AI & COVID-19

Davide Bacciu^a, Emanuela Girardi^{b,*}, Marco Maratea^c and Jose Sousa^d ^aUniversity of Pisa, Italy ^bPop AI, Turin, Italy ^cUniversity of Genova, Italy ^dSANO-Centre for Computational Medicine, Krakow, Poland

Abstract. The COVID-19 pandemic has influenced our lives significantly since March 2020, and a number of initiatives have been put forward in order to tackle its effects, including those focused on technological solutions. In this paper, we present one of such initiatives, i.e. the CLAIRE's taskforce on AI and COVID-19, in which Artificial Intelligence methodologies and tools are being developed to help the society contrasting the pandemic. We present the different lines of development within the taskforce, some fields in which they are used, and draw few recommendations.

Keywords: Artificial intelligence, COVID-19

1. Introduction

For several decades we have been increasingly facing several natural disasters that are killing people, destroying houses, workplaces, fields, and cities. In the last 18 months we faced the first global pandemic of the XXI century, which dramatically changed our lives. The COVID-19 pandemic, which could be a direct consequence of this ecological debt, has been a wake-up call for the world's developed countries to acknowledge the biggest challenges of our society and that we need a new global approach to face them. These new challenges can be tackled with international cooperation and the support of technology. The new algorithms of Artificial Intelligence, and the availability of data and high-performance computing, can be used to measure and monitor natural resources. climate change and biodiversity. With the combination of different technologies, predictive models and decision support tools can help policy makers to evaluate the economical, social and environmental impact of the governments' policy. These new digital

*Corresponding author: Emanuela Girardi, Pop AI, Turin, Italy. E-mail: emanuela.girardi@popai.me.

systems could represent an important support to improve the effectiveness and efficiency of the actions taken by governments. A very innovative project that aims to support policy makers in tackling climate change is Destination Earth¹, a digital twin of our Planet promoted by the European Commission to measure, control and test the impact of the government's plans. The digital twin of Planet Earth will allow researchers to test and develop new solutions to face the global challenges, in a safe and secure environment, and provide feedback to decision makers to improve their decisions and policy.

When the pandemic hit Europe, in February 2020, several initiatives started to emerge within the scientific community to collaboratively develop tools, models, and apps that could bring concrete support to political decision makers, health organizations, medical doctors and citizens to fight the pandemic.

One of the most successful European initiative is the CLAIRE's taskforce on AI and COVID-19² that, in just a few days, gathered over 150 of the best European scientists, researchers and experts from all the

¹https://digital-strategy.ec.europa.eu/en/policies/destinationearth

²https://covid19.claire-ai.org/

fields of Artificial Intelligence. They worked together to contrast the pandemic leveraging Artificial Intelligence technologies. Organized in seven working groups according to the different expertise of the participants, the taskforce addressed these main topics:

- 1. Epidemiological data analysis
- 2. Mobility and monitoring data analysis
- 3. Bioinformatics
- 4. Image analysis
- 5. Social dynamics and networks monitoring
- 6. Robotics
- 7. Scheduling and resource management

This article analyses the results and difficulties faced by these groups and in addition considers how Artificial Intelligence technologies have been used in the following fields to fight the pandemic:

- 1. Patient clinical data analysis
- 2. Tracing apps
- 3. Artificial Intelligence and vaccine

2. Case studies and AI application to counter the pandemic

In this section we report a number of topics, with related case studies and Artificial Intelligence applications, that have been put in place in order to counter the COVID-19 pandemic. We will devote one paragraph to each topic.

Epidemiological data analysis. Recently, epidemiological modeling made a lot of progress. The quite simple compartment models, such as SIR [31] and SEIR [25] models that look at the epidemic at a macroscopic view, have now been extended to metapopulation models and Individual Based Models (IBM), also referred to as agent based models [25]. While the meta-population models allow instantiating compartment models for subpopulations based on e.g., age and location, and express their interactions, IBMs allow to capture important details that have an impact on how the epidemic evolves. They allow modeling important heterogeneity of the population and to not only get insight in how the epidemic is going to unfold in expectation, so what is the average outcome, but also the spread of the possible outcomes. Therefore, providing much richer information. Another important difference between the compartment models and the IBMs is that the former are predictive models, while the latter can be seen as

prescriptive models and allow to predict the outcome of measurements or policies. Therefore, they are an important tool for policy makers, as understanding the dynamics of an epidemic is not easy, given that its behavior is exponential. Moreover, the system has also a significant time delay, meaning that the effect of measurements only become clear after some time. For COVID-19 this is from 2 to 3 weeks.

Artificial Intelligence (AI) has contributed to the field in several ways. First, in the fitting of the models. The more complex the models are, the more data are needed to instantiate the models. Moreover, not all data can be measured directly. In the case of COVID-19, we know that there are quite some asymptomatic patients, which are often not tested but who contributes to the spreading of the virus. In machine learning terms we speak about hidden variables, which need to be estimated. The fact that data are not that uniformly collected over the different countries, and moreover testing strategies are changing over time even within a country, makes this a challenging problem. Second, as the models become more complex, the traditional methods used by epidemiologists to propose and evaluate prevention or containment strategies are no longer adequate. Here, AI can also play an important role, as it can learn, based on the models, which course of actions can be taken at which stage of the epidemic in order to have the most effect of the efforts that policies imply. Hereby balancing not only health factors but also economical aspects and the well-being of people.

Mobility and monitoring data analysis. In order to allow a machine to use the self-reported data it would be necessary to develop machine self-learning capabilities. There are two approaches: one that uses statistical learning, developed since the beginning of AI in the 1950's, and the other exploiting logical learning where rules are defined to create a description of the element of interest. It is assumed that input data are from outcomes or from rules, and it is always provided by humans [30, 34, 35].

In a pandemic, the progression of mobility is the first non-pharmacological intervention that public health decision makers have to address. And this pandemic reflected it when we saw governments around the world acting on it. Monitoring the pandemic is the only way to create evidence on how the pandemic is progressing and allows the adoption of measures to control it, something that in a pandemic normally relates to controlling mobility [14, 32, 43]. Moreover, in a pandemic there isn't historical information to be able to use data hungry analytical tools, such as deep learning, to develop insights from the existing data [2]. From the beginning it was visible a focus on the development of apps for collecting monitoring and mobility data, and publicly available data such as flights routes, population comorbidities and prescription could be sources of data [4, 36, 42].

Disease symptoms clustering was one of early use of self-reported data taken from traditional statistical modelling; machine learning (ML) much lately started to allow the development of risk assessment and prevalence models. The evidence was that developing ML under uncertainty is challenging because ML relies on a finite description of the world, being it a huge amount of data (big data) with the aim to reduce uncertainty or a well-defined outcome, something that from the pandemic perspective is quite impossible. We started by looking into a preprocessing of data that would allow the data to flow into the ML system always in the same format and from where a ML self-learning approach using Complex Networks would assemble knowledge graphs (KG's). Those KG's would then be quantified using entropy to determine state changes, and inference would be driven from communities and weights [10, 41].

Bioinformatics. Bioinformatics is an umbrella term covering several aspects at the interaction between computer science and biomedical data. One of the characterizing challenges of bioinformatics is the need of dealing with data that is noisy, highdimensional, and often highly heterogeneous in nature, integrating clinical evidence, genomic and proteomic information, as well as molecular data. In such a context, it is natural to turn the attention towards ML methods, whose data-driven nature and flexibility allow to accommodate the complexities of multi-sourced data as well as integrate it for predictive purposes. The analysis of COVID-19 data has been no exception, in this sense, with one additional challenge linked to the scarcity of sample data available in the early phases of the pandemic, a fact that heavily affects data-driven methods. That is why most of the work in this context focused on applications and ML methods where the few available sample data could be integrated with existing bio-medical knowledge. A notable example in this sense has been that of drug repurposing which aims at identifying new therapeutic effects for existing approved drug within the context of COVID-19 treatment, in a clear attempt to shorten the time needed to identify and put into operation COVID-19 therapies. Drug repurposing, in particular, has been tackled by leveraging prior knowledge available under the form of protein interactions (within the human and also between the host and the viral proteins), gene networks as well as data describing known drugprotein relationships. In [7], it has been provided one of the first resource collecting in one place all the clinical evidence on COVID-19 and the human genomic and proteomic information available at the time of release. The repository contains data characterizing molecular aspects of human diseases, drugs and protein-protein interactions between the human organism and the COVID-19, made freely available for actively supporting the COVID-19 research community. The kind of information available in such repositories is of relational nature, which is amenable to be processed by network science methods and ML models for structured data, such as Deep Graph Networks (DGN) [8]. One of the early work in the context of COVID-19 drug repurposing is [47], which leverages a combination of network proximity measures on protein-protein data with genomic data analysis. In [26], classical networks science proximity measures are integrated with DGN methods. Lately [29, 46], have framed drug re-purposing as a link prediction task in a biological knowledge-base of drug-disease relationships augmented with known relationships for coronaviruses.

Image analysis. Diagnostic image analysis has been the primary application domain for AI methodologies since the early onset of the COVID-19 pandemic, also due to early release of publicly available datasets. Several research groups have begun to revamp the pipelines developed to classify lesions to recognize interstitial pneumonia damages resulting in a plethora of scientific works being quickly released, mostly dealing with lungs CT scans by means of Convolutional Neural Network solutions. Initially, these works focused on fast release of results obtained in single-centre data, rather than providing clearly reproducible empirical settings, performing multicentric studies and defining standardized setups to allow confronting the performance of different AI solutions [20, 44]. As such it had been difficult to identify the most promising and robust research directions. Following up this initial exploratory phase, the community engaged in developing more robust and general solutions, such as HPC platforms and cloud software engineering methodologies enabling large scale experimentation of AI models for medical imaging [16], while also taking into consideration

explainability and reproducibility aspects [39]. Lately, the attention of the community has started to focus on medical imaging methodologies characterized by an increased portability of the equipment, such as X-rays and ultrasound, even at the costs of reduced quality and resolution of the sample. These are the imaging data where the use of AI models can possibly provide the most tangible added value. Several of the works in this context focused on developing deep learning solutions which can be used in practice, on aspects such as certification from medical equipment [37] and deployment in portable resource-constrained devices [33].

Social dynamics and networks monitoring. This topic focuses on the analysis of information circulating on social media, and specifically on the popular microblogging platform Twitter, based on a wide spectrum of AI-based techniques including natural language processing for psycholinguistics analysis, social bot classification and network science. Challenges are related to identifying, quantifying and monitoring the spread of disinformation and information on social media platforms, a phenomenon named "infodemic" by the World Health Organization in early February 2020. A relevant work in this direction has been developed as part of the CLAIRE COVID-19 initiative, which has tackled considerable challenges connected to the lack of theoretical and computational tools designed for infodemic monitoring purposes, as well as the lack of existing publicly available data to tune existing techniques. Therefore, a dedicated pipeline has been developed to gather, store and analyse in nearly real-time the big flow of social media data, consisting in more than four millions posts per day about coronavirus and COVID-19, with an estimate coverage of more than 60% of the public discussion worldwide. Some outcomes of the analysis show that the data provide significant information about infodemic waves in 127 countries [40], analyzing more than one billion posts, publicly releasing the data to speed up the research efforts to fight disinformation and misinformation spreading³. Other initiatives in this direction are the WHO Information Network for Epidemics (EPI-WIN) team, to speed up the development of a stable and publicly available tool - namely the COVID-19 Infodemic Observatory⁴, and the Twitter COVID-19 Working Group's efforts, obtaining from Twitter a dedicated

³https://osf.io/n6upx/ ⁴https://covid19obs.fbk.eu/#/ access to their firehose, i.e. the total flow of messages about COVID-19 in all languages, filtered by more than 500 keywords selected by human annotators. To date, this huge volume of data is worth more than 6 TB, in more than 0.7 billion public messages with a 100% coverage across the world.

The lack of a dedicated computing infrastructure, either more powerful and specific for such data, can be a major challenge to perform devoted research in the area. On a broader perspective, the circumstances have put in evidence the need for hardware and researchers working on infodemic, especially in the view of future events and challenges – such as climate change – where significant infodemic waves are expected. The access to social media data requires several efforts: for the future, there would be the need to have a mediator to facilitate the data gathering and access to a dedicated computing infrastructure for AIbased data analytics of social and network dynamics. The role of infodemic for policy-making in public health is rapidly becoming critical.

Robotics. The goal in this area is to empower with AI the robots that can better help mitigate the effects of the COVID-19 pandemics. A common pitfall is that there is a mismatch between the expectations raised on what robotics could have done to mitigate this emergency, and what it could actually do, analyzed in the following. Robotic experts and observers alike agree that robots have a tremendous potential to help in a pandemic situation: opportunities include providing care to isolated people, easing communication during lockdown, delivering food and goods, monitoring isolated people, disinfecting places, ensuring compliance to safety rules, and even companionship and entertainment. In face of these strong expectations, there are relatively few robots that were actually deployed, and robotics cannot certainly be said to have had a major impact in the mitigation of the current pandemics. Two types of challenges that hindered the impact of robotics are: socio-economic challenges, and technological challenges. The former include the lack of pre-existing connections between robotic researchers and the health sector, be it government or private, as well as the lack of suitable technological and organisational infrastructure. Creating these connections or infrastructure during the crisis turned out not to be feasible. As for the technological challenges, in order to be effectively deployed and used in a pandemic situation, a robotic system needs to be reliable (it can operate for a long time without failures), resilient (able to adapt to situations

different from the nominal ones), flexible (it must be easy to reprogram it for a different task or environment) and user-friendly (it must be possible for non-technical people to use it with minimal or no training). Unfortunately, and despite the impressive advances in robotics in the last two decades, robots are not yet sufficiently advanced in any of the above aspects. This is because robots are complex, integrated systems that interact with the physical world using noisy sensors and unreliable actuators. Moreover, the above aspects are interdependent: for instance, making a robot reliable often requires strong specialization in the hardware and/or in the algorithms, which reduces flexibility. In this context AI technologies can be pivotal in overcoming the above technological challenges: these include intelligent

failure detection and recovery to increase reliability, long-life learning and adaptation to increase resiliency, automated planning to increase flexibility, and natural language understanding and user modelling to increase user-friendliness.

Scheduling and resource management. The possibility of automatically scheduling certain activities and treatments, together with the ability to manage resources efficiently, have gained even more attention during the pandemic, given the needs of having very efficient scheduling to be able to treat more patients, and/or being able to treat also non COVID patients, and the scarcity of resources.

Modeling and solving real problems and contingent situations usually leverages classical AI planning and scheduling techniques, These are often based on knowledge representation and reasoning methodologies, such as Answer Set Programming [12, 22–24], possibly hybridized with constraint programming [9], and extended to work on parallel architectures, in which a problem (defined in terms of e.g., requirements, constraints, input and preferences) is modeled using a knowledge representation language, and solving is done automatically. Such solvers can parse and interpret the language and are then employed to automatically compute a solution (a schedule) that corresponds to the solution of the original problem. Such classical AI techniques can be complemented by machine learning methods that analyze input data and compute ML models to "parametrize" the scheduling problem.

Concrete problems that can be analyzed and solved are: nurse scheduling [5, 17], to define the workforce organization of nurses; operating room scheduling in presence of scarce resources (e.g. ICU beds) [19], where patients are assigned to operating rooms taking into account the required specialty and ensuring the presence of an ICU bed if needed; chemotherapy and rehabilitation scheduling [13, 18], for planning cyclic chemotherapy treatments and rehabilitation physiotherapy sessions, respectively, and generation of priority lists.

Effective solutions to these problems, that can be profitably used in practice and made available to the community (in terms of web applications, and/or open platforms, in the spirit of e.g., [6]), require the availability of precise descriptions and specifications about the problem to be analyzed and solved, and about its dynamics: these, are equally important to having access to clinical data. During the hype of the pandemic, there have been difficulties in accessing fresh specifications and data; some data were already at our disposal, or synthetic data were often employed. More recently, the availability of data has increased and is now possible to test some of the proposed solutions on real data, e.g., data about patient management in the ASL1 of the Liguria Region, for what concerns the operating room scheduling; chemotherapy sessions performed by the S. Martino Hospital⁵ in Genova, Italy; and rehabilitation sessions managed by ICS Maugueri⁶.

Patient clinical data anlysis. The digitalization of patient records is key to facilitate the transition towards personalized medicine and, in the specific case of the COVID-19, to enable a faster response to the pandemic emergency. A key issue that has surfaced in this sense is that while several hospitals and clinical centres had in place procedures to collect patient data in electronic form or to rapidly digitalize physical information, lesser attention had been devoted to design shared patient record schemes as well as procedures for data sharing between centres. As a result of that, the use of multicentric patient data is extremely limited in AI studies [45]. Much of the work in this field focuses on single-centre patient medical data, where ML methods are typically used to predict the evolution of the disease, its severity and to anticipate adverse events [11]. Several works along this line of research have explored a variety of discriminative ML methodologies to predict the risk of the patient to develop acute respiratory distress, also at different level of severity, based on features from hospitalization records. The interested reader

⁵https://www.ospedalesanmartino.it/ ⁶https://www.icsmaugeri.it/

can refer to [3] for a specialized review. Several of these works also leveraged the trained ML models to identify the key features influencing more strongly the prediction, in an attempt to help the clinicians in the identification of critical risk factors for the outcome. In this respect, some clinical indicators have been consistently and repeatedly identified by different independent studies [11]. However, it is also widely known how discriminative ML methodologies can be heavily affected by biases and confounders in the data, leading to misleading conclusions induced by distorsive aspects in the data. In the context of pulmonary disease [15], describes a popular example of a discriminative predictor which considered asthma as a feature reducing the risk of pneumonia critical outcomes due to data biases. Causal learning, in this sense, provides methodologies that allow to robustly infer causation relationships in patient clinical data. In the context of COVID-19 [21], has recently proposed an approach that leverages Bayesian Structure Learning to infer a graph representing the causal relationships among the features of patient hospitalization records, also allowing to incorporate prior clinical knowledge as concerns implausible relationships to be discarded by the data-driven process.

Tracing apps. Tracing apps were wrongly pointed in some context as tracing the infectious people where they should be tracing symptoms and that created low levels of engagement to use it. In the cases where it was promoted as a symptoms tracking it had a huge impact and allowed the collection and development of very early evidence of the progression. The two cases that we explored were the ZOE app as part of the COVID Symptoms study⁷ and the COVIDCare app ⁸ as part of work done within the taskforce with the Northern Ireland Public Health Agency in a machine learning approach to model the disease progression. A close relation between the app self-reported symptoms and the disease positive cases validated by lab testing was developed, while at the same time the community of the most prevalent systems had a close relation with the symptoms reported by hospital inpatients.

AI and vaccine. The availability of secure and efficient vaccines has brought the attention of AI researchers also on how AI can help in this new phase of the pandemic. Of course both ML and scheduling

can help in this issue, and become more important with the increasing availability of doses. For what concern the application of scheduling methodologies in this area, building automated tools for vaccination planning is a plus. At the moment, such planning is done manually or using custom systems with relative "Intelligence". Instead, solutions based on AI planning and scheduling techniques employing knowledge representation and reasoning methodologies are being developed, with the aim of verifying the quality of the scheduling done so far, and hopefully supporting further vaccination phases with AI methods [1, 38]. This involves both scheduling and rescheduling in case some scheduled appointment is canceled for the unavailability of either operators or patients. For what concern, instead, the application of ML techniques, they can allow to understand the vaccination effects and incorporate that knowledge in the modelling of the pandemic progression. ML has the capability to integrate different data in near real time and integrate it into a computational model to provide actionable knowledge. However, current ML based applications rely on an expert labelling of the expected outcome. This limitation should be addressed in order to be able to build models accounting for vaccination effects. Self-reported data and self-learning approaches seem promising directions to allow to integrate vaccination-related information as part of an open learning approach [28].

3. Conclusion and recommendations

Invest in research. What we are seeing is a huge effort on bringing AI to the front of public health approaches to understand the diseases progression and to create conditions to allow the development of evidence based public health. Several of these approaches are under development in the UK with a clear fundamental role of the UK national institute for health data science (HDRUK) by acting as a data HUB, SAIL databank by acting as a common repository for different data sets, from mental health data to self-reported, and a new lighthouse institute to explore novel models for disease prevention. The CLAIRE Task Force, having multidisciplinary approaches, can be in forefront of impacting on such a change.

Multidisciplinary approach. A key learning from the CLAIRE's taskforce experience and from the several AI working groups that emerged during the pandemic

⁷https://covid.joinzoe.com
⁸https://covid-19.hscni.net/covidcare-ni-mobile-app/

is the need of multidisciplinary teams where AI scientists and AI experts work together with domain experts to better identify the complexity of the context, define the priorities and work on feasible solutions.

Data availability, integration and infrastructure. AI needs to be capable of ingesting heterogeneous data from a multitude of sources, trying not to rely only on the data-induced knowledge but being capable of embracing an open-world approach and life-long learning process. Interoperable data is essential but we also need secure infrastructures where data can be collected and we need protocols that regulate sharing and utilisation of data according to the trustworthy human-centric way put forward in the European AI regulation⁹.

Need for a European research center for AI. The fragmentation of the European AI & COVID-19 initiatives urges for a creation of a European Center for AI, in close collaboration with other center all over the world to share data and knowledge. The center will create a network of excellence including the best AI scientists, researchers and AI experts and fostering the research of AI technologies based on the European values. The European AI Center will work with Industry, Governments and Civil Organisation to bring the benefits of AI technologies into our society.

Al for sustainable development. Al technologies represent a very powerful tool for humans to address the challenges of our society and to develop new paradigm to reach a more sustainable development from the economical, societal and environmental point of view.

Acknowledgments

The authors wish to thank all volunteers of the CLAIRE COVID-19 taskforce for their contribution. In particular, we would like to acknowledge the other members of the CLAIRE core: Gianluca Bontempi, Ricardo Chavarriaga, Hans De Canck, Holger Hoos, Iarla Kilbane-Dawe, and Tonio Ball, and the other topic coordinators: Marco Aldinucci, Manlio De Domenico, Ann Nowé, and Alessandro Saffiotti, who have supported this work.

References

- [1] A. Abdulla, B. Wang, F. Qian, T. Kee, A. Blasiak, Y.H. Ong, L. Hooi, F. Parekh, R. Soriano, G.G. Olinger, J. Keppo, C.L. Hardesty, E.K. Chow, D. Ho and X. Ding, Project IDentif.AI: Harnessing artificial intelligence to rapidly optimize combination therapy development for infectious disease intervention, *Advanced Therapeutics* **3**(7) (2020), 2000034. ISSN 2366–3987. doi: 10.1002/adtp.202000034
- [2] D. Alahakoon, R. Nawaratne, Y. Xu, D. De Silva, U. Sivarajah and B. Gupta, Self-building artificial intelligence and machine learning to empower big data analytics in smart cities, *Information Systems Frontiers* (2020). ISSN 1387-3326. doi: 10.1007/s10796-020-10056-x
- [3] N. Alballa and I. Al-Turaiki, Machine learning approaches in covid-19 diagnosis, mortality, and severity risk prediction: A review, *Informatics in Medicine Unlocked* 24 (2021), 100564, ISSN 2352-9148. doi: https://doi.org/10.1016/j.imu.2021.100564.
- [4] H. Alsdurf, E. Belliveau, Y. Bengio, T. Deleu, P. Gupta, D. Ippolito, R. Janda, M. Jarvie, T. Kolody, S. Krastev, T. Maharaj, R. Obryk, D. Pilat, V. Pisano, B. Prud'homme, M. Qu, N. Rahaman, I. Rish, J.-F. Rousseau, A. Sharma, B. Struck, J. Tang, M. Weiss and Y.W. Yu, COVI White Paper. *arXiv*, (2020).
- [5] M. Alviano, C. Dodaro and M. Maratea, An advanced answer set programming encoding for nurse scheduling, In Floriana Esposito, Roberto Basili, Stefano Ferilli, and Francesca A. Lisi, editors, Advances in Artificial Intelligence -Proceedings of the 16th International Conference of the Italian Association for Artificial Intelligence (AI*IA 2017), volume 10640 of Lecture Notes in Computer Science, pages 468–482. Springer, (2017).
- [6] A. Armando, C. Castellini, E. Giunchiglia, M. Idini and M. Maratea, TSAT++: an open platform for satisfiability modulo theories, *Electronic Notes in Theoretical Computuer Science* 125(3) (2005), 25–36.
- [7] D. Bacciu, F. Errica, A. Gravina, F. Landolfi, L. Madeddu, M. Podda and G. Stilo, Covid19 initiative: A curated network of protein-drug-gene data and virus-host interactions for drug-repurposing research, *Technical report, CLAIRE COVID-19 Taskforce* (2020). https://github.com/CLAIRE-COVID-T4/covid-data.
- [8] D. Bacciu, F. Errica, A. Micheli and M. Podda, A gentle introduction to deep learning for graphs, *Neural Networks* 129 (2020), 203–221.
- [9] M. Banbara, B. Kaufmann, M. Ostrowski and T. Schaub, Clingcon: The next generation, *Theory and Practice of Logic Programming* 17(4) (2017), 408–461.
- [10] A.-L. Barabási, The network takeover. *Nature Physics* 8(1) (2012), 14–16. ISSN 1745–2473. doi: 10.1038/nphys2188
- [11] J. Bullock, A. Luccioni, K.H. Pham, C.S.N. Lam and M. Luengo-Oroz, Mapping the landscape of artificial intelligence applications against covid-19, *Journal* of Artificial Intelligence Research 69 (2020). doi: 10.1613/JAIR.1.12162
- [12] F. Calimeri, M. Gebser, M. Maratea and F. Ricca, The design of the fifth answer set programming competition, *CoRR*, *abs/1405.3710*, (2014). URL http://arxiv.org/abs/1405.3710.
- [13] M. Cardellini, P. De Nardi, C. Dodaro, G. Galatà, A. Giardini, M. Maratea and I. Porro, A twophase ASP encoding for solving rehabilitation scheduling, In *Proceedings of the 5th International Joint Conference on Rules and Reasoning*

⁹https://digital-strategy.ec.europa.eu/en/library/proposalregulation-laying-down-harmonised-rules-artificial-intelligence

(*RuleML*+*RR* 2021), Lecture Notes in Computer Science. To appear, (2021).

- [14] A. Cartenii; L. Di Francesco and M. Martino, How mobility habits influenced the spread of the COVID-19 pandemic: Results from the Italian case study, *The Science of the Total Environment* **741** (2020), 140489, doi: 10.1016/j.scitotenv.2020.140489
- [15] R. Caruana, Y. Lou, J. Gehrke, P. Koch, M. Sturm and N. Elhadad, Intelligible models for healthcare: Predicting pneumonia risk and hospital 30-day readmission, In *Proceedings of the 21th ACM SIGKDD International Conference on Knowledge Discovery and Data Mining*, (2015), 1721–1730.
- [16] I. Colonnelli, B. Cantalupo, I. Merelli and M. Aldinucci, Streamflow: cross-breeding cloud with hpc, *IEEE Trans*actions on Emerging Topics in Computing (2020). doi: 10.1109/TETC.2020.3019202
- [17] C. Dodaro and M. Maratea, Nurse scheduling via answer set programming, In *Marcello Balduccini and Tomi Janhunen*, editors, Proceedings of the 14th International Conference on Logic Programming and Nonmonotonic Reasoning (LPNMR 2017), volume 10377 of Lecture Notes in Computer Science, pages 301–307. Springer, (2017).
- [18] C. Dodaro, G. Galatà, M. Maratea, M. Mochi and I. Porro, An ASP-based solution to the chemotherapy treatment scheduling problem, *Theory and Pratice of Logic Programming* 21(6) (2021), 835–851.
- [19] C. Dodaro, G. Galatà, M.K. Khan, M. Maratea and I. Porro, Operating room (re)scheduling with bed management via ASP, *Theory and Practice of Logic Programming*. To appear, (2022).
- [20] D. Dong, Z. Tang, S. Wang, H. Hui, L. Gong, Y. Lu, Z. Xue, H. Liao, F. Chen, F. Yang, R. Jin, K. Wang, Z. Liu, J. Wei, W. Mu, H. Zhang, J. Jiang, J. Tian and H. Li, The role of imaging in the detection and management of covid-19: A review, *IEEE Reviews in Biomedical Engineering* 14 (2021), 16–29. doi: 10.1109/RBME.2020.2990959
- [21] E. Ferrari, L. Gargani, G. Barbieri, L. Ghiadoni, F. Faita and D. Bacciu, A causal learning framework for the analysis and interpretation of COVID-19 clinical data, *CoRR*, *abs/2105.06998*, (2021). URL https://arxiv.org/abs/2105.06998.
- [22] M. Gebser, M. Maratea and F. Ricca, What's hot in the answer set programming competition. In Dale Schuurmans and Michael P. Wellman, editors, *Proceedings of the Thirtieth AAAI Conference on Artificial Intelligence (AAAI 2016),* pages 4327–4329. AAAI Press, (2016).
- [23] M. Gebser, M. Maratea and F. Ricca, The design of the seventh answer set programming competition, In Marcello Balduccini and Tomi Janhunen, editors, Proceedings of the 14th International Conference on Logic Programming and Nonmonotonic Reasoning (LPNMR 2017), volume 10377 of Lecture Notes in Computer Science, pages 3–9. Springer, (2017).
- [24] M. Gebser, M. Maratea and F. Ricca, The seventh answer set programming competition: Design and results, *Theory Pract. Log. Program.* 20(2) (2020), 176–204.
- [25] V. Grimm, U. Berger, F. Bastiansen, S. Eliassen, V. Ginot, J. Giske, J. Goss-Custard, T. Grand, S.K. Heinz, G. Huse, et al., A standard protocol for describing individual-based and agent-based models, *Ecological Modelling* **198**(1-2) (2006), 115–126.
- [26] D.M. Gysi, Í.D. Valle, M. Zitnik, A. Ameli, X. Gan, O. Varol, S.D. Ghiassian, J.J. Patten, R. Davey, J. Loscalzo and A.-L. Barabási, Network medicine framework for identifying

drug repurposing opportunities for covid-19, *ArXiv*, (2020).

- [27] K. Heng and C.L. Althaus, The approximately universal shapes of epidemic curves in the susceptibleexposed infectious-recovered (seir) model, *Scientific Reports* 10(1) (2020), 1–6.
- [28] Y. Hu, J. Jacob, G.J.M. Parker, D.J. Hawkes, J.R. Hurst and D. Stoyanov, The challenges of deploying artificial intelligence models in a rapidly evolving pandemic, *Nature Machine Intelligence* 2(6) (2020), 1–3. doi: 10.1038/s42256-020-0185-2
- [29] V.N. Ioannidis, D. Zheng and G. Karypis, Few-shot link prediction via graph neural networks for covid-19 drugrepurposing, arXiv, (2020).
- [30] W. Jin, T. Derr, H. Liu, Y. Wang, S. Wang, Z. Liu and J. Tang, Self-supervised Learning on Graphs: Deep Insights and New Direction, *arXiv*, (2020).
- [31] W.O. Kermack and A.G. McKendrick, A contribution to the mathematical theory of epidemics, *Proceedings of the royal* society of london. Series A, Containing papers of a mathematical and physical character, 115(772) (1927), 700–721.
- [32] M.U.G. Kraemer, C.-H. Yang, B. Gutierrez, C.-H. Wu, B. Klein and D.M. Pigott, Open COVID-19 Data Working Group[†], L. du Plessis, N.R. Faria, R. Li, W.P. Hanage, J.S. Brownstein, M. Layan, A. Vespignani, H. Tian, C. Dye, O.G. Pybus and S.V. Scarpino, The effect of human mobility and control measures on the COVID-19 epidemic in China. *Science* 368(6490) eabb4218-10, 03 (2020). doi: 10.1126/science.abb4218
- [33] X. Li, C. Li and D. Zhu, Covid-mobilexpert: On-device covid-19 patient triage and follow-up using chest xrays, In 2020 IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2020), pages 1063–1067, (2020). doi: 10.1109/BIBM49941.2020.9313217
- [34] X. Liu, F. Zhang, Z. Hou, L. Mian, Z. Wang, J. Zhang and J. Tang, Self-supervised Learning: Generative or Contrastive, *IEEE Transactions on Knowledge and Data Engineering* **PP**(99) (2021), 1–1, ISSN 1041-4347. doi: 10.1109/tkde.2021.3090866
- [35] Y. Liu, M. Jin, S. Pan, C. Zhou, F. Xia and P.S. Yu, Graph Self-Supervised Learning: A Survey. arXiv, (2021).
- [36] M.N. Lochlainn, K.A. Lee, C.H. Sudre, T. Varsavsky, M.J. Cardoso, C. Menni, R.C.E. Bowyer, L.H. Nguyen, D.A. Drew, S. Ganesh, J.L. du Cadet, A. Visconti, M.B. Freydin, M. Modat, M.S. Graham, J.C. Pujol, B. Murray, J.S. El Sayed Moustafa, X. Zhang, R. Davies, M. Falchi, T.D. Spector, A.T. Chan, S. Ourselin and C.J. Steves, Key predictors of attending hospital with COVID19: An association study from the COVID Symptom Tracker App in 2,618,948 individuals. medRxiv, (2020), pages 1–14, doi: 10.1101/2020.04. 25.20079251
- [37] K. Murphy, H. Smits, A.J.G. Knoops, M.B.J.M. Korst, T. Samson, E.T. Scholten, S. Schalekamp, C.M. Schaefer-Prokop, R.H.H.M. Philipsen, A. Meijers, J. Melendez, B. van Ginneken and M. Rutten, Covid-19 on chest radio-graphs: A multireader evaluation of an artificial intelligence system, *Radiology* 296(3) (2020). doi: 10.1148/radiol. 2020201874
- [38] E. Ong, M.U. Wong, A. Huffman and Y. He, COVID-19 Coronavirus Vaccine Design Using Reverse Vaccinology and Machine Learning, *Frontiers in Immunology* **11** (2020), 1581. doi: 10.3389/fimmu.2020.01581
- [39] M. Pennisi, I. Kavasidis, C. Spampinato, V. Schinina, S. Palazzo, F.P. Salanitri, G. Bellitto, F. Rundo, M. Aldinucci, M. Cristofaro, P. Campioni, E. Pianura, F. Di Stefano,

A. Petrone, F. Albarello, G. Ippolito, S. Cuzzocrea and S. Conoci, An explainable ai system for automated covid-19 assessment and lesion categorization from ct-scans, *Artificial Intelligence in Medicine* (2021), 102–114, ISSN 0933-3657.

- [40] G. Riccardo, V. Francesco, C. Nicola, S. Pierluigi and D.D. Manlio, Assessing the risks of 'infodemics' in response to covid-19 epidemics, *Nature Human Behavior* 4 (2020). doi: https://doi.org/10.1038/s41562-020-00994-6.
- [41] M. Salathé, L. Bengtsson, T.J. Bodnar, D.D. Brewer, J.S. Brownstein, C. Buckee, E.M. Campbell, C. Cattuto, S. Khandelwal, P.L. Mabry and A. Vespignani, Digital Epidemiology, *PLoS Computational Biology* 8(7) (2012), e1002616. ISSN 1553-734X. doi: 10.1371/journal.pcbi.1002616
- [42] E. Segal, F. Zhang, X. Lin, G. King, O. Shalem, S. Shilo, W.E. Allen, F. Alquaddoomi, H. Altae-Tran, S. Anders, R. Balicer, T. Bauman, X. Bonilla, G. Booman, A.T. Chan, O. Cohen, S. Coletti, N. Davidson, Y. Dor, D.A. Drew, O. Elemento, G. Evans, P. Ewels, J. Gale, A. Gavrieli, B. Geiger, Y.H. Grad, C.S. Greene, I. Hajirasouliha, R. Jerala, A. Kahles, O. Kallioniemi, A. Keshet, L. Kocarev, G. Landua, T. Meir, A. Muller, L.H. Nguyen, M. Oresic, S. Ovchinnikova, H. Peterson, J. Prodanova and J. Rajagopal, G.R. x000E4 tsch, H. Rossman, J. Rung, A. Sboner, A. Sigaras, T. Spector, R. Steinherz, I. Stevens, J. Vilo and P. Wilmes, Building an international consortium for tracking coronavirus health status, *Nature Medicine* 105 (2020), 1–4. doi: 10.1038/s41591-020-0929-x
- [43] J. Sousa and J. Barata, Tracking the Wings of Covid-19 by Modeling Adaptability with Open Mobility Data, *Applied*

Artificial Intelligence (2020), 1–22, ISSN 0883-9514. doi: 10.1080/08839514.2020.1840196

- [44] L. Wang, Z.Q. Lin and A. Wong, Covidnet: A tailored deep convolutional neural network design for detection of covid-19 cases from chest x-ray images, *Scientific Reports* 10(1) (2020), 1–12.
- [45] L. Wynants, B. Van Calster, G.S. Collins, R.D. Riley, G. Heinze, E. Schuit, M.M.J. Bonten, D.L. Dahly, J.A. Damen, T.P.A. Debray, V.M.T. de Jong, M. De Vos, P. Dhiman, M.C. Haller, M.O. Harhay, L. Henckaerts, P. Heus, M. Kammer, N. Kreuzberger, A. Lohmann, K. Luijken, J. Ma, G.P. Martin, D.J. McLernon, C.L.A. Navarro, J.B. Reitsma, J.C. Sergeant, C. Shi, N. Skoetz, L.J.M. Smits, K.I.E. Snell, M. Sperrin, R. Spijker, E.W. Steyerberg, T. Takada, I. Tzoulaki, S.M.J. van Kuijk, B.C.T. van Bussel, I.C.C. van der Horst, F.S. van Royen, J.Y. Verbakel, C. Wallisch, J. Wilkinson, R. Wolff, L. Hooft, K.G.M. Moons and M. van Smeden, Prediction models for diagnosis and prognosis of covid-19: systematic review and critical appraisal, *British Medical Journal* **369** 2020. doi: 10.1136/bmj.m1328
- [46] X. Zeng, X. Song, T. Ma, Q. Pan, Y. Zhou, Y. Hou, Z. Zhang, K. Li, G. Karypis and F. Cheng, Repurpose open data to discover therapeutics for covid-19 using deep learning, *Journal* of Proteome Research (2020).
- [47] Y. Zhou, Y. Hou, J. Shen, Y. Huang, W. Martin and F. Cheng, Network-based drug repurposing for novel coronavirus 2019-ncov/sars-cov-2, *Cell Discovery* 6(1) (2020), 1–18.