In the arrangement of leaves, Fibonacci numbers relate the number of spirals going in one direction to the number of spirals in the other. There are many conflicting reports in botany, for example, in sunflowers. In a large-scale experiment of popular science with over 600 sunflowers in 2016, only three out of four of the parastichies on sunflowers were direct Fibonacci numbers. The other one-quarter were approximate or modified Fibonacci and Lucas numbers, derived series, or irregular. If only three-quarters are described by Fibonacci series (derived series are easy to generate), it is hard to argue that this is the ultimate model for phyllotaxy. The volume fails to mention this research; in fact, the list of references hardly mentions any botanical works.

The essence is recurrence series. One point raised by the author is that leaves and scales on pine cones are discrete structures. But then one should focus on difference equations and polynomials to study phyllotaxy. Consider a homogeneous linear second order difference equation with constant coefficients: u_0; u_1; $u_{n+1} = au_n + bu_{n-1}$. If a and b are polynomials in x, a sequence of polynomials is generated. In particular if $a = 2x$ and $b = -1$, we obtain Chebyshev polynomials. They are of the first kind $T_n(x)$ for $u_0 = 1$; $u_1 = x$ and of the second kind $U_n(x)$ for $u_0 = 1$; $u_1 = 2x$. Fibonacci numbers F_n rise for $a = b = 1$; $u_0 = 0$; $u_1 = 1$. For $a = b = 1$; $u_0 = 2$; $u_1 = 1$, we obtain Lucas numbers L_n. Therefore, if in Chebyshev polynomials $i = \sqrt{-1}$ is used with $x = \frac{i}{2}$ the results are Lucas numbers L_n for Chebyshev polynomials of the first kind T_n, and Fibonacci numbers F_n for those of the second kind U_n. Rather than focus on numerology, difference and differential equations (for the underlying processes, since leaves and scales connect in space and time to the rest of the plant) remain central to understand natural processes.

This book is a nice introduction on mathematical phyllotaxis and recurrence, but the link to botany is lacking. Rozin provides many illustrations and videos, and claims that the study of real botany to prove his thesis will rely on ever better methods of computer vision. Apart from the questionable status of resolution, the choices made in such programs largely determine the outcome that one wishes for. The challenge to understand plant phyllotaxis remains wide open.

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MICROBIOLOGY

Bats and Viruses: Current Research and Future Trends.

Edited by Eugenia Corrales-Aguilar and Martin Schwemmle. Norfolk (United Kingdom): Caister Academic Press. $319.00 (paper). iv + 224 p.; ill.; index. ISBN: 978-1-912530-14-4 (pb); 978-1-912530-15-1 (eb). 2020.

Timing is everything. What could be more timely than a volume on bats and viruses published in 2020? Yet, as the editors themselves point out in the introduction, there are important gaps in the hypothesized connections between bats and zoonotic virus outbreaks. Thus, a book-length synthesis of the state of knowledge on this subject, even as it stood before the avalanche of new research in 2020, is very valuable. This volume provides a much-needed synthesis, with chapters summarizing the state of their fields as of 2019, including experimental studies, knowledge gaps and challenges, and guidance for future directions. As a panoramic review of bats and viruses spanning virology, immunology, and its subdisciplines, this book could be a mine of useful information and thoughtful synthesis and guidance, made all the more urgent by the COVID-19 pandemic. Regrettably, the volume is unlikely to reach its audience for reasons that have nothing to do with its relevance or content.

With a large diversity of viruses and bat hosts to survey, the book is organized into three broad sections. The first section focuses on chapter-by-chapter surveys of virus families and the second is centered on bats as hosts, their immunity, and any other special traits relevant to their interactions with viruses. Although coronaviruses are the focus of sustained global attention at the moment, and the corresponding chapter is a good introduction to the state of the art just before the COVID-19 pandemic, other virus families hold the imagination as well. In the flavivirus summary, for example, we learn that Tamana cave, Trinidad, is also the home of the Tamana bat virus with no known arthropod vector (X. de Lamballerie et al. 2002. *Journal of General Virology* 83:2443–2454). There are, however, curious omissions, with no chapter on filoviruses or paramyxoviruses (e.g., henipaviruses), both of which groups are of growing interest because of recent hypothesized or recorded spillover events originating in bats (J. F. Drexler et al. 2012. *Nature Communications* 3:796; C. E. Brook et al. 2020. *eLife* 9:e48401). Perhaps the current state of evidence at the time the book was assembled was insufficient for the kind of summary presented in each of the other chapters (E. C. Teeling et al. 2018. *Annual*

Review of Animal Biosciences 6:23–46; D. J. Becker et al. 2019. *Biology Letters* 15:20190423). Three chapters, on innate immunity, adaptive immunity, and traits that may make bats special viral hosts provide a good introduction to the rapidly growing—but still nascent—field of bat host biology (e.g., M. L. Baker and T. Schountz. 2018. Mammalia: Chiroptera: immunology in bats. Pages 839–862 in *Advances in Comparative Immunology*, edited by E. L. Cooper. Cham (Switzerland): Springer International Publishing; A. Banerjee et al. 2020. *Frontiers in Immunology* 11:26; A. T. Irving et al. 2020. *Cell Reports* 33:108345). A final section, on methods, presents in vitro, in vivo, and field-based methods for viral surveillance, rounding off this wide-ranging survey of the evolution and ecology of bat-borne viruses.

Although the book provides good syntheses on bat biology, solid summaries of (some) bat-borne viruses, and careful surveys of a range of methods, this volume will unfortunately be largely inaccessible to most of its potential audience. Due to its high price for the print or electronic version, only very well-resourced libraries will be able to afford it. Students seeking brief introductions to the subject, scientists in developing countries, or those in developed countries with shrinking library budgets will have to instead turn to individual articles, some of which are open access (e.g., Banerjee et al. 2020). Although open access publishing is too costly for many authors, there are successful examples of edited volumes accessible to all (e.g., C. C. Voigt and T. Kingston. 2016. *Bats in the Anthropocene: Conservation of Bats in a Changing World.* Cham (Switzerland): Springer International Publishing). In this case, the price stands in the way of the book meeting its readers; the authors would have been better served by publishing their concise and pithy chapters in open access or society journals.

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AVIAN VIROLOGY: CURRENT RESEARCH AND FUTURE TRENDS.

Edited by Siba K. Samal. Norfolk (United Kingdom): Caister Academic Press. $399.00 (paper). v + 411 p.; ill.; index. ISBN: 978-1-912530-10-6 (pb); 978-1-912530-11-3 (eb). 2019.

DEFROSTING ANCIENT MICROBES: EMERGING GENOMES IN A WARMER WORLD.

By Scott O. Rogers and John D. Castello. Boca Raton (Florida): CRC Press (Taylor & Francis Group). $129.95 (hardcover); $64.95 (paper). xxiv + 230 p.; ill.; index. ISBN: 978-0-367-22350-2 (hc); 978-0-367-22262-8 (pb). 2020.

Through many eons, life has adapted and caused profound changes on our planet. How do we reconstruct events that happened in the past, which undoubtedly shaped the Earth biome of today? Answering this question is essential for understanding life on Earth and the search for life in the universe. There are very few conserved test beds that allow biologists to travel back in time. The biological record consists of specific genetic, molecular, and architectural patterns that compose vibrant, extant life. The geologic record relies upon interpreting chemical, environmental, and fossil traces of deceased life preserved in the rocks. Both of these records are indirect and incomplete pictures of past life, mainly because they are restricted in their own ways to those traces that are amenable to study.

Rogers and Castello focus on another and more direct record to revive the ancient biology on Earth: ice. Unlike their more fragile eukaryotic cousins (trees, animals, mushrooms), microbes persist quite well under extreme freezing conditions, and can often be "resurrected" after prolonged exposure to plunging temperatures. Resurrecting life frozen in time provides a much more direct glimpse of ancient genomes and atmospheric composition. The ice record is subject to its own unique restrictions; most pointedly, the oldest ice on Earth is on the order of about a few million years old, while Earth is a staggering 4.5 billion years old.

What sets the ice record truly apart is that it inhabits the vast gray gulf of inanimacy between the dynamically vibrant and resolutely deceased endmembers respectively covered by the biological and geological datasets. We have not yet encountered natural conditions where life spontaneously emerges, and we cannot yet engineer such conditions in an idealized laboratory setting. This indicates that there is a tremendous gap in our understanding of what separates the living and nonliving. For this reason alone, we need access to every dataset available to probe the extent (and limits) of living systems.

The authors take us on a comprehensive and insightful journey, centered on life preserved in ice, which allows us to grasp the overwhelming complexity and diversity of life on Earth from protist evolution to the impact of viruses for evolution and sustainability of life on Earth, as well as the science behind studying permafrost microbiology. They comprehensively discuss how ice can preserve essential clues to life's past, origins, and likely presence