC CORDS), a de-identified EHR of PCR-confirmed SARS-CoV-2-positive patients in California. The purposes were to (1) describe the prevalence of PASC, (2) describe COVID-19 symptoms and symptom clusters, and (3) identify risk factors for PASC. Data were subjected to non-negative matrix factorization to identify symptom clusters, and a predictive model of PASC was developed. PASC prevalence was 11% (277/2,153), and of these patients, 66% (183/277) were considered asymptomatic at days 0–30. Five PASC symptom clusters emerged and specific symptoms at days 0–30 were associated with PASC. Women were more likely than men to develop PASC, with all age groups and ethnicities represented. PASC is a public health priority.

Keywords
COVID-19, long-COVID, electronic health record, machine learning

Background and Significance
In the United States, over 83 million people have been infected with SARS-CoV-2, the virus responsible for COVID-19 (Johns Hopkins University, 2021), and the cumulative hospitalization rate has exceeded 1,300 persons per 100,000 since early 2020 (Centers for Disease Control and Prevention, 2021). Hospitalized patients account for 1% of COVID-19 patients, yet most of the COVID-19 research focuses on in-patients with severe disease (Bergquist et al., 2020). Among non-hospitalized patients, little is known about the medium- and long-term consequences of COVID-19. The most recent statistics show that 10–30% non-hospitalized patients, those with mild to moderate COVID-19 cases, will not recover quickly, within the expected time-frame for symptom resolution (Carfì et al., 2020; Greenhalgh et al., 2020; Lamberti & Survivor Corps, 2020; Rubin, 2020). These individuals, termed “long-haulers,” or persons with post-acute sequelae of SARS-CoV-2 (PASC) infection, as recently termed by the United States National Institutes of Health, struggle with debilitating, persistent, and ever-evolving symptoms that last for weeks and can exceed 1 year after SARS-CoV-2 infection. In short, COVID-19 has resulted in a cohort of millions of long-haulers worldwide, and we know little about the diagnosis and treatment. There is no cure.

It is not uncommon for infectious diseases to have late sequelae; however, the reason is unclear. For PASC, some scientists believe that late sequelae reflects primary organ involvement during acute infection; others believe that long-term signs and symptoms are promoted by aberrant inflammatory immune responses. PASC is yet to be

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Objectives

The objectives of this study were to (1) determine the prevalence of PASC, (2) to describe medically documented symptoms (EHR) of non-hospitalized patients with PCR-confirmed SARS-CoV-2-positive \( n = 2,153 \) tests at days 0–30 and 180+ days, and (3) to identify the factors that increase risk to develop symptoms at 180+ days.

Materials and Methods

Sample Size and Inclusion Criteria

University of California CoVid Research Data Set (UC CORDS as of 03/17/2021) is a de-identified EHR for 52,083 patients treated in facilities throughout California and is available to University of California researchers. Because this is one of the first studies to characterize long-haul symptoms, it was important to ensure accurate temporal ordering of symptoms that were not subject to limitations of patient recall and used the gold standard of recording medical data, the EHR. Symptoms recorded in the EHR are documented by a medical provider, who receives information from the patient, and conducts a medical assessment. Using medically documented symptoms through the EHR increased our confidence in the accurate reporting of symptoms and their temporal order. This approach worked to overcome the limitations of prior work that relied on patient retrospective recall of symptoms by patients months following SARS-CoV-2 infection and lacked symptom history data and was plagued by the inability to determine the temporal order of symptoms or if symptoms were new or pre-existing before COVID-19. To validly capture the symptoms that could be attributed to COVID-19, we employed strict inclusion/exclusion criteria that yielded a sample \( N = 2,153 \) of never-hospitalized SARS-CoV-2-infected individuals with COVID-19 symptoms. Patients hospitalized for COVID-19 were excluded as were out-patients with false-positive PCR results—having a positive and negative test within the same visit—or documented reinfection with SARS-CoV-2. In addition, patients needed to have records within the system before SARS-CoV-2 infection for at least a year and symptoms reported before infection were excluded in the analysis. The data captured in the EHR reflect a time before vaccines were publicly available. Figure 1 provides a schematic of how we achieved the sample size of 2,153.

Non-Negative Matrix Factorization for Subgroup Identification

Non-negative matrix factorization (NMF) was employed to identify and quantitatively derive the subgroups of patients based on initial symptom presentation data. NMF is an unsupervised learning algorithm that can extract meaningful features from high-dimensional data sets (Lee & Seung, 1999). It is widely used to extract interpretable components from data in various domains such as image processing, data mining, and genomics. In principle, NMF could be used in any application for meaningful components extraction where the elements in input data are non-negative. We formulate our input data as a matrix A of m rows and n columns with each element \( A_{ij} \geq 0 \), where m is the number of subjects and n is the total number of symptoms of interest, each element denotes the count of a symptom documented within a specific time range for a given patient. NMF searches for matrices W of size \( m \times k \) and H of size \( k \times n \), such that \( A = WH \). The matrices W and H are derived by minimizing the squared Frobenius norm \( ||A - WH||^2 \) with some suitable optimization algorithms such as coordinate descent. Here \( k \) is a hyperparameter and its value is determined by the user. In the context
of symptom cluster discovery, \( k \) would be the number of symptom clusters; its value should be smaller than the smallest of \( m \) and \( n \). The matrix \( W \) is also known as the basis matrix, and \( H \) is called coefficient matrix. Note that the value of an element inside matrix \( A \) can be approximated in terms of the dot product of a basis vector (rows of \( W \)) and the corresponding coefficients (columns of \( H \)). Plenty of questions can be explained by the \( W \) matrix and \( H \) matrix. First of all, we can recognize which subgroup a patient resides in by inspecting the basis vector where the \( i \)th element of the basis vector can be interpreted as how likely the patient belongs to the \( i \)th subgroup, and given that the patient belongs to the \( i \)th subgroup, the chances of developing each symptom are represented by the coefficient vector in matrix \( H \). Second, we can identify the most representative symptoms in each subgroup by aggregating and sorting the coefficient vectors.

**Network Analysis to Determine Symptom Associations**

Association study methods are typically based on correlations and to derive the associations, a common way is to set an arbitrary threshold (e.g., significance of \( \alpha = .05 \)) via null-hypothesis testing, one often has to execute a considerable number of significance tests and deal with it through Bonferroni corrections, which will lead to a loss of power. To circumvent the above problems, we applied Graphical lasso (Glasso) which uses model selection to find the simplest model (sparse network) with sparsity achieved by imposing L1 penalty on model coefficients. Glasso operates on symptom occurrence counts data and yields pairwise associations of symptoms which are represented by an undirected network where each vertex represents a symptom. The network structure can be estimated by applying a lasso regression using each variable in the graph as the response and the others as predictors. After network structure estimation using Glasso, we employed the walktrap algorithm which is a standard community detection algorithm on graphs to further cluster nodes in the network (Friedman et al., 2008; Pons & Latapy, 2005).

**Analysis to Identify Predictors of PASC**

To identify factors leading to the development of persistent symptoms, we developed a predictive model that inputs multiple potential key factors to predict whether a subject with SARS-CoV-2 infection will become a long-hauler. By

**Model Selection of NMF**

We used Akaike information criterion (AIC) (Akaike, 1974), a method originated from information theory and widely applied in statistics and machine learning for model selection to determine the optimal \( k \), the formula of AIC is given as follows:

\[
AIC = -2\log L + K(N + M)
\]

where \( L \) is the likelihood of the model, and \( K(N + M) \) is the number of parameters in the model. When there are several candidate models, the best choice is identified as the one corresponding to the minimum AIC, and the intuition is that when the likelihood is identical for two models, the better model is the one with less parameters. We further normalized likelihood term and model complexity term in the original AIC formula because without proper normalization, the second term would usually dominate the equation and thus suggest \( K = 1 \) all the time. We found out that AIC works the best and the optimal \( K \)s derived are 5 for both early-stage symptoms and long-haul symptoms. More details are found in our supplemental materials.

**Figure 1.** Flowchart depicting how records were screened for inclusion in the study.
inspecting the model’s coefficient strength, we can identify the key predictors. We formulated socio-demographics, symptoms the individuals experienced in the first 30 days, and whether a patient was asymptomatic in the first 30 days as input features and then applied logistic regression as our predictive model. To alleviate the effect of multicollinearity, which may cause misinterpretation of predictor importance, we performed hierarchical clustering on the Spearman rank-order correlations of input features.

One of the key properties of supervised machine learning techniques (e.g., logistic regression) is their predictive nature. In these techniques also known as classification, by analyzing a set of features (e.g., symptoms from the first 30 days) from an existing set of labeled samples (e.g., COVID-19 long-hauler vs. not COVID-19 long-hauler), a model can be learned to predict the probability of those classes/labels (e.g., becoming a long-hauler or not) for a new sample. Such predictive models do not require a control group for predictions since the labels (e.g., positive/negative) intrinsically provide information regarding both classes (in binary classification), assuming that enough samples were observed by the model to learn from. Once can then analyze the learned models to calculate the contribution/correlation of each of the features (e.g., symptoms) to the final classification.

Results

Features and Symptoms Among Community-Dwelling Individuals with COVID-19: Days 0–30 and 180 + Days

Table 1 shows the sample distribution related to age, sex, and ethnicity at days 0–30 and at 180 + days. Comorbidities included asthma (~13%), hypertension (~43%), diabetes mellitus (~24%), chronic obstructive pulmonary disease (~1%), hyperlipidemia (~38%), major depressive disorder (~15%), congestive heart failure (~7%), anemia (~21%), cerebrovascular disease (~1%), and hypothyroidism (~13%). Approximately 22% had 1 comorbidity, 16% had 2 comorbidities, 32% had three or more, and 30% of the sample did not have any of these comorbidities. Figure 2 shows the prevalence of symptoms reported at days 0–30 and 180 + days. Prevalent symptoms at days 0–30 include (in descending order) cough, dyspnea, fever, chest pain, headache, among others. Symptoms reported among those with PASC (180 + days) include (in descending order) dyspnea, chest pain, abdominal pain, headache, low back pain, among other symptoms.

Using NMF five symptom clusters with the co-occurrence of symptoms were identified at days 0–30 (Figure 3a) and 180 + days (Figure 3b). At days 0–30 symptom clusters included: dyspnea—diarrhea (N=283), cough—diarrhea (N=378), chest pain—heart palpitations (N=173), fever—nausea (N=270), and tachycardia—heart palpitations (N=337). Symptom network analysis was used to identify the strength of association between symptoms, wherein the darker the line connecting nodes indicates a stronger relationship. Symptom clusters observed among PASC (180 + days) included the following: dyspnea—cough (N=41), chest pain—cough (N=40), heart palpitations—anxiety (N=29), headache—low back pain (N=53), and nausea—fatigue (N=64). Symptom network analysis was again used to identify the strength of association between symptoms, wherein the darker the line connecting nodes indicates a stronger relationship.

Symptoms at Days 0–30 and Their Predictive Value for PASC and Specific Symptom Cluster

Table 1 provides the distribution of age, sex, and ethnicity among patients with PASC, those reporting symptoms at 180 + days. This group was distributed across all age groups, including among those <18, ethnicities, and included more women than men. In Figure 4, features associated with developing PASC were identified and included an initial asymptomatic presentation at the time of testing, as well as reporting alopecia, chronic rhinitis, joint or throat pain, and tinnitus, among many others. Conversely, an initial presentation of dysgeusia, or loss of taste, was negatively associated with developing PASC.

Features present at days 0–30 that most likely result in grouping within one of five symptom clusters identified among PASC survivors are reported in Figure 5. The greatest
magnitude between a feature and membership within a cluster included initial presentation with fatigue with the dyspnea–cough cluster, asymptomatic with heart palpitations–anxiety cluster, and muscle pain with nausea–fatigue cluster. Of the non-modifiable factors such as age, sex, and ethnicity, age 18–29 was associated with the nausea–fatigue symptom cluster and White race was associated with headache–low back pain cluster.

**Figure 2.** Symptoms prevalence among SARS-CoV-2 infected community dwellers at days 0–30 and 180+ days. Bar graphs showing prevalence of symptoms reported at days 0–30 and 180+ days. Symptoms with very low prevalence are omitted in this graph.

**Figure 3.** Symptom clusters among SARS-CoV-2-infected community dwellers at days (a) 0–30 and (b) 180+ days. NMF determined symptom clusters depicted in bar graphs with symptom ranking within each cluster, graph demonstrating optimal k means clustering, and graph demonstrating symptom network analysis showing relationship between each reported symptom. Each symptom is denoted as a node, with darker lines connecting symptoms indicating stronger relationships. NMF = non-negative matrix factorization.
Discussion

The current study provides much needed insight into early factors predisposing individuals for developing PASC. These novel findings warrant additional investigations, discussion, and context within current knowledge about long-haulers/ PASC. In reviewing our findings, we believe there are several key take-home points from our analyses.

First, we found the PASC prevalence to be 11%. While our method captured symptoms attributable to COVID-19, it is likely the symptoms reported in the EHR are not comprehensive. Patient visits are typically short, and patients often report the most bothersome symptoms, the symptoms they see as most related to the suspected illness, and refrain from discussing symptoms that may be stigmatized or cause embarrassment. The understanding of COVID-19 symptoms and openness of providers in validating patient accounts have evolved over time. While this study estimated PASC prevalence at 11%, it is possible that there are more patients with symptoms that did not disclose for one the aforementioned reasons. Therefore, our estimate is conservative and is likely at the lower bounds of prevalence. Of note, of those that developed PASC, 66% were asymptomatic days 0–30. The reason for testing is unclear, but the implication that many asymptomatic, SARS-CoV-2-infected persons suggest PASC may be difficult to diagnose because of a lack of COVID-19 symptoms or COVID-19 disease among non-hospitalized people. Moreover, this could represent a significant number of people that may be omitted from any supportive services that would assist in recovery where documentation of a PCR-positive test is required.

Second, the UC CORDS data set provides both patient-reported and clinician-documented symptoms from SARS-CoV-2-infected patients. These symptoms are reported and recorded in real time, which minimizes retrospective recall that has been used in the limited studies to date and includes any symptoms uncovered by the medical provider (Carfì et al., 2020; Carvalho-Schneider et al., 2020). A few other important strengths from using the UC CORDS data set and the analytic techniques are exclusion of symptoms attributed to chronic diseases (e.g., asthma, heart failure, etc.). By excluding symptoms reported prior to SARS-CoV-2 infection, we increase confidence in the identified symptoms being attributable to becoming a long-hauler. However, it is important to note that while exclusion of symptomat comorbidities may raise confidence in the symptoms attributable to PASC, a potential limitation with our model is that it did not account for asymptomatic or well-controlled comorbid conditions, nor does it account for the potential impact of comorbidities on PASC and symptoms/symptom clusters. However, the use of the data set allowed for a broad swath of symptoms, rather than being limited to a narrowly focused checklist of symptoms, which allows for a more sophisticated understanding of symptoms among long-haulers. Symptoms were obtained through a clinical encounter and are documented by the provider; however, this does not mean that all symptoms experienced were captured. It is likely that symptoms that were causing the patient the most problems were reported, and only symptoms that patients believe were associated with the primary problem. Thus, it is
possible that dominant symptoms of each symptom cluster were potentially the most bothersome to patients. Also, it is worth considering that a feature of PASC may be the acceleration of symptoms that could be attributed to worsening or progression of underlying comorbidities, a nuance not currently being considered in attempting to understand and define PASC.

Third, our observations suggest a developing picture of long-haulers potentially reflecting that middle age and female sex as common features specific to a subset of long-haulers. Although similar descriptions have been provided in other investigations (Huang et al., 2021) and the lay media, further corroboration is warranted. We observed a near normal distribution of age among long-haulers (Table 1), including those under the age of 18—with the mean age at 10.92 years. Although our study supported a potential association with male sex and higher likelihood of becoming a long-hauler, race also appeared to be predictive for both Caucasian and Hispanic ethnicity. Blacks were at decreased risk (Figure 4), and a larger sample is needed to validate this finding. Age distribution of all SARS-CoV-2-infected individuals at days 0–30 very closely mimicked that of the long-haulers, suggesting the latter group are distributed across all age groups with persons ages 50–59 range (±20 years) representing more than 75% of the long-hauler population.

Next, the symptom experience among those who become long-haulers changes over time and may be influenced by the circulating viral strain. In this study, founder and alpha strains were the dominant strains, and symptoms associated with SARS-CoV-2 infection have evolved as newer strain emerge. However, data from multiple studies converge to illustrate that many hospitalized and non-hospitalized survivors of COVID-19 experience persistent symptoms (Chopra et al., 2020; Davis et al., 2020; Goertz et al., 2020; Halpin et al., 2021; Huang et al., 2021; Mandal et al., 2020; Meys et al., 2020). The reported incidence of persistent symptoms varies; however, in the current study, we report that 11% of people-reported symptoms after 180+ days. Some of the variability in symptom reporting and symptom association with long-haulers in other studies may be due to limitations inherent in rapid screening questionnaires in as much as these questionnaires inquire about symptoms that predominantly impact those with severe disease. Also, questionnaires may fail to inquire about emerging symptoms such as cognitive dysfunction (including “brain fog”), limiting the ability to accurately document such symptoms. Asymptomatic individuals may be less often intensely monitored due to an inherent notion of low risk for severe acute disease; however, this is problematic as asymptomatic individuals account for 60% of the long-haulers observed in this study. Since the start of the pandemic, we have learned that COVID-19 affects nearly every body system, and there is a wide variety of symptoms. It is possible that patients who reported symptoms did not mention during their office visit with the provider symptoms that they did not connect as related to their primary complaint. Because long-haul among non-hospitalized patients has not been well characterized, we took a conservative approach to symptom identification with increased confidence that symptoms documented were not pre-existing and because information was collected in real time during office visits, it was not subject to recall. We see these symptom clusters as a foundation to build from in future studies and enrich and continue to validate with other data sources. The symptom clusters observed among long-haulers vary compared to those at initial presentation. The evolution of these clusters may provide insight into the etiology of long-haulers in which elucidating sites of evolving tissue damage, and alterations in innate and adaptive immune inflammatory pathways might provide clarity in understanding the underlying pathophysiology.

In October 2020, the Tony Blair Institute for Global Change identified key characteristics among long-haulers, specifically that women appear to be at greater risk and those who are of working age (mean of age 45) (Sleat et al., 2020). Our data align with these observations. Therefore, to our third key point, we observed that all ethnicities and races were affected as well as individuals who were initially asymptomatic. However, our use of ethnicity and race is limited to broad groups and lacks needed specificity, a limitation imposed by how data are recorded in the EHR.

Larger population-based studies will be needed to confirm and expand upon these observations, particularly studies using large databases that can incorporate the methods used here would be insightful in determining emerging variants and their symptom patterns with the development of PASC. Undertaking detailed immune profiling through emerging technologies such as the -omics platforms may identify key host phenotypes associated with the symptom clusters that we have described. We hope this article will prompt the development and implementation of longitudinal prospective studies that garner patient-generated reports of symptoms, rather than patient responses to questions generated by researchers—this latter approach inherently constrained the answers we obtained. With such a new phenomenon, an ethnographic approach that focuses on understanding patients’ experiences would add an important lens to our analyses.

**Conclusion**

This study utilized machine learning techniques to develop and test an algorithm designed to predict individuals at risk for the development of PASC. In addition, we identified symptoms and symptom clusters among individuals with persistent symptoms at 180+ days post-SARS-CoV-2 infection. Indeed, data suggest that infection with SARS-CoV-2 leads to prolonged and persistent symptoms in a subset of persons known as long-haulers. However, the long-term consequences of becoming a long-hauler are unclear, and further research is urgently needed to corroborate our findings.
These findings include identifying a cohort of long-haulers with non-modifiable risk factors, which may have predicted the likelihood of persistent symptoms and/or assignment within given symptom clusters. Further research is needed to understand the underlying pathophysiology including host phenotypes associated with aberrant innate and adaptive immune responses following SARS-CoV-2 infection.

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**Supplemental Material**
Supplemental material for this article is available online.

**References**
Akaike, H. (1974). A new look at the statistical model identification. *IEEE Transactions on Automatic Control*, 19(6), 716–723. https://doi.org/10.1109/TAC.1974.1100705
Bergquist, S. H., Partin, C., Roberts, D. L., O’Keefe, J. B., Tong, J., Zreloff, J., Jarrett, T. L., & Moore, M. A. (2020). Non-hospitalized adults with COVID-19 differ noticeably from hospitalized adults in their demographic, clinical, and social characteristics. *SN Comprehensive Clinical Medicine*, 2(9), 1349–1357. https://doi.org/10.1007/s42399-020-00453-3
Carfì, A., Bernabei, R., & Landi, F. Gemelli Against COVID-19 Post-Acute Care Study Group. (2020). Persistent symptoms in patients after acute COVID-19. *Jama*, 324(6), 603–605. https://doi.org/10.1001/jama.2020.12603
Carvalho-Schneider, C., Laurent, E., Lemaignen, A., Beaufils, E., Bourbou-Tournois, C., Laribi, S., Flament, T., Ferreira-Maldent, N., Bruyère, F., Stefic, K., Gaudy-Griffon, C., Grammatico-Guillon, L., & Bernard, L. (2020). Follow-up of adults with noncritical COVID-19 two months after symptom onset. *Clinical Microbiology and Infection: The Official Publication of the European Society of Clinical Microbiology and Infectious Diseases*, 27(2), 258–263. https://doi.org/10.1016/j.cmi.2020.09.052 [pii]
Centers for Disease Control. (2021). COVID-19 laboratory confirmed hospitalizations. https://gis.cdc.gov/grasp/covidnet/COVID19_5.html
Chopra, V., Flanders, S. A., O’Malley, M., Malani, A. N., & Prescott, H. C. (2020). Sixty-day outcomes among patients hospitalized with COVID-19. *Annals of Internal Medicine*, 174(4), 576–578. https://doi.org/10.7326/M20-5661
Davis, H. E., Assaf, G. S., McCorkell, L., Wei, H., Low, R. J., Re’em, Y., Redfield, S., Austin, J. P., & Akrami, A. (2020). Characterizing long COVID in an international cohort: 7 months of symptoms and their impact. *MedRxiv*, 38, 101019. https://doi.org/10.1101/2020.12.24.20248802
Friedman, J., Hastie, T., & Tibshirani, R. (2008). Sparse inverse covariance estimation with the graphical lasso. *Biostatistics (Oxford, England)*, 9(3), 432–441. https://doi.org/10.1093/biostatistics/kxm045
Goertz, Y. M. J., Van Herck, M., Delbressine, J. M., Vaes, A. W., Meys, R., Machado, F. V. C., Houben-Wilke, S., Burtin, C., Posthuma, R., Franssen, F. M. E., van Loon, N., Hajian, B., Spies, Y., Vrijbriel, H., van ‘t Hul, A. J., Janssen, D. J. A., & Spruit, M. A. (2020). Persistent symptoms 3 months after a SARS-CoV-2 infection: The post-COVID-19 syndrome? *ERJ Open Research*, 6(4), 00542–2020. https://doi.org/10.1183/23120541.00542-2020
Greenhalgh, T., Knight, M., A’Court, C., Buxton, M., & Husain, L. (2020). Management of post-acute covid-19 in primary care. *BMJ*, 370, m3026. https://doi.org/10.1136/bmj.m3026
Halpin, S. J., McIvor, C., Whyatt, G., Adams, A., Harvey, O., McLean, L., Walshaw, C., Kemp, S., Corrado, J., Singh, R., Collins, T., O’Connor, R. J., & Sivan, M. (2021). Postdischarge symptoms and rehabilitation needs in survivors of COVID-19 infection: A cross-sectional evaluation. *Journal of Medical Virology*, 93(2), 1013–1022. https://doi.org/10.1002/jmv.26368
Huang, C., Huang, L., Wang, Y., Li, X., Ren, L., Gu, X., Kang, L., Guo, L., Liu, M., Zhou, X., Luo, J., Huang, Z., Tu, S., Zhao, Y., Chen, L., Xu, D., Li, Y., Li, C., Peng, L., . . . Cao, B. (2021). 6-month consequences of COVID-19 in patients discharged from hospital: A cohort study. *The Lancet (London, England)*, 397(10270), 220–232. https://doi.org/10.1016/S0140-6736(20)32656-8
Johns Hopkins University. (2021) COVID-19 dashboard by the center for systems science and engineering. https://gisanddata.maps.arcgis.com/apps/opsdashboard/index.html#/bda7594740fd40299423467b48e9ecf6
Lambert, N. J., & Survivor Corps. (2020). COVID-19 “long-hauler” symptoms survey report (Survey report). Indiana University School of Medicine.
Lee, D. D., & Seung, H. S. (1999). Learning the parts of objects by non-negative matrix factorization. *Nature*, 401(6755), 788–791. https://doi.org/10.1038/44565
Mandal, S., Barnett, J., Brill, S. E., Brown, J. S., Dennyen, E. K., Hare, S. S., Heightman, M., Hillman, T. E., Jacob, J., Jarvis, H. C., Lipman, M. C. I., Naidu, S. B., Nair, A., Porter, J. C., Tomlinson, G. S., Hurst, T. R., & ARC Study Group. (2020). ‘Long-COVID’: A cross-sectional study of persisting symptoms, biomarker and imaging abnormalities following hospitalisation for COVID-19. *Thorax*, 76(4), 396–398. https://doi.org/10.1136/thoraxjnl-2020-215818
Meys, R., Delbressine, J. M., Goertz, Y. M. J., Vaes, A. W., Machado, F. V. C., Van Herck, M., Burtin, C., Posthuma, R.,
Spaetgens, B., Franssen, F. M. E., Spies, Y., Vijlbrief, H., van’t Hul, A. J., Janssen, D. J. A., Spruit, M. A., & Houben-Wilke, S. (2020). Generic and respiratory-specific quality of life in non-hospitalized patients with COVID-19. *Journal of Clinical Medicine, 9*(12), 3993. https://doi.org/10.3390/jcm9123993

Pons, P., & Latapy, M. (2005). Computing communities in large networks using random walks. In: Yolum, p., Güngör, T., Gürgen, F., & Özturan, C. (eds.), *Computer and information sciences - ISCIS 2005. ISCIS 2005. Lecture notes in computer science* (long version, vol. 3733, pp. 284–293). Berlin, Heidelberg: Springer.

Rubin, R. (2020). As their numbers grow, COVID-19 “Long haulers” stump experts. *JAMA, 324*(14), 1381–1383. https://doi.org/10.1001/jama.2020.17709

Sleat, D., Wain, R., & Miller, B. (2020). *Long Covid: Reviewing the science and assessing the risk*. https://institute.global/sites/default/files/articles/Long-Covid-Reviewing-the-Science-and-Assessing-the-Risk.pdf

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