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Chair's Column

February 15, 2022. The past year and a half has brought changes to all of our lives and to the Mathematical Optimization Society (MOS). One of MOS's most visible changes was the postponement to August 2022 of the 24th International Symposium on Mathematical Programming (ISMP) that was scheduled to be held in Beijing in August 2021. The continued uncertainty regarding international travel in 2022 may require still additional changes in the format of that meeting (e.g., as a hybrid virtual and in-person meeting), but we hope to confirm any changes soon and look forward to your participation in continuing the ISMP's tradition of showcasing the best of mathematical optimization.

While the ISMP did not proceed as planned, we had two successful gatherings of the Integer Programming and Combination Optimization (IPCO) conference that have taken place virtually. IPCO XXI was held in June 2020 and hosted at the London School of Economics, while IPCO XXII took place in May 2021 at the Georgia Institute of Technology. For 2022, in addition to the ISMP, we also have IPCO XXIII at Eindhoven University of Technology in June and the next International Conference on Continuous Optimization (ICCOPT) at Lehigh University in July. Looking forward to 2023, the next International Conference on Stochastic Programming (ICSP) will be at University of California, Davis, in July. We also recently announced that the 25th ISMP will be held in Montreal, Canada, in July 2024.

Besides demonstrating the value of mathematical optimization through our meetings, our journals, Mathematical Programming, Series A and Series B, and Mathematical Programming Computation, continue to attract the state-of-the-art in mathematical optimization research. Jon Lee is completing the end of his term as Editor-in-Chief at Mathematical Programming, Series A, at the end of 2021, and Sven Leyffer finishes his term as Editor-in-Chief at Mathematical Programming, Series B, as well, while Jonathan Eckstein continues as Editor-in-Chief at Mathematical Programming Computation and Jesús De Loera continues as Editor of the MOS-SIAM book series. While we thank Jon, Sven, Jonathan, and Jesús for their skillful guidance of these pre-eminent archival series, we look forward to announcing Jon and Sven's successors shortly.

Our other major activity of awards also continued over this pandemic period, despite our not having a physical ISMP at which to celebrate the award winners' achievements. We announced the winners of the Beale–Orchard–Hays Prize, Dantzig Prize, Fulkerson Prize, Lagrange Prize, Tucker Prize, and Tseng Lectureship at a virtual event in July 2021, which was held during the SIAM Annual Meeting which also recognized our joint awards with SIAM (the Dantzig and Lagrange prizes). You can read about the award winners and their work in this issue, and you can find a recording of the ceremony on our website at www.mathopt.org/prizes/mosawards_2021.mp4.

You may have also noticed that our website, www.mathopt.org, after an extended period of stasis, is now reflecting current information about MOS thanks to the valued efforts of our web editor, Timo Berthold. We are also fortunate to have Sebastian Pokutta's leadership in reviving Optima with this issue and continuing this important connection to our community. Finally, we all benefit from Steve Wright's ongoing efforts to ensure Optimization Online provides our community access to the latest work in our field.

While these past two years have brought us all challenges, they have also brought mathematical optimization to the forefront of research in many ways through its ubiquitous use in applications that guide the lives of so many. Our work is having an ever growing impact on the world around us, and we should all be excited by the possibilities ahead. I look forward to witnessing that growth with you and to hearing and reading of your latest achievements at one of our upcoming meetings and in our journals.

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Note from the Editors

We are pleased to take on the editorial duties of OPTIMA for this period. While the COVID-19 pandemic has posed serious personal and organizational challenges to our start, it has also provided a unique opportunity for our optimization community to contribute towards solutions for this global problem. To this end, in this issue, Dimitris Bertsimas and Michael Li introduce us to their perspective and epidemiological method to predict the progression of the pandemic. They highlight how this optimization approach can affect the design of trials and distributions of vaccines. We complement this discussion with comments from experts in this area. We are grateful for the detailed and outstanding technical production work of Christoph Eyrich and sincerely hope that you will enjoy reading this and future issues of Optima! We welcome suggestions and ideas for topics you would like to read about.

Sebastian Pokutta, Editor
Swati Gupta, Co-Editor
Omid Nohadani, Co-Editor

I am very happy to have both Swati Gupta and Omid Nohadani as my co-editors for OPTIMA. Their breadth of research areas, judgment, and creativity will be a great asset for OPTIMA. I am looking forward to editing OPTIMA together.

Sebastian Pokutta, Editor

The Delphi Model for Epidemiological Predictions for COVID-19 and Its Applications

Dimitris Bertsimas and Michael Lingzhi Li

In this paper, we present the DELPHI model, an epidemiological model developed in [7] for COVID-19 and its application in prioritizing site selection for the Johnson and Johnson clinical trials for its Covid-19 vaccine and in developing an optimization model for vaccine allocation reported in [3]. This work is part of a broader effort regarding Covid-19 that started in March, 2020 and resulted in the website covidanalytics.io that is being maintained until today at MIT's Operations Research Center.

Epidemiological Predictions and Application to Vaccine Trial Design

Since the initial Wuhan outbreak in December 2019, the world has been upended by the COVID-19 pandemic, a severe acute respiratory disease caused by the SARS-CoV-2 coronavirus. As of May 2021, over 160 million cases and 3.3 million deaths have been reported globally. To curtail the viral spread of SARS-CoV-2, most governments implemented non-pharmaceutical interventions (NPIs) spanning social distancing, self-isolation and travel restrictions, culminating in partial to full lockdowns in many parts of the world. As a result, the pandemic also engendered unprecedented socio-economic strain, leading to growing unemployment and recessions in some of the world's largest economies. To help mitigate the impact of the pandemic, many research groups have created epidemiological models to help policymakers plan during the pandemic and adapt the interventions as necessary. A large class of models utilize some flavor of the SEIR compartmental model [6], which attempt to model large population dynamics by assuming the population divides into four compartments based on epidemiological states: Susceptible (S), Exposed (E), Infected (I), and Recovered (R). The flow from S through E and I to R is then governed through ordinary differential equations with the most central equation being the differential equation measuring the flow of people being exposed to the virus and thus moving from S to E. The equation contains a bilinear term between the number of susceptible individuals S and the number of infected individuals I:

$$\frac{S}{t} = -\alpha S I \qquad (1)$$

In the standard SEIR model, α, the rate of infection, is deemed to be a constant [1]. Some models create further subdivisions based on age groups and symptom severity to account for heterogeneity [2]. Furthermore, many modeling approaches supplement SEIR models with additional behavioral data such as mobility and governmental policies [4, 13] to adjust for compliance and non-pharmaceutical interventions. There is also significant work on approaches that do not model the disease dynamics directly, such as utilizing deep learning for predicting week-ahead mortality [11], or treating the past epidemiological data as a time-series forecasting problem [9].

One particular model of note is the DELPHI (Differential Equations Lead to Predictions of Hospitalizations and Infections) model [7]. One of DELPHI's key innovations is to extend the SEIR model to account explicitly for the effect of societal response as a multiplicative sigmoid term $\gamma(t)$, so that the central dynamic equation for DELPHI is:

$$\frac{S}{t} = -\alpha\gamma(t) S I \qquad (2)$$

where $\gamma(t)$ is defined as (with $t_0 \ll t_r$):

$$\gamma(t) = 1 + \frac{2}{\pi}\arctan\left(\frac{-(t-t_0)}{k}\right) + c\exp\left(-\frac{(t-t_r)^2}{2\sigma^2}\right).$$

DELPHI stipulates that the initial response is modeled by an (inverted) sigmoid process to capture a concave-convex effect. The initial concave shift models the decline in infection rate as restrictions come into effect, while the latter convex flattening reflects the diminishing marginal utility of additional measures. The particular choice of arctan is due to its slow asymptotic decay behavior (as $t \to \infty$, $\gamma(t) \sim \frac{1}{t}$) which has been shown to match initial responses for previous epidemics better than other common sigmoid functions (e.g. the logistic function). The parameters t_0 and k capture, respectively, the timing and the strength of the response. The additional exponential term models a resurgence of magnitude c that peaks at time t_r and decays over a characteristic period σ. All of these parameters are fitted by minimizing a recency-weighted mean squared error metric with respect to the total predicted cases (C_t) and deaths (D_t) over the training period T:

$$\sum_{t=1}^{T} t \cdot \left(\mathrm{MSE}(C_t) + \lambda \cdot \mathrm{MSE}(D_t)\right),$$

where λ weighs the relative importance of cases and deaths. This flexible parametric formulation allows DELPHI to adjust to the effect of different non-pharmaceutical interventions as they have been implemented in various regions, while retaining the key benefits of compartmental models, including parameter interpretability.

To optimize the parameters in the resulting non-convex differential equation model, DELPHI utilizes a dual-track optimization approach. Daily iterative parameter updates are done through the

Table 1. Median out-of-sample MAPE aggregated per region (prediction made on July 15th, 2020 and MAPE evaluated over 15 days, 30 days, and 45 days)

		Cases			Deaths		
Region	1c# Areas	15 days	30 days	45 days	15 days	30 days	45 days
Africa	50	11.0 %	17.2 %	21.9 %	10.0 %	15.5 %	23.3 %
Asia	37	9.9 %	14.4 %	17.6 %	12.7 %	14.1 %	15.0 %
Europe	43	5.0 %	9.5 %	14.1 %	2.4 %	5.1 %	5.9 %
North America	70	8.0 %	11.7 %	15.3 %	6.9 %	8.5 %	9.5 %
Oceania	12	2.4 %	2.9 %	3.6 %	0.0 %	0.0 %	0.0 %
South America	8	6.8 %	14.6 %	21.6 %	6.5 %	11.0 %	13.8 %
United States	51	8.4 %	12.0 %	16.6 %	8.7 %	8.9 %	9.4 %
World	**221**	**8.0 %**	**11.8 %**	**16.2 %**	**6.9 %**	**9.4 %**	**10.8 %**

Table 2. Implementation length and effect of each policy category as implemented across the world

Restrictions	Area-Days	Residual Infection Rate
None	2142	100 %
Travel and Work	2049	88.9 ± 4.5 %
Mass Gathering, Travel, and Work	340	59.0 ± 5.2 %
Mass Gathering, School, Travel, and Work	1460	41.7 ± 4.3 %
Stay-at-Home Order	6585	25.6 ± 3.7 %

truncated newton (TN) method, while dual annealing is run weekly to capture any paradigm shift in the parameters that TN is unable to assess. This ensures that in case of large changes in the pandemic behavior (e.g., new dominant strains, treatments or government restrictions), the model could respond in an efficient manner.

Since its inception in late March 2020, DELPHI provided accurate predictions both short and long term to more than 200 countries/regions worldwide. The DELPHI model was one of the first to predict the United States would have millions of cases by mid May 2020, and again was one of the first to predict large outbreaks in India, Russia and South Africa long before they materialized in early June 2020. As an example of its accuracy, the following are the results of an exhaustive backtest from predictions generated on July 15th 2020 during the 2^{nd} wave resurgence, and evaluated their Mean Absolute Percentage Error (MAPE) over three time periods (15, 30 and 45 days), as reported in Table 1.

Its two weeks out-of-sample Worldwide Median MAPE over 221 areas is 8.0 % for cases and 6.9 % for deaths, while for a six weeks backtest period, they are respectively 16.2 % and 10.8 %. Compared to other top-performing models used by the CDC, Figure 1 shows DELPHI consistently ranked in the Top 2 (with two exceptions) for prediction accuracy on US deaths in the second wave.

Furthermore, using the modeling of $\gamma(t)$, [7] was able to analyze NPIs in over 150 countries during this pandemic, and quantified the effect of interventions on the infection rate in mutually exclusive and collectively exhaustive categories. Important categories

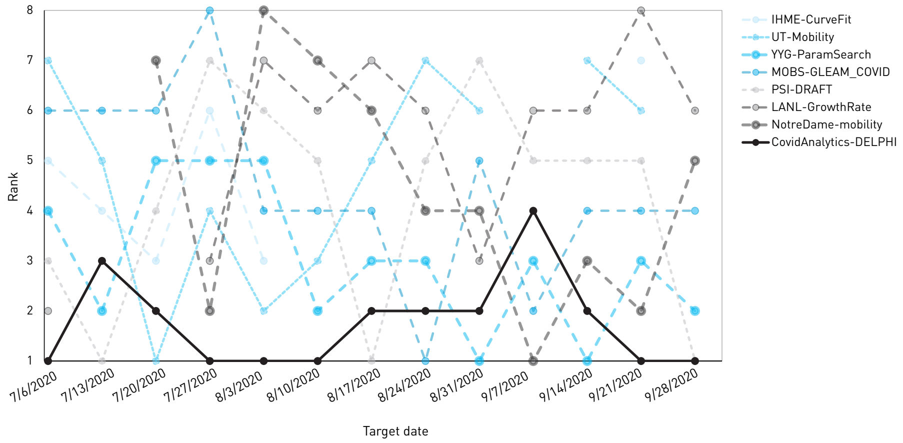

Figure 1. Model rank for US wide – 4 week ahead deaths predictions: DELPHI ranks 1^{st} on average for the 4-week ahead US deaths prediction among all models used by the CDC over the 3 months in the 2^{nd} wave (July to September). It ranks 1^{st} 5 weeks out of 13 and never worse than 4^{th}.

include: (1) *No measure*; (2) *Restrict travel and work only*; (3) *Restrict mass gatherings, travel and work*; (4) *Restrict mass gatherings, schools, travel and work*; and (5) *Stay-at-Home*. The results of this analysis is shown in Table 2.

They show that mass gathering restrictions generate a large reduction in infection rate, with the incremental reduction between travel and work restrictions compared to mass gathering, travel, and work restrictions is 29.9 ± 6.9 %. This is further supported by the large residual infection rate of 88.9 ± 4.5 % when travel and work restrictions are implemented, but mass gatherings are allowed. Additionally, closing schools also generate a large reduction in the infection rate, with an incremental effect of 17.3 ± 6.6 % on top of mass gathering and other restrictions. Stay-at-home orders produced the strongest reduction in infection rate across the different countries, with a residual infection rate of just 25.6 ± 3.7 % compared to when no measure was implemented. Importantly, these results demonstrate that if COVID-19 has an average basic reproductive number R_0 of 2.5-3 ([8, 14]), then on average, only the strongest measure (Stay-at-Home orders) are sufficient to control a COVID-19 epidemic in reducing R_0 to be less than 1.

However, the unbearable societal cost of stay-at-home orders meant that NPIs cannot be the solution to the pandemic. Therefore, there has been extensive research in clinical solutions to COVID-19, with much hope being placed in vaccines. Unlike therapeutics and diagnostics, vaccines intervene at the upstream to immunize patients against the virus, potentially offering the society a solution to return to normal. Many pharmaceutical companies and academic institutions have explored different technologies toward a COVID-19 vaccine [5, 12]. These span (i) inactivated or live-attenuated virus vaccines, which induce an immune response from weakened or killed pathogens (used by the Wuhan Institute of Biological Products, for instance); (ii) viral vector vaccines, which exploit non-replicating adenoviruses to deliver an antigenic element (used by Johnson and Johnson, for instance); (iii) subunit vaccines, which use a minimal structural component of a pathogen such as a protein (used by Clover Biopharmaceuticals, for instance); (iv) nucleic acid vaccines, which deliver DNA or mRNA of viral proteins (used by Pfizer and Moderna, for instance). As of October 2020, there are over 100 experimental SARS-CoV-2 vaccines globally, 11 of which are in latest phases of clinical trials—an unprecedented speed for vaccine development.

However, to further complicate the already daunting task of developing a vaccine, it is difficult to quickly ascertain if a vaccine indeed offers immunity. Usually, this is done through Phase III vaccine trials, where large number of volunteers are recruited at a certain location, and a random portion is selected to receive the vaccine (while the rest receive a placebo). The trial then monitors the infection rate for such disease in both the vaccinated and placebo group over a period of time. The vaccine is only deemed effective if at some point there is a statistically significant difference between the infection rate in the two groups.

Given the extraordinary humanitarian and economic cost of the pandemic, it is thus imperative for the Phase III trial to be completed as soon as possible. One of the key ways to reduce the trial time is by selecting trial locations with high incidence rates ("hotspots"), so that the infections develop quicker, allowing an earlier comparison between the two groups. To do so, however, requires knowledge of the future COVID-19 infection rate. In May 2020, Janssen selected DELPHI as one of two core models from a group of more than 10 leading modeling efforts to serve as the foundation for its predictive forecasting for identifying hotspots for the Phase III trial of its single-dose vaccine candidate, Ad26.Cov2.S.

Due to practical constraints on vaccine trial planning, Janssen needed to predict where hotspots would be on a 4+ months out on the level of country, province, and sub-provinces/counties. Therefore, immediately after selecting DELPHI, Janssen selected a core group of countries in May that were predicted to have high incidence in September to begin site feasibility assessment.

Then, since late May 2020, Janssen worked closely with MIT to further refine the prediction methodology to produce long-term forecasts at the province/state and county level. Based on feedback from Janssen in uncovering disease propagation dynamics across various geographies, MIT adapted the modeling process to better account for repeated disease emergence in previously impacted

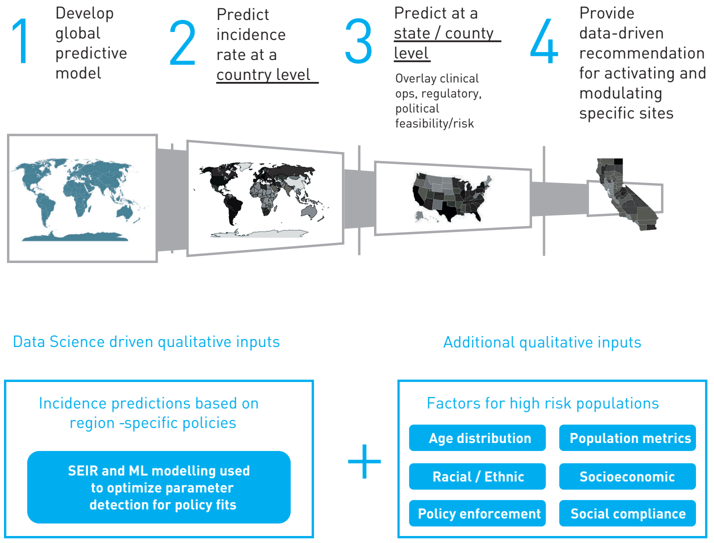

Figure 2. Janssen data-driven process for site selection and activation based on MIT DELPHI incidence forecasts and other factors for high risk populations

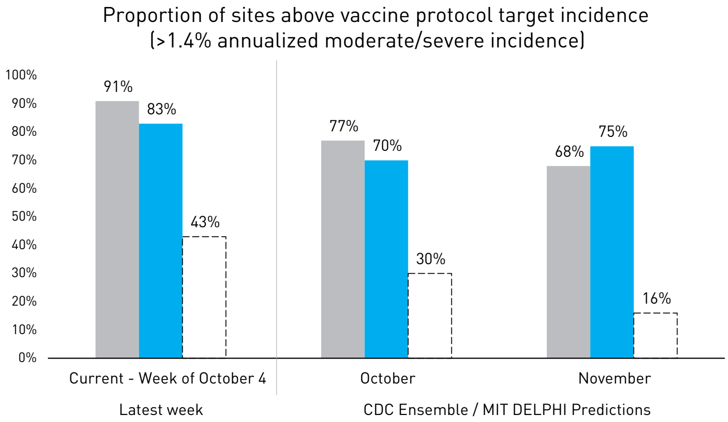

Figure 3. DELPHI/Janssen COVID-19 predicted hotspots in May 2020 were accurate in selecting true hotspots in October 2020 (light/dark blue – predicted hotspots in/starting trial, white – predicted non-hotspots).

areas, as well as allowing for the dynamic modulation of shifting policy input as regions enter/exit/re-enter partial lockdowns. Building on this foundation, Janssen then combined the DELPHI incidence predictions with additional layers of qualitative factors to identify the highest risk populations who would most benefit from the vaccine–age distribution, population metrics, racial/ethnic demographics, and policy and compliance metrics specific to each province, state, or county (Figure 2).

By September 2020, it was clear that the results of the DELPHI-driven country selection process in May 2020 were directionally highly accurate with the reality of COVID-19's spread in August and September 2020. DELPHI, combined with the Janssen layering of demographic/age/policy-driven factors, accurately identified high incidence (defined as greater than 1.4 % moderate-to-severe COVID-19 incidence) in ~70–90 % of the hotspots predicted. In comparison, only a minority of non-hotspot areas (~16–40 %) have achieved this level of incidence, as shown in Figure 3. Janssen then utilized the province/state/county high resolution predictions in real-time as an input for site activation and rollout planning in the accurately forecasted high incidence countries of United States, Brazil, Colombia, Argentina, Mexico, Chile and Peru. The final DELPHI-driven location selection achieved 90 %+ accuracy in choosing sites with high COVID-19 incidence, as shown in Figure 4. This data-driven methodology accelerated the Phase III trial time by 6–8 weeks while simultaneously reducing the trial size from 60,000 to 45,000 individuals. Areas of high COVID-19 incidence also are the most likely places to produce variants. Therefore, by utilizing DELPHI to identify hotspots, this enabled Janssen to have the only Phase III trial to date that is directly tested against important variants in Brazil and South Africa. Such direct evidence of variant protection has contributed to the decision by the South Africa authorities to utilize the Janssen vaccine for its frontline healthcare workers.

Currently, there has been more than 13 million vaccinations in the United States, 11.9 million vaccinations in the European Union, and 500,000 vaccinations in South Africa with the Ad26.Cov2.S vaccine. The current vaccinations alone are estimated to have already saved thousands of deaths by COVID-19. Janssen is expecting to eventually manufacture over 1 billion doses – fulfilling orders from the U.S. government (up-to-300 million doses), European Union (up-to-400 million doses), and with a commitment of up-to-500 million doses to lower-income countries next year as part of the Communiqué on Global Access to ensure that people have access to potential COVID-19 innovation everywhere. The Janssen vaccine only requires storage between 2 °C and 8 °C; combined with the single-shot nature, Janssen's vaccine is a prime vaccine for reaching lower-income countries, and vulnerable or hard-to-reach communities around the world.

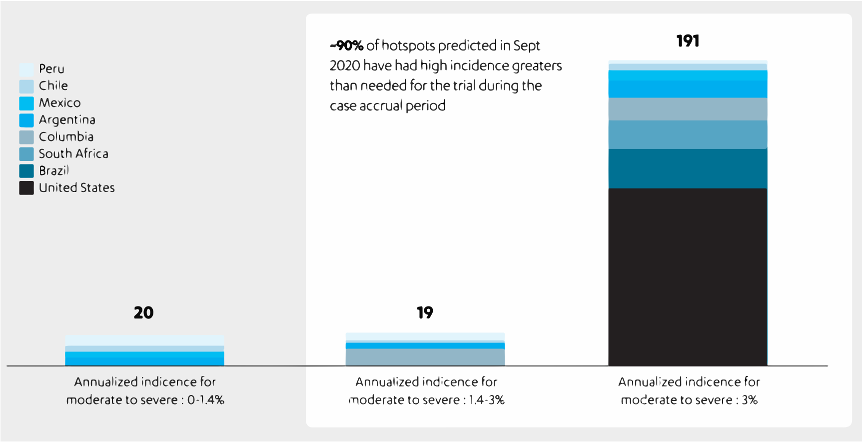

Figure 4. Over 90 % of hotspots chosen by DELPHI/Janssen in September 2020 for the actual trial had incidence higher than needed for the trial.

Comment by Sheldon H. Jacobson

The COVID-19 pandemic has been fast moving, disruptive, and unpredictable. This has challenged data scientists, epidemiologists, and mathematical modelers, stretching their toolbox of methodologies beyond everyone's comfort zone.

The Delphi model provide a unique balance between analytical rigor and practical value. Building upon existing differential equation population models, Delphi adds realistic extension that capture system dynamics of an infectious disease in a population that are specific to the SARS-CoV2 virus. Their modeling efforts are enhanced by optimizing the model parameters appropriately, something that is often lacking in such types of efforts.

Forecasts on the spread of the virus and fatalities are impressive when compared to what actually occurred. The application of supporting locations of clinical trials for vaccines is clever, with areas of high virus transmission and concentration are ideal settings for evaluating the efficacy of vaccines. As new variants continue to emerge, the value of Delphi will continue to grow, providing a valuable tool that fills a void during these challenging times.

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Vaccine Allocation

Unfortunately, discovering and developing a vaccine for COVID-19 was just the beginning – it takes months to produce, distribute, and deliver vaccines at scale. The world has quickly come to the realization that vaccines cannot be made available immediately to everyone, and policy makers need to make tough decisions to pilot vaccine distribution. A global consensus has naturally emerged to prioritize to healthcare workers, other front line workers, and vulnerable populations such as older people and people with comorbidities [see, e.g., 10]. Within these general principles, each jurisdiction is designing more detailed eligibility guidelines to distribute vaccines effectively and equitably *within a population*, based on demographic, clinical and geographic factors. However, a question remains open: how to plan vaccine distribution *across populations*, that is, how to allocate a limited vaccine supply across communities, across provinces, and even across countries?

In the United States, this question gained prominence in the midst of a presidential transition. In particular, the new Biden administration relies on higher extents of federal coordination in vaccine distribution, as opposed to a more decentralized approach at the state level. In one of its first major decisions, the administration started opening mass vaccination sites, with many more planned over the next few weeks (www.nbcnews.com/politics/white-house/federal-government-opening-first-mass-covid-19-vaccination-sites-california-n1256611). This environment raises the critical question of where to locate these vaccination sites. Obviously, these decisions need to adhere to a number of political and fairness considerations – most notably, there must be at least one site per state. Yet, there remains flexibility to use mass vaccination sites as a strategic lever to effectively combat the pandemic.

In [3], the authors addresses this question with a novel data-driven approach, combining epidemiological modeling and prescriptive analytics, leveraging the DELPHI epidemiological model and integrated it into a (prescriptive) optimization model for vaccine allocation. Specifically, the goal is to optimize the deployment of mass vaccination sites, and the subsequent allocation of vaccines to minimize the death toll of the pandemic.

The number of vaccines allocated, C_t, on day t directly affect V_t, the vaccinations done that day. To link between vaccinations V_t and the epidemic, the authors designed the following equation, connecting V_t with the population eligible for vaccination $\bar{S}_t$ and the total susceptible population in the population S_t as followed:

$$\bar{S}_{t+1} = \bar{S}_t - V_t - (S_t - \beta V_t - S_{t+1}),$$

where β is the efficacy of the vaccine. This equation reflects that people could leave the eligible population through two means: vaccination (V_t), or infection ($S_t - \beta V_t - S_{t+1}$). Note that βV_t left the susceptible state due to effective vaccination and thus they need to be removed from the calculation for the number infected.

With this linkage, the authors then discretized DELPHI (accounting for vaccinations) in the optimization model as constraints to model the evolution of S (and other compartments). For example, Equation 2 in DELPHI is discretized to:

$$S_{t+1} = S_t - \beta V_t - \alpha\gamma(t)(S_t - \beta V_t)I_t, \tag{1}$$

where $S_t - \beta V_t$ is the effective susceptible population at the end of day t after βV_t people successfully gained immunity. The other DELPHI equations are similarly discretized and the death compartment D_t is minimized in the objective.

However, the bilinear nature of Equation 1 means that the eventual optimization model is non-convex. To solve it efficiently in realistic large-scale settings, they proposed a coordinate descent algorithm. First, one would initialize some vaccination strategy V_t. Then, the procedure would loop between the following two steps:

1. (Simulate) With V_t and initial conditions from DELPHI, simulate the spread of the pandemic and extract the infected population over time I_t.

Table 3. Summary of the results of vaccine allocation optimization for 100 sites in the United States. The number of lives saved are calculated within the period of simulation, between February 1st and April 30th of 2021. Multiple heuristic baselines are included as reference.

Solution	Center locations	Vaccine distributions	Saved lives	
Baseline 1	Most populous cities	Uniform across centers	19,045	(base)
Baseline 2	Pro-rata population	Uniform across centers	19,709	(+3.5%)
Baseline 3	Pro-rata active cases	Uniform across centers	21,037	(+10.5%)
Proposed	Optimized: minimizes deaths Fair: inter-state equity	Optimized: minimizes deaths Fair: inter-center equity	23,000	(+20.8%)

Comment by Julie Swann

Mathematical modelers and operations researchers have much to offer in the domain of public health. Contributing to research, knowledge, and translation into practice may require new perspectives, such as the importance of equity in public health decisions and the role of human behavior in systems. One thing that I really appreciate about the disease forecasting model presented in this paper is that they incorporate the societal response to the pandemic to predict the future spread. This is critical, as when infections greatly increase and hospitals become overwhelmed, then the model adopts accordingly. The model also validates its predictions and shows the accuracy 5, 30, and 45 days after the forecast (US and other countries), and the model was a top performer in those submitted to the CDC Covid forecasting hub. The forecasting was also used to help determine the locations for clinical trials of the Johnson & Johnson Covid-19 vaccine – perhaps that is one factor in that vaccine's continued effectiveness to other variants. The authors also consider the allocation of vaccine to locations taking into account the impact that vaccinations will have on the susceptibility "tomorrow". It is a critical factor that they incorporated the relationship between vaccine allocation and the future disease spread rather than simply allocating according to locations that have disease hot-spots today (where vaccine would likely arrive too late to have meaningful impact). This article may help inspire future mathematical optimizers to dive into problems of societal importance, where sophisticated methods can meet interesting and challenging new domains.

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2. (Optimize) Fix I_t in the optimization model so that Equation 1 is linear in the remaining variables. Solve the (linear) optimization problem to get V_t.

This procedure is extremely efficient and the experimental results are stable against a variety of initial V_t. The solution using this method for optimized vaccine allocation between February and April of 2021 with 100 sites is included in Table 3. The outcomes suggest that the locations of vaccination sites can have a massive impact on the effectiveness of the vaccination campaign. As compared to several benchmarks based on demographic information (e.g., city and state population) and epidemiological information (e.g., case counts), the optimization approach increases the number of lives saved by the vaccines by 20 %, or 4,000 lives over a three-month period in the United States. These results underscore the necessity to consider both demographics and epidemiological dynamics when determining the locations of vaccination sites and subsequent vaccine allocation. In addition, the optimization approach can ensure equity between states and across vaccination sites, thus alleviating the death toll of the pandemic in some states without hurting others. The authors also show that these benefits are highly robust to misspecifications and fluctuations in the DELPHI epidemiological parameters. Practically speaking, even though tactical decisions (e.g., vaccine allocation) need to be revised continuously in response to the latest information available throughout the vaccination campaign, strategic decisions (i.e., the location of vaccination sites) are highly robust to noise and uncertainty.

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MOS Prizes and Citations 2021

George B. Dantzig Prize

⇝ *Michel Goemans and Hédy Attouch* The Dantzig Prize is awarded to Michel Goemans for his outstanding contributions to the field of combinatorial optimization; most notably, the initiation of new research directions, introduction of novel and deep techniques, and ingenious use of sampling, rounding, and geometric ideas to significantly advance several fields, including the pioneering use of semi-definite programming for the design of approximation algorithms.

The Dantzig Prize is awarded to Hédy Attouch for his fundamental contributions to modern variational analysis and nonsmooth optimization, including new notions of variational convergence, the introduction of novel topologies for the study of quantitative stability of variational systems, and their application in algorithm design and analysis, dynamical systems and partial differential equations.

Lagrange Prize

⇝ *Léon Bottou, Frank E. Curtis, and Jorge Nocedal* for their paper, "Optimization methods for large-scale machine learning", *SIAM Review* 60(2), 2018, which provides a foundational and insightful review of optimization methods for large-scale machine learning, including a new perspective for the simultaneous consideration of noise reduction and ill-conditioning and the foundations and analysis of second-order stochastic optimization methods for machine-learning.

Fulkerson Prize

⇝ *Béla Csaba, Daniela Kühn, Allan Lo, Deryk Osthus and Andrew Treglown* for "Proof of the 1-factorization and Hamilton decomposition conjectures", *Memoirs of the American Mathematical Society*, vol. 244, no. 1154, 2016.

This paper proves three longstanding conjectures in graph theory that were open since the 70s and 80s: the 1-factorization conjecture for regular graphs, the Hamilton decomposition conjecture for regular graphs, and a conjecture of Nash–Williams on the number of Hamilton cycles that can be packed into an n-vertex graph in which every vertex has degree at least $n/2$. The proof of these conjectures is obtained via a unified approach, first replacing the original graph by a "clean" graph, and then decomposing the clean graph via an absorption approach. The techniques introduced in this paper have since been applied to solve other classical problems in graph theory.

⇝ *Jin-Yi Cai and Xi Chen* for "Complexity of counting CSP with complex weights", *Journal of the ACM*, vol. 64, no. 3, 2017.

This paper resolves the complexity of computing partition functions that are sums of products of complex-valued functions, proving that every class of partition function is either computable in polynomial time or is $\#P$ complete. The computation of partition functions is one of the most fundamental computational problems. They are essential to understanding sampling problems, Bayesian probability and statistical physics. This result is the culmination of a two-decade long research effort that builds on impressive contributions by many researchers.

⇝ *Ken-Ichi Kawarabayashi and Mikkel Thorup* for "Deterministic edge connectivity in near-linear time", *Journal of the ACM*, vol. 66, no. 1, 2018.

Determining the edge connectivity of a graph is one of the most fundamental graph problems. Karger's 1996 breakthrough gave a randomized algorithm that runs in near-linear time. It took a long time, and a lot of new ideas, before Kawarabayashi and Thorup could find a deterministic algorithm. This work does not just improve the running time of the algorithm, impressive as that is. Its main contributions are conceptual: the paper introduces powerful and impactful new ideas that will have a long-lasting influence on the field. The most powerful of these ideas is a fast deterministic sparsification that essentially preserves all the non-trivial minimum cuts of the graph.

Beale–Orchard-Hays Prize

⇝ *Alberto Costa and Giacomo Nannicini* for the work in the following papers:

- Alberto Costa and Giacomo Nannicini, RBFOpt: An open-source library for black-box optimization with costly function evaluations. *Mathematical Programming Computation* **10** (2018) 597–629.
- Giacomo Nannicini, On the implementation of a global optimization method for mixed-variable problems. *Open Journal of Mathematical Optimization* **2** (2021).

The work described in these papers develops multiple innovations in optimization of expensive derivative-free and black-box functions. The resulting package RBFOpt is notable for allowing continuous, discrete, and categorical variables; automatically learning the best surrogate model class for the objective; speeding convergence by use of low-cost approximations together with full objective evaluations; asynchronously evaluating objective values at different points in parallel; and combining effective global search approaches with multiple local search strategies. These and other ideas are tightly integrated in a computational package that has shown exceptional performance on a variety of problems from different domains. The papers offer an exemplary presentation of this work, combining lucid mathematical and algorithmic development, computational tests showing the benefits of individual innovations, and benchmark comparisons demonstrating the superior performance of RBFOpt as a whole.

⇝ *Iain Dunning, Joey Huchette, and Miles Lubin* for the work in their paper "JuMP: A modeling language for mathematical optimization". *SIAM Review* **59** (2017) 295–320.

New ideas introduced in this paper touch upon all significant aspects of algebraic modeling language design, and have been successfully integrated into JuMP, a new package for building optimization applications that has attracted users from many fields. Notable innovations of JuMP include efficient embedding of objective and constraint expressions into the Julia programming language through the use of syntactic macros; integration of user-defined functions into model formulations and derivative computations; and a design that facilitates extensions to structured problem classes.

The paper is particularly notable for its detailed discussion of the language design and software engineering considerations that had to be addressed in order to combine new ideas effectively into a general-purpose system.

A. W. Tucker Prize

⇝ *Jakub Tarnawski (Winner):* Thesis title: New graph algorithms via polyhedral techniques

Tarnawski's thesis achieves a breakthrough on a fundamental optimization problem: the Traveling Salesperson Problem (TSP). Given n cities with inter pair distances, the goal is to find the shortest tour that visits all the cities. The most successful algorithms for the problem are based on linear programming methods, both theoretically and computationally. One of the most well-studied linear programming based formulations is known as the Held-Karp relaxation and a central question has been to give tight bounds on how good this relaxation is, along with the study of algorithms that can produce tours that are provably close to being optimal. In the case of the asymmetric version of the problem, where the distance between two cities may be different depending on the direction of travel, for decades it was not clear if the quality of the Held-Karp relaxation degrades with the size of the problem instance, or remains the same no matter how many cities are involved. Tarnawski's thesis shows that the latter is true by giving an algorithm that produces a tour whose cost is at most a constant (independent of instance size) times larger than the Held-Karp lower bound, resolving a question that remained open for many decades in spite of sustained efforts from the optimization community.

Tarnawski's thesis also makes progress on another open question in combinatorial optimization: parallel algorithms for the matching problem. Randomized parallel algorithms for matching had been known for three decades, but deterministic versions had eluded researchers until a recent result by Fenner, Gurjar, and Thierauf that worked for bipartite graphs. Tarnawski's work extends this result to the general setting and introduces significant new ideas to deal with the general perfect matching polytope.

Tarnawski's thesis is groundbreaking because it resolves one of the most well-studied and hardest questions in optimization and discrete mathematics. Along with other significant achievements in fundamental and core problems in combinatorial optimization, this makes Tarnawski's thesis highly deserving of the 2021 A. W. Tucker Prize.

⇝ *Georgina Hall (Finalist):* Thesis title: Optimization over nonnegative and convex polynomials with and without semidefinite programming

Hall's thesis is outstanding in both its scope and its depth. The chapters of this thesis make several exceptional contributions to the field of mathematical optimization and its interface with computational convex algebraic geometry. Together, Hall's results span deep mathematical theory involving real algebraic geometry, computational techniques to make her ideas more tractable in software, and applications of these optimization models to robotics, statistics and optimal control. Amongst the many theoretical results dealing with algebraic aspects of convexity and polynomial optimization, one remarkable result shows how to avoid the use of semidefinite programming (SDP) in certain contexts of polynomial optimization, replacing SDPs with much simpler algebraic operations. On the computational side, Hall shows how to take advantage of techniques from discrete optimization to design more efficient algorithms for polynomial optimization. The final two chapters of Hall's thesis apply these algebraic and polynomial optimization techniques to the problem of representing 3D objects in computer vision and robotics, and to shape regression in statistics.

In summary, Hall's thesis makes significant contributions to the active area of polynomial optimization and its interface with real algebraic geometry. It is impressive in its scope, straddling theory, computation and applications, making it exceptionally well-rounded while simultaneously opening new directions of research in the area.

⇝ *Yair Carmon:* Thesis title: The complexity of optimization beyond convexity

Carmon's dissertation effectively settles the analytical (oracle) and algorithmic complexity of smooth nonconvex optimization. The corresponding theory for convex optimization had been established in the 70s and 80s by seminal work from Yudin, Nemirovskii and Nesterov. Carmon establishes information-theoretic lower bounds on the complexity of computing stationary points for smooth, nonconvex functions and gives algorithms that either match these lower bounds exactly or get very close to these lower bounds in complexity. Some of these algorithms are classical ones from the literature while others are newly designed in this thesis. In some of the key algorithm design innovations, the thesis combines insights from smooth convex optimization with new ways to exploit downward curvature, in a framework that Carmon terms "Convex until proven guilty".

Carmon's thesis reads like a textbook on the complexity theory of smooth nonconvex optimization. It is a self-contained treatise on a topic of broad interest, nailing several fundamental open questions in the area of smooth nonconvex optimization.

Tseng Memorial Lectureship

⇝ *Ya-Xiang Yuan* (The Chinese Academy of Sciences)

Ya-xiang Yuan has made highly impactful and technically deep contributions to the development of trust region methods, composite optimization and quasi-Newton methods. He gave an elegant optimality condition for the two ball constrained trust-region subproblem, and proved a surprising result about the ability of the trust-region conjugate gradient method to produce a significant reduction in the model compared to the optimal reduction (the so called "1/2 conjecture" for the truncated conjugate gradient method). He has been a remarkable educator, having trained, through his teaching and mentoring, more major researchers in optimization for Asia Pacific region than anyone else. Apart from teaching and research, Ya-xiang Yuan has been an influential academic leader in mathematics who has led major mathematics journals and institutions in China for several decades. His leadership has helped to significantly increase the research funding and vastly improved the physical infrastructure and computing resources for optimization in China.

Obituary – Donald W. Hearn

Donald W. Hearn, Ph.D., Professor Emeritus of the Department of Industrial & Systems Engineering at the University of Florida, passed away on July 9, 2021, in Pinehurst, NC. Dr. Hearn received a bachelor's degree in physics from the University of North Carolina, where he was named a Morehead Scholar. He then went on to receive both a master's and a doctorate degree in management science and operations research from Johns Hopkins University. In 1971, Dr. Hearn joined the faculty of the Department of Industrial & Systems Engineering at the University of Florida. Dr. Hearn was elected as Fellow of the Institute of Operations Research and Management Science in 2004, and from 2007–2012, he served as a program manager for Optimization and Discrete Mathematics at the Air Force Office of Scientific Research. In addition to this, Dr. Hearn also served as co-program manager and consultant for Service, Manufacturing, and Operations Research at the National Science Foundation. Dr. Hearn authored and co-authored many articles and books, and was the founding editor of OPTIMA, the newsletter of the Mathematical Programming Society.

Courtesy of the Department of Industrial & Systems Engineering at the University of Florida, USA

CONFERENCES AND WORKSHOPS

ICCOPT and MOPTA 2022 – Bethlehem, Pennsylvania

The seventh International Conference on Continuous Optimization (ICCOPT) and the Modeling and Optimization: Theory and Applications (MOPTA) conference will jointly take place at Lehigh University in Bethlehem, Pennsylvania, 2022. The program will consist of a Summer Program (July 23–24) and Conference (July 25–28) with plenary and semi-plenary talks, organized and contributed sessions, a Best Paper for Young Researchers in Continuous Optimization session, a best poster competition, and the 14th AIMMS-MOPTA Optimization Modeling Competition.

Attendees will enjoy exploring Bethlehem's rich history and contemporary culture where they can experience an array of diverse offerings in food, shopping, entertainment, and more. The conference will take place on the picturesque Lehigh University Campus, which is located 1.5 hours from New York City and Philadelphia.

Plenary Speakers

Ten distinguished researchers will deliver plenary and semi-plenary lectures at the conference:

- Ernesto Birgin (University of São Paulo, Brasil)
- Jean-Bernard Lasserre (Laboratory for Analysis and Architecture of Systems, Toulouse, France)
- Asu Ozdaglar (Massachusetts Institute of Technology, Cambridge, USA)
- Defeng Sun (Hong Kong Polytechnic University, Hong Kong)

Semi-Plenary Speakers

- Daniel Kuhn (EPFL, Lausanne, Switzerland)
- Guanghui (George) Lan (Georgia Institute of Technology, Atlanta, USA)
- Angelia Nedich (Arizona State University, Tempe, USA)
- Pablo Parillo (MIT, Cambridge, USA)
- Suvrit Sra (MIT, Cambridge, USA)
- Akiko Takeda (The University of Tokyo and Center for Advanced Intelligence Project, RIKEN, Tokyo, Japan)

Summer School

The summer school will take place July 23–24 at the scenic Mountaintop Campus of Lehigh University.

Distributionally Robust Optimization

Mathematical optimization problems traditionally model uncertainty via probability distributions. However, observable statistical data can often be explained by many strikingly different distributions. This "uncertainty about the uncertainty" poses a major challenge for optimization problems with uncertain parameters: estimation errors in the parameters' distribution are amplified through the optimization process and lead to biased (overly optimistic) optimization results as well as post-decision disappointment in out-of-sample tests.

This workshop provides an overview of the emerging field of distributionally robust optimization (DRO), which studies optimization models whose solutions are optimized against all distributions consistent with the given prior information. Recent findings have shown that many DRO models can be solved in polynomial time even when the corresponding stochastic models are intractable. DRO models also offer a more realistic account of uncertainty and mitigate the post-decision disappointment characteristic of stochastic models.

The workshop addresses four main topics. First, we develop a rigorous and general theory of static DRO using the language of convex analysis. Next, we investigate how the theory developed for static DRO extends to dynamic problems, where the values of the uncertain problem parameters are revealed sequentially over time, and where future decisions can depend on the parameter values that have already been observed. Subsequently, we address DRO problems that hedge against all distributions in a neighborhood of some nominal distribution with respect to the Wasserstein distance and establish connections to regularization. Finally, we develop statistical methods for certifying a good out-of-sample performance in Wasserstein DRO while optimally recovering regularization parameter choices advocated in high-dimensional statistics.

Lecturers

- Jose Blanchet (Stanford University, USA);
- Soroosh Shafieezadeh-Abadeh (Carnegie Mellon University, USA)
- Daniel Kuhn (Ècole Polytechnique Fédérale de Lausanne, Switzerland)
- Wolfram Wiesemann (Imperial College, London, United Kingdom)

Mathematical Optimization in Julia with JuMP

In this workshop, we will cover the basics of programming in Julia with a focus on mathematical optimization. You will learn how to write simple programs in Julia and to solve mathematical optimization problems in JuMP. The tutorial will cover three classes of problems: integer linear programs, nonlinear programs and conic programs. In addition, we will cover data manipulation, visualization and analysis.

Julia is a high-level, high-performance dynamic language for technical computing. It is dynamically typed so it feels like a scripting language and has good support for interactive use. At the same time, Julia programs compile to efficient native code for multiple platforms via LLVM hence its performance is comparable to C or Fortran.

JuMP is a modeling language and software ecosystem for mathematical optimization in the Julia programming language. JuMP makes it easy to formulate and solve linear programming, semidefinite programming, integer programming, convex optimization, constrained nonlinear optimization, and related classes of optimization problems.

Lecturers

- Benoît Legat (Massachusetts Institute of Technology, Cambridge, USA)
- Miles Lubin (Hudson River Trading, New York City, USA)

14th AIMMS-MOPTA Optimization Modeling Competition

Hospitals are complex and expensive systems to manage. One department of particular interest that poses major managerial challenges is the operating room (OR) department. The OR department generates about 40–70 % of revenues and incurs 20–40 % of operating costs in a hospital. It also demands significant hospital resources and directly influences patient flow and efficiency of care delivery. Thus, hospital managers are constantly seeking better OR and surgery scheduling approaches to improve OR utilization, surgical care, and quality, as well as to minimize operational costs.

Stochasticity is an intrinsic characteristic of OR and surgery scheduling problems since surgical activities are subject to multiple sources of uncertainty. This competition focuses on an elective surgery planning problem (ESP) in flexible ORs, where emergency patients are accommodated in the existing elective surgery schedule. Elective cases can be scheduled weeks or months in advance. In contrast, the arrival of emergency surgeries is random, and must be performed on the day of arrival. The goal is to construct a plan that specifies the assignments of a subset of elective cases from a waiting list to available OR surgery blocks and the scheduled start times of surgeries assigned to each block. The surgical blocks are typically designed to allow for multiple surgeries to be scheduled during the surgery block's time length. The plan's quality is a function of costs related to performing or delaying elective surgeries, costs related to OR overtime and idle time, costs related to surgery waiting times, and costs related to canceling scheduled surgeries to accommodate emergency surgeries. Your team's goal is to develop an efficient and implementable method to solve ESP that managers can use in practice.

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- Luis Zuluaga

Deadline

June 1: Deadline for registration

Conference Website

iccopt2022.lehigh.edu

We invite researchers and practitioners working in the field of optimization to join us in enjoying exciting mathematics in the summer of 2022!

Daniel P. Robinson and Frank E. Curtis
Co-Chairs of the Organizing Committee

ISMP 2022

The Organizing Committee of ISMP 2021/2022 in Beijing together with the Program Committee and Mathematical Optimization Society Leadership have reached the decision not to hold an in-person meeting in the end, because an international meeting is not possible in Beijing in August, due to strict quarantine requirements.

For the past few months the Program Committee has considered possibilities of an alternative location, but due to the wave of Omicron and other constraints, no suitable alternative has been found.

It was thus decided that ISMP in 2022 will consist ONLY of virtual invited talks. They will be streamed live during the originally scheduled week (August 15–19) as well as recorded and will be available to all MOS members.

The list of the speakers is as follows:

Tseng Memorial Lecture
- Yin Zhang, Chinese University of Hong Kong

Plenary speakers
- Yuhong Dai, Chinese Academy of Sciences, China
- Dick den Hertog, Tilburg University
- Rekha Thomas, University of Washington
- Yinyu Ye, Stanford University

Semi-plenary speakers
- Amitabh Basu, Johns Hopkins University
- Sébastian Bubeck, Microsoft Research
- Coralia Cartis, Oxford University
- Alexandre d'Aspremont, CNRS, Paris, École Normale Supérieure
- Stefanie Jegelka, Massachusetts Institute of Technology
- Simge Küçükyavuz, Northwestern University
- Georgia Perakis, Massachusetts Institute of Technology
- Chung Piaw Teo, National University of Singapore
- Juan Pablo Vielma, Google Research

The talks will be scheduled and streamed one at a time (no parallel talks) using Zoom webinar platform. Each talk will be followed by a Q&A session. The talks will be scheduled at different times of the day in an effort to reach the world-wide MOS community. The recording will be available from the MOS website.

The webinar and the recording will be accessible to anyone with an MOS membership, by using the email associated with the MOS membership. No special registration is required, however, the participants need to make sure to renew their membership no later than August 7th!

IMPRINT
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