References

Aktuell

Alvarez 2021

Luis Alvarez, Miguel Colom, Jean-David Morel & Jean-Michel Morel, *Computing the daily reproduction number of COVID-19 by inverting the renewal equation using a variational technique.* PNAS **118** (2021), e2105112118. DOI:10.1073/pnas.2105112118.

pnas118-e2105112118-Supplement.pdf

The COVID-19 pandemic has undergone frequent and rapid changes in its local and global infection rates, driven by governmental measures or the emergence of new viral variants. The reproduction number Rt indicates the average number of cases generated by an infected person at time t and is a key indicator of the spread of an epidemic. A timely estimation of Rt is a crucial tool to enable governmental organizations to adapt quickly to these changes and assess the consequences of their policies. The EpiEstimmethod is themostwidely accepted method for estimating Rt . But it estimates Rt with a significant temporal delay. Here, we propose a method, EpiInvert, that shows good agreement with EpiEstim, but that provides estimates of Rt several days in advance. We show that Rt can be estimated by inverting the renewal equation linking Rt with the observed incidence curve of new cases, it . Our signal-processing approach to this problem yields both Rt and a restored it corrected for the "weekend effect" by applying a deconvolution and denoising procedure. The implementations of the EpiInvert and EpiEstim methods are fully open source and can be run in real time on every country in the world and every US state.

Keywords: COVID-19 | renewal equation | reproduction number | integral equations

Significance: Based on a signal-processing approach, we propose a method to compute the reproduction number Rt , the transmission potential of an epidemic over time. Rt is estimated by minimizing a functional that enforces: 1) the ability to produce an incidence curve it corrected of the weekly periodic bias produced by the "weekend effect," obtained from Rt through a renewal equation; and 2) the regularity of Rt . A good agreement is found between our Rt estimate and the one provided by the currently accepted method, EpiEstim, except that our method predicts Rt several days closer to present. We provide the mathematical arguments for this shift.

Bates 2021

Timothy A. Bates et al., *Antibody Response and Variant Cross-Neutralization After SARS-CoV-2 Breakthrough Infection.* Journal of the American Medical Association (2021), preprint, 1–3. DOI:10.1001/jama.2021.22898.

Results of this study showed substantial boosting of humoral immunity after breakthrough infection, despite predominantly mild disease. Boosting was most notable for IgA, possibly due to the differences in route of exposure between vaccination and natural infection. In addition, breakthrough sera demonstrated improved variant crossneutralization, and Delta breakthrough infections in particular exhibited improved potency against Delta vs WA1, suggesting that the protective

immune response may be broadened through development of variant boosters with antigenic inserts matching the emerging SARS-CoV-2 variants. Limitations of this study include the small number of samples and the difference in time from initial vaccination to serum collection between the breakthrough and control groups, which emerging evidence suggests may contribute to the development of variant cross-neutralizing antibody responses.

Timothy A. Bates, Savannah K. McBride, Bradie Winders, Devin Schoen, Lydie Trautmann, Marcel E. Curlin, Fikadu G. Tafesse

Callaway 2021

Ewen Callaway, *Omicron likely to weaken Covid vaccine protection.* nature **600** (2021), 367–368.

Existing vaccines could be less effective against the fast-spreading coronavirus variant, but boosters should improve immunity.

Cernuschi 2021

Tania Cernuschi, Stefano Malvolti, Matthew Downham, Dominique Maugeais, David Robinson & Alejandro Cravioto, *COVID-19 impact on infant and adolescent vaccine supplies.* science **374** (2021), 1438–1441. DOI:10.1126/science.abl7019.

Vaccine production is quadrupling rapidly, creating supply chain challenges.

Dejnirattisai 2021

Wanwisa Dejnirattisai et al., *Reduced neutralisation of SARS-COV-2 Omicron-B.1.1.529 variant by postimmunisation serum.* medRxiv **2021**, Dec. 11. DOI:10.1101/2021.12.10.21267534.

In this report, we present live neutralisation titres against SARS-CoV-2 Omicron variant, compared with neutralisation against Victoria, Beta and Delta variants. Sera from day-28 post second-dose were obtained from participants in the Com-COV2 study who had received a two-dose COVID-19 vaccination schedule with either AstraZeneca (AZD1222) or Pfizer (BNT162b2) vaccines. There was a substantial fall in neutralisation titres in recipients of both AZD1222 and BNT16b2 primary courses, with evidence of some recipients failing to neutralise at all. This will likely lead to increased breakthrough infections in previously infected or double vaccinated individuals, which could drive a further wave of infection, although there is currently no evidence of increased potential to cause severe disease, hospitalization or death.

Wanwisa Dejnirattisai, Robert H. Shaw, Piyada Supasa, Chang Liu, Arabella S. V. Stuart, Andrew J. Pollard, Xinxue Liu, Teresa Lambe, Derrick Crook, Dave I. Stuart, Juthathip Mongkolsapaya, Jonathan S. Nguyen-Van-Tam, Matthew D. Snape, Gavin R. Screaton & the Com-COV2 study group

Elliott 2021

Paul Elliott, David Haw, Haowei Wang, Oliver Eales & Steven Riley et al., *Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant.* science **374** (2021), 1463. DOI:10.1126/science.abl9551.

s374-1463-Supplement.pdf

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infections were rising during early summer 2021 in many countries as a result of the Delta variant. We assessed reverse transcription polymerase chain reaction swab positivity in the

Real-time Assessment of Community Transmission–1 (REACT-1) study in England. During June and July 2021, we observed sustained exponential growth with an average doubling time of 25 days, driven by complete replacement of the Alpha variant by Delta and by high prevalence at younger, less-vaccinated ages. Prevalence among unvaccinated people [1.21 % (95 % credible interval 1.03 %, 1.41 %)] was three times that among double-vaccinated people [0.40 %(95 % credible interval 0.34 %, 0.48 %)]. However, after adjusting for age and other variables, vaccine effectiveness for double-vaccinated people was estimated at between ≈50 % and ≈60 % during this period in England. Increased socialmixing in the presence of Delta had the potential to generate sustained growth in infections, even at high levels of vaccination.

Paul Elliott, David Haw, Haowei Wang, Oliver Eales, Caroline E. Walters, Kylie E. C. Ainslie, Christina Atchison, Claudio Fronterre, Peter J. Diggle, Andrew J. Page, Alexander J. Trotter, Sophie J. Prosolek, The COVID-19 Genomics UK (COG-UK) Consortium, Deborah Ashby, Christl A. Donnelly, Wendy Barclay, Graham Taylor, Graham Cooke, Helen Ward, Ara Darzi & Steven Riley

Kupferschmidt 2021

Kai Kupferschmidt, *Scientists see a 'really, really tough winter' with Omicron.* science **374** (2021), 1421–1422. DOI:10.1126/science.acz9834.

Another major pandemic wave seems inevitable. The big question is how much severe disease it will bring.

Kupferschmidt 2021

Kai Kupferschmidt, *Missed Shots.* science **374** (2021), 1434–1435. DOI:10.1126/science.acz9824.

By total doses delivered, the COVID-19 vaccine rollout was a spectacular success. By other measures, it went tragically awry.

Li 2021

Juan Li, Shengjie Lai, George F. Gao & Weifeng Shi, *The emergence, genomic diversity and global spread of SARS-CoV-2.* nature **600** (2021), 408–418. DOI:10.1038/s41586-021-04188-6.

Since the first cases of COVID-19 were documented in Wuhan, China in 2019, the world has witnessed a devastating global pandemic, with more than 238 million cases, nearly 5 million fatalities and the daily number of people infected increasing rapidly. Here we describe the currently available data on the emergence of the SARS-CoV-2 virus, the causative agent of COVID-19, outline the early viral spread in Wuhan and its transmission patterns in China and across the rest of the world, and highlight how genomic surveillance, together with other data such as those on human mobility, has helped to trace the spread and genetic variation of the virus and has also comprised a key element for the control of the pandemic. We pay particular attention to characterizing and describing the international spread of the major variants of concern of SARS-CoV-2 that were first identified in late 2020 and demonstrate that virus evolution has entered a new phase. More broadly, we highlight our currently limited understanding of coronavirus diversity in nature, the rapid spread of the virus and its variants in such an increasingly connected world, the reduced protection of vaccines, and the urgent need for coordinated global surveillance using genomic techniques. In summary, we provide important information for the prevention and control of both the ongoing COVID-19 pandemic and any new diseases that will inevitably emerge in the human population in future generations.

RICHELLE 2021

Matthieu Richelle, *"No", A Reply to Benjamin Sass.* Semitica (2021), preprint, 1–3. .

> In the end, I have expressed my views in my Semitica article; Sass did the same in his own article. It is unlikely that we will convince each other on the subject of the Shapira strips, but that is perfectly fine. I respect him and look forward to learning from him on other subjects in future publications.

VÖHRINGER 2021

Harald S. Vöhringer et al., *Genomic reconstruction of the SARS-CoV-2 epidemic in England.* nature **600** (2021), 506–511. DOI:10.1038/s41586-021-04069-y.

> n600-0506-Supplement.pdf

> The evolution of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) virus leads to new variants that warrant timely epidemiological characterization. Here we use the dense genomic surveillance data generated by the COVID-19 Genomics UK Consortium to reconstruct the dynamics of 71 different lineages in each of 315 English local authorities between September 2020 and June 2021. This analysis reveals a series of subepidemics that peaked in early autumn 2020, followed by a jump in transmissibility of the B.1.1.7/Alpha lineage. The Alpha variant grew when other lineages declined during the second national lockdown and regionally tiered restrictions between November and December 2020. A third more stringent national lockdown suppressed the Alpha variant and eliminated nearly all other lineages in early 2021. Yet a series of variants (most of which contained the spike E484K mutation) defied these trends and persisted at moderately increasing proportions. However, by accounting for sustained introductions, we found that the transmissibility of these variants is unlikely to have exceeded the transmissibility of the Alpha variant. Finally, B.1.617.2/Delta was repeatedly introduced in England and grew rapidly in early summer 2021, constituting approximately 98 % of sampled SARS-CoV-2 genomes on 26 June 2021.

> Harald S. Vöhringer, Theo Sanderson, Matthew Sinnott, Nicola De Maio, Thuy Nguyen, Richard Goater, Frank Schwach, Ian Harrison, Joel Hellewell, Cristina V. Ariani, Sonia Gonçalves, David K. Jackson, Ian Johnston, Alexander W. Jung, Callum Saint, John Sillitoe, Maria Suciu, Nick Goldman, Jasmina Panovska-Griffiths, The Wellcome Sanger Institute COV- Surveillance Tea, The COV- Genomics U. K. Consortiu, Ewan Birney, Erik Volz, Sebastian Funk, Dominic Kwiatkowski, Meera Chand, Inigo Martincorena, Jeffrey C. Barrett & Moritz Gerstung

Anthropologie

MCNUTT 2021

Ellison J. McNutt et al., *Footprint evidence of early hominin locomotor diversity at Laetoli, Tanzania.* nature **600** (2021), 468–471.

> n600-0468-Supplement.pdf

> Bipedal trackways discovered in 1978 at Laetoli site G, Tanzania and dated to 3.66 million years ago are widely accepted as the oldest unequivocal evidence of obligate bipedalism in the human lineage1–3. Another trackway discovered two years earlier at nearby site A was partially excavated and attributed to a hominin, but curious affinities with bears (ursids) marginalized its importance to the paleoanthropological community, and the location of these footprints fell into obscurity3–5. In 2019, we located, excavated and cleaned the site A trackway, producing a digital archive using 3D photogrammetry and laser scanning. Here we

compare the footprints at this site with those of American black bears, chimpanzees and humans, and we show that they resemble those of hominins more than ursids. In fact, the narrow step width corroborates the original interpretation of a small, cross-stepping bipedal hominin. However, the inferred foot proportions, gait parameters and 3D morphologies of footprints at site A are readily distinguished from those at site G, indicating that a minimum of two hominin taxa with different feet and gaits coexisted at Laetoli.

Ellison J. McNutt, Kevin G. Hatala, Catherine Miller, James Adams, Jesse Casana, Andrew S. Deane, Nathaniel J. Dominy, Kallisti Fabian, Luke D. Fannin, Stephen Gaughan, Simone V. Gill, Josephat Gurtu, Ellie Gustafson, Austin C. Hill, Camille Johnson, Said Kallindo, Benjamin Kilham, Phoebe Kilham, Elizabeth Kim, Cynthia Liutkus-Pierce, Blaine Maley, Anjali Prabhat, John Reader, Shirley Rubin, Nathan E. Thompson, Rebeca Thornburg, Erin Marie Williams-Hatala, Brian Zimmer, Charles M. Musiba & Jeremy M. DeSilva

Melillo 2021

Stephanie M. Melillo, *Hominin footprints reveal a walk on the wild side.* nature **600** (2021), 388–390.

Bipedalism is a defining feature of the human lineage, but not all hominin species walked in the same way. New data from a famous palaeoanthropology site reveal that at least two differently bipedal hominins roamed eastern Africa.

Bibel

Richelle 2021

Matthieu Richelle, *Was the Tower of Babel Really Left Uninished? Genesis 11:5 in Light of Hebrew Syntax, the Septuagint, and Jewish Reception.* Semitica **63** (2021), 125–139.

Exegetes have long been torn between two constraints: a grammatical one in v. 5, which should lead to the translation "had built;" a contextual one, stemming from v. 8, which implies that the construction of the city is still ongoing at the time referred to in that verse. Some commentators have felt a tension between these two constraints, and their solution has been to bend the meaning of v. 5. However, a simpler option exists, that gives the last verb of v. 5 its full force while not introducing a tension with v. 8: to limit the referent of the relative clause in v. 5 to the tower, and thus to understand: "The Lord came down to see the city, and [also] the tower that the men had built."

Richelle 2021

Matthieu Richelle, *The Shapira Strips in Light of Paleography, Six Impossible Things Before Breakfast.* Semitica **63** (2021), 243–294.

The script of the Shapira strips exhibits an accumulation of anomalies that are indicative of forgeries (anomalous stances, letterforms unparalleled in Old Hebrew script but relecting a mixture of letterforms from other alphabets or from the Moabitica, mixture of letterforms from diferent periods, ligatures). One could imagine that the strips were forged by someone who used a variety of script sources as models: the Moabite Stone, Nabatean inscriptions, Phoenician inscriptions, and so on (as was done before for the Moabitica). But there is a convergence of factors indicating that they were simply made by the same person(s) who forged the Moabitica. Which echoes the circumstances of their appearance: they were offered for sale by the same man who had sold the Moabitica.

SASS 2021

Benjamin Sass, *Can a Unique Letterform Clinch the Authenticity of the Shapira Leather Manuscripts? A Rejoinder to Matthieu Richelle.* Semitica **63** (2021), 223–242.

Semitica63-223-Comment.pdf

A comparison with Ginsburg's largely inexact drawings of the Mesha and Siloam letterforms leads me to conclude that the drawings of Shapira's manuscripts by Ginsburg and most other 1880s scholars are also unlikely to be facsimiles. Hence these drawings of the lost manuscripts are unsuited for confirming or denying authenticity. The sole exception is the zigzag yod of The Graphic. The potential for genuineness of that yod has a soundness of its own: Taken at face value, the combined Samaria, Rehov and Haror comparisons show this letter, hence the Shapira manuscripts at large, to be genuine. For if not, how could a forger in the 1880s foresee a letterform, the next attestation of which, at Samaria, lay three decades in the future? To be sure, excusing away The Graphic's meandering yod as clumsy (Richelle), or incidental, or immaterial, is no option, as noted below; the clearly drawn form is too highly diagnostic to be unintended.

Biologie

LIEBERMAN 2021

Daniel E. Lieberman, Timothy M. Kistner, Daniel Richard, I-Min Lee & Aaron L. Baggish, *The active grandparent hypothesis, Physical activity and the evolution of extended human healthspans and lifespans.* PNAS **118** (2021), e2107621118.

The proximate mechanisms by which physical activity (PA) slows senescence and decreases morbidity and mortality have been extensively documented. However, we lack an ultimate, evolutionary explanation for why lifelong PA, particularly during middle and older age, promotes health. As the growing worldwide epidemic of physical inactivity accelerates the prevalence of noncommunicable diseases among aging populations, integrating evolutionary and biomedical perspectives can foster new insights into how and why lifelong PA helps preserve health and extend lifespans. Building on previous life-history research, we assess the evidence that humans were selected not just to live several decades after they cease reproducing but also to be moderately physically active during those postreproductive years. We next review the longstanding hypothesis that PA promotes health by allocating energy away from potentially harmful overinvestments in fat storage and reproductive tissues and propose the novel hypothesis that PA also stimulates energy allocation toward repair and maintenance processes. We hypothesize that selection in humans for lifelong PA, including during postreproductive years to provision offspring, promoted selection for both energy allocation pathways which synergistically slow senescence and reduce vulnerability to many forms of chronic diseases. As a result, extended human healthspans and lifespans are both a cause and an effect of habitual PA, helping explain why lack of lifelong PA in humans can increase disease risk and reduce longevity.

Keywords: physical activity | exercise | lifespan | healthspan | evolution

Datierung

NIESPOLO 2021

Elizabeth M. Niespolo & Tim D. White et al., *Integrative geochrono-*

logy calibrates the Middle and Late Stone Ages of Ethiopia's Afar Rift. PNAS **118** (2021), e2116329118.

pnas118-e2116329118-Supplement.pdf

The Halibee member of the Upper Dawaitoli Formation of Ethiopia's Middle Awash study area features a wealth of Middle and Later Stone Age (MSA and LSA) paleoanthropological resources in a succession of Pleistocene sediments. We introduce these artifacts and fossils, and determine their chronostratigraphic placement via a combination of established radioisotopic methods and a recently developed dating method applied to ostrich eggshell (OES). We apply the recently developed 230Th/U burial dating of OES to bridge the temporal gap between radiocarbon (14C) and 40Ar/39Ar ages for the MSA and provide 14C ages to constrain the younger LSA archaeology and fauna to ≈24 to 21.4 ka. Paired 14C and 230Th/U burial ages of OES agree at ≈31 ka for an older LSA locality, validating the newer method, and in turn supporting its application to stratigraphically underlying MSA occurrences previously constrained only by a maximum 40Ar/39Ar age. Associated fauna, ora, and Homo sapiens fossils are thereby now xed between 106 ± 20 ka and 96.4 ± 1.6 ka (all errors 2σ). Additional 40Ar/39 Results on an underlying tuff rene its age to 158.1 ± 11.0 ka, providing a more precise minimum age for MSA lithic artifacts, fauna, and H. sapiens fossils recovered ≈9 m below it. These results demonstrate how chronological control can be obtained in tectonically active and stratigraphically complex settings to precisely calibrate crucial evidence of technological, environmental, and evolutionary changes during the African Middle and Late Pleistocene.

Elizabeth M. Niespolo, Giday WoldeGabriel, William K. Hart, Paul R. Renne, Warren D. Sharp, M. Steven Shackley, Stanley H. Ambrose, Berhane Asfaw, Yonas Beyene, Marianne F. Brasil, Joshua P. Carlson, Yonatan Sahle & Tim D. White

Significance: Understanding the evolution, dispersals, behaviors, and ecologies of early African Homo sapiens requires accurate geochronological placement of fossils and artifacts. We introduce open-air occurrences of such remains in sediments of the Middle Awash study area in Ethiopia. We describe the stratigraphic and depositional contexts of our discoveries and demonstrate the effectiveness of recently developed uranium-series dating of ostrich eggshell at validating and bridging across more traditional radioisotopic methods (14C and 40Ar/39Ar). Homo sapiens fossils and associated Middle Stone Age artifacts are placed at >158 and ≈96 ka. Later Stone Age occurrences are dated to ≈21 to 24 ka and ≈31 to 32 ka, firmly dating the upper portion of one of the longest records of human evolution.

Energie

Tang 2021

Kechao Tang, Kaichen Dong & Jiachen Li et al., *Temperature-adaptive radiative coating for all-season household thermal regulation.* science **374** (2021), 1504–1509.

s374-1504-Supplement.pdf

The sky is a natural heat sink that has been extensively used for passive radiative cooling of households. A lot of focus has been on maximizing the radiative cooling power of roof coating in the hot daytime using static, cooling-optimized material properties. However, the resultant overcooling in cold night or winter times exacerbates the heating cost, especially in climates where heating dominates energy consumption. We approached thermal regulation from an all-season

perspective by developing a mechanically flexible coating that adapts its thermal emittance to different ambient temperatures. The fabricated temperature-adaptive radiative coating (TARC) optimally absorbs the solar energy and automatically switches thermal emittance from 0.20 for ambient temperatures lower than 15°C to 0.90 for temperatures above 30°C, driven by a photonically amplified metal-insulator transition. Simulations show that this system outperforms existing roof coatings for energy saving in most climates, especially those with substantial seasonal variations.

Kechao Tang, Kaichen Dong, Jiachen Li, Madeleine P. Gordon, Finnegan G. Reichertz, Hyungjin Kim, Yoonsoo Rho, Qingjun Wang, Chang-Yu Lin, Costas P. Grigoropoulos, Ali Javey, Jeffrey J. Urban, Jie Yao, Ronnen Levinson & Junqiao Wu

Wang 2021

Shancheng Wang, Tengyao Jiang, Yun Meng, Ronggui Yang, Gang Tan & Yi Long, *Scalable thermochromic smart windows with passive radiative cooling regulation.* science **374** (2021), 1501–1504.

s374-1501-Supplement.pdf

Radiative cooling materials spontaneously radiate long-wave infrared (LWIR) to the cold outer space, providing cooling power that is preferred in hot seasons. Radiative cooling has been widely explored for walls and roofs but rarely for windows, which are one of the least energy-efficient parts of buildings. We fabricated scalable smart windows using a solution process giving different emissivity (e) at high (eLWIR-H of 0.61) and low (eLWIR-L of 0.21) temperatures to regulate radiative cooling automatically while maintaining luminous transparency and near-infrared (NIR) modulation. These passive and independent visible–NIR–LWIR regulated smart windows are capable of dynamic radiative cooling for self-adapting applications across different climate zones.

Kultur

Brown 2000

David Brown, John Fermor & Christopher Walker, *The Water Clock in Mesopotamia.* Archiv für Orientforschung **46** (2000), 130–148.

This paper discusses the evidence pertaining to water clocks in Mesopotamia, revealing the serious flaws that exist in our current understanding of the devices and attempting to remedy this, while recognising the limitations inherent in the exercise. We possess no recognised examples, however fragmentary, from ancient Mesopotamia of outflowing water clocks. Any reconstruction of them relies on textual evidence and what is known to be both physically possible and impossible. J. Fermor undertook the experimental work. This paper also presents BM 29371, which was edited by C. B. F. Walker and published in a photograph in Astronomy before the Telescope (1996, ed. C. B. F. Walker) p. 47. BM 29371 describes weights, times and the lengths of shadows on various days through the year and was inscribed during the Late Babylonian period.

Politik

Hangartner 2021

Dominik Hangartner, Gloria Gennaro, Fabrizio Gilardi & Karsten Donnay et al., *Empathy-based counterspeech can reduce racist*

Despite heightened awareness of the detrimental impact of hate speech on social media platforms on affected communities and public discourse, there is little consensus on approaches to mitigate it. While content moderation—either by governments or social media companies—can curb online hostility, such policies may suppress valuable as well as illicit speech and might disperse rather than reduce hate speech. As an alternative strategy, an increasing number of international and nongovernmental organizations (I/NGOs) are employing counterspeech to confront and reduce online hate speech. Despite their growing popularity, there is scant experimental evidence on the effectiveness and design of counterspeech strategies (in the public domain). Modeling our interventions on current I/NGO practice, we randomly assign English-speaking Twitter users who have sent messages containing xenophobic (or racist) hate speech to one of three counterspeech strategies—empathy, warning of consequences, and humor—or a control group. Our intention-totreat analysis of 1,350 Twitter users shows that empathy-based counterspeech messages can increase the retrospective deletion of xenophobic hate speech by 0.2 SD and reduce the prospective creation of xenophobic hate speech over a 4-wk follow-up period by 0.1 SD. We find, however, no consistent effects for strategies using humor or warning of consequences. Together, these results advance our understanding of the central role of empathy in reducing exclusionary behavior and inform the design of future counterspeech interventions.

Keywords: hate speech | social media | counterspeech | field experiment

Dominik Hangartner, Gloria Gennaro, Sary Alasiri, Nicholas Bahrich, Alexandra Bornhoft, Joseph Boucher, Buket Buse Demirci, Laurenz Derksen, Aldo Hall, Matthias Jochum, Maria Murias Munoz, Marc Richter, Franziska Vogel, Salomé Wittwer, Felix Wüthrich, Fabrizio Gilardi & Karsten Donnay