



A 16th-century mathematician's role in determining the closest packing formation of spheres is described. And another 16th-century history lesson is offered on the heretical ideas of Giordano Bruno: "He found it easy to accept the Copernican view that Earth moved around the sun because he thought Earth itself was alive and so, of course, it could move....For Bruno, the entire universe was alive." Proposed nomenclature guidelines for the genetic classification of HIV-1 strains are outlined. And it is suggested that a dynamic system (a laser beam) that appears chaotic on short time scales but was found to produce regular patterns when observed over longer periods of time might be an example of symmetric chaos.

From Cannon Balls to Yeast Cells

In connection with the News Focus article "Random packing puts mathematics in a box" (Charles Seife, 17 Mar., p. 1910) about "random" versus "close" packing of uniform spheres, it is worth mentioning that English mathematician Thomas Harriot (1560–1621) performed some of the first packing calculations. His correspondence with Johannes Kepler (1) subsequently led to Kepler's famous "conjecture" on the most efficient density, which is close to 74%. Harriot was intellectual advisor to Sir Walter Raleigh, who was at the time most interested in stacking cannonballs on his ships. The same principles hold for all sizes of spheres. For example, mature yeast cells have a packing density of about 78% (2); the small difference from theory is primarily attributed to a slight departure from spherical shape.

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References and Notes

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Background on Bruno

I should like to raise two points about Giordano Bruno's martyrdom (Random Samples, "Burned by history," 10 Mar., p. 1743). In 1600, Bruno, a Dominican friar, was declared a heretic by the Inquisition and burned at the stake, an event the Catholic Church has now said was a "sad episode." Although Bruno is endeared to scientists for having "embraced Copernicus's heliocentric model of the solar system" and having "declared that Earth might be only one of an infinite number of worlds inhabited by beings entirely foreign to humans," in fact he went much further than most scientists today might

find endearing. He found it easy to accept the Copernican view that Earth moved around the sun because he thought Earth itself was alive and so, of course, it could move. And he taught not only that the infinite worlds were inhabited, but that they too were alive. For Bruno, the entire universe was alive. The stars consisted of living worlds prowling through space like Blake's Tyger, burning bright in the forests of the night.

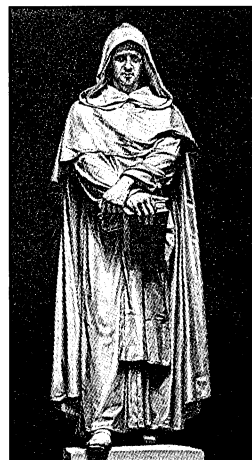
Of course, none of these ideas were based on observational evidence, or on anything resembling a scientific theory, but that does not excuse the Catholic Church for burning him alive. Cardinal

Angelo Sodano referred to this event as an "atrocious death," according to the Random Samples item, but his implied justification for burning Bruno at the stake, that the Inquisition used then-common methods, is nearly as atrocious as the act itself. It begs the question, to whom were these methods common? Only to such monsters as the Inquisition.

Cardinal Sodano said further that the Inquisition "did everything possible to save his life." What they actually did was carry him through the streets of Rome, naked, gagged, and tied to a stake. In the Square of the Flowers before the Theatre of Pompey, the Master Inquisitor stood in front of Bruno with a lit torch in one hand and a picture of Christ in the other, demanding repentance. When Bruno turned his head away, the fire was lit.

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HIV-1 Nomenclature Proposal

A clear and consistent genetic classification of human immunodeficiency virus–type 1 (HIV-1) strains continues to be of great utility in epidemiological tracking of the AIDS pandemic and in vaccine design. It also provides a foundation for detecting any biological differences that may have evolved during the diversification of these viruses. Over the past few years, expanding access to diverse HIV-1 samples from throughout the world, coupled with improved polymerase chain reaction (PCR) amplification and sequencing technologies, has led to the discovery of ever-increasing numbers of sequences that do not fit well into the standard HIV-1 subtyping nomenclature. Two issues of particular importance that have needed to be resolved were the classification of related recombinant viruses that are epidemic strains and the minimum criteria for designating a new subtype. A working group was convened to discuss HIV-1 nomenclature, and the participants arrived at a proposal (1) that resolves current ambiguities and retains as much as possible of the nomenclature system that has been adopted over the past 10 years. The salient points of the proposal are the following.

♦ The three distantly related "groups" of HIV-1 viruses that have been previously established are M (for main), N (for non-M, non-O), and O (for outlier) (2). If new groups are discovered, they should be named by continuing through the alphabet: P, Q, R, etc.

♦ Subtypes will continue to refer to the distinctive lineages within group M, the group of viruses that dominates the AIDS pandemic. The subtype designations A to D, F to H, J, and the newly defined K (3) will be retained. As new subtypes are discovered, they will be named by continuing through the alphabet, so that there could eventually be a group M, subtype N virus (written M:N when a distinction is required).

♦ Sub-subtype designations will be used to describe distinctive lineages that are not genetically distant enough to justify designating a new subtype. For example, distinct lineages that form sister clades within subtype F have been named sub-subtypes F1 and F2 (3).

♦ Recombinant viruses that are epidemic strains will be called circulating recombinant forms (CRFs) (4) and numbered sequentially, with the first fully sequenced virus of a CRF serving as the prototype. There are currently four defined CRFs (1). For example, CRF02_AG

(IbNg) refers to the second CRF that was defined; it is common in parts of Africa and contains regions that resemble A and G subtypes, with a prototype sequence called IbNg. Mosaic viruses with regions that resemble four or more subtypes will be called complex, and designated cpx.

It has become apparent that two previously designated subtypes, E and I, are problematic. Subtype E has a high prevalence in many parts of Asia and is considered a recombinant between subtypes A and E (5), although no full-length subtype E representatives have been found. Some participants at the meeting argued that mechanisms other than recombination might underlie the observed phylogenetic patterns found among these viruses (J.P.A. and G.H.L., also J. I. Mullins, University of Washington, Seattle, WA, USA, and A. G. Rodrigo, University of Auckland, Auckland, New Zealand). Most participants, however, thought that recombination was the most likely explanation of the data and thus voted to rename subtype E as CRF01_AE, retaining the E subtype designation in the name to refer to the non-subtype A regions. In the future, such CRF segments for which a parental strain cannot be determined will be labeled U for

unknown; the CRFs will retain a numerical descriptor so they will be distinguishable. Similarly, it was decided that previously designated "subtype I" viruses (6) should now be designated CRF04_cpx.

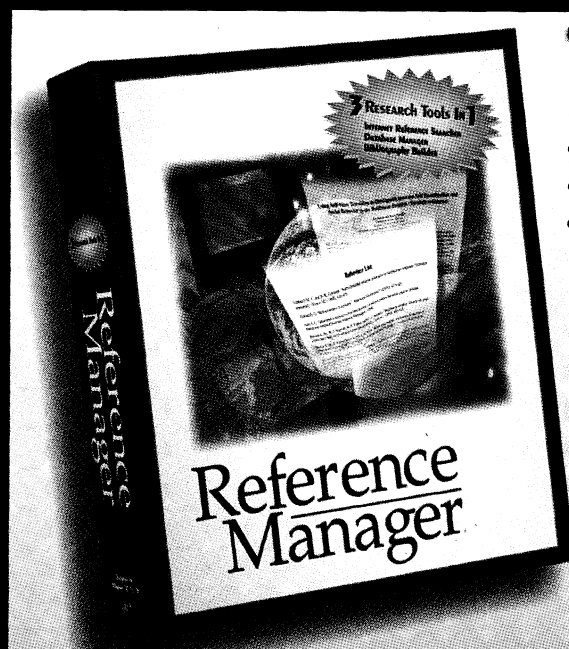
Before a new subtype, sub-subtype, or CRF is named, three representative full-length genomes should be sequenced that are obtained from individuals who do not have direct epidemiologically linked infections. Under circumstances where only two complete genomes are available, a new designation can be made if a partial sequence or sequences cluster tightly with them (to define a CRF, the partial sequences must also confirm the CRF's mosaic structure). Unusual variants should be designated U until classification criteria are met. An interactive tool has been developed to aid researchers in distinguishing between subtypes and sub-subtypes on the basis of genetic distance analyses (7). It should be emphasized, however, that all distance analyses should be backed up with detailed phylogenetic and recombination analyses. Authors should consult the HIV database before designating a new subtype to ensure that new designations are only assigned once (contact B.K. at btkt@t10.lanl.gov, or C.K. at kuiken@t10.lanl.gov). Finally, it would

be helpful to the field if a simplified version of the World Health Organization nomenclature to name HIV sequences (8) was more generally adopted, specifying the time and place of origin. In particular, sequences should be named with two digits to indicate the year of sampling, a two-letter country code designation that refers to the country where the person was living when sampled, and a unique laboratory identifier. For example, 92UG.seqID refers to a sequence derived from a Ugandan, sampled in 1992; seqID would be the study-specific designation for the sequence.

The full text of this proposal can be found at the Los Alamos HIV Sequence Database Web site (<http://hiv-web.lanl.gov>).

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9. We thank D. Birx and F. McCutchan of the U.S. Army and the Henry M. Jackson Foundation; J. Bradac of the National Institute of Allergy and Infectious Dis-

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Traces of Symmetric Chaos

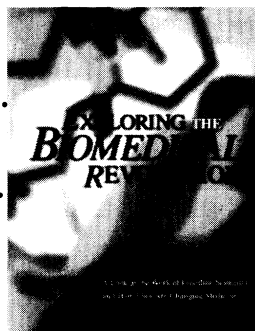
The Editors' Choice selection entitled "Chaos underlying order" (Phillip D. Szuro-mi, 18 Feb., p. 1169) describes the work of Encinas-Sanz *et al.* (1), in which regular pat-terns arise when a system that is chaotic on short time scales (a few nanoseconds) is ob-served over longer time scales (around 100 nanoseconds). Their system is a laser beam, the nonchaotic dynamics of which is well known to exhibit many symmetric patterns. This fact, together with the reference to "rolls" in the long-term pattern, suggests that this effect is probably an example of "symmetric chaos," in which a symmetric dynamical system has a chaotic attractor (2). This attractor usually has symmetry, al-though not necessarily the same symmetry as the overall system because of the possibil-ity that the symmetry could be broken. Short-term "snapshots" of the state of the system appear unstructured because short-term observations explore too small a region of the attractor for the overall symmetry to become apparent. Longer-term observations

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