Inside *Nature*:
visual communication in science publishing

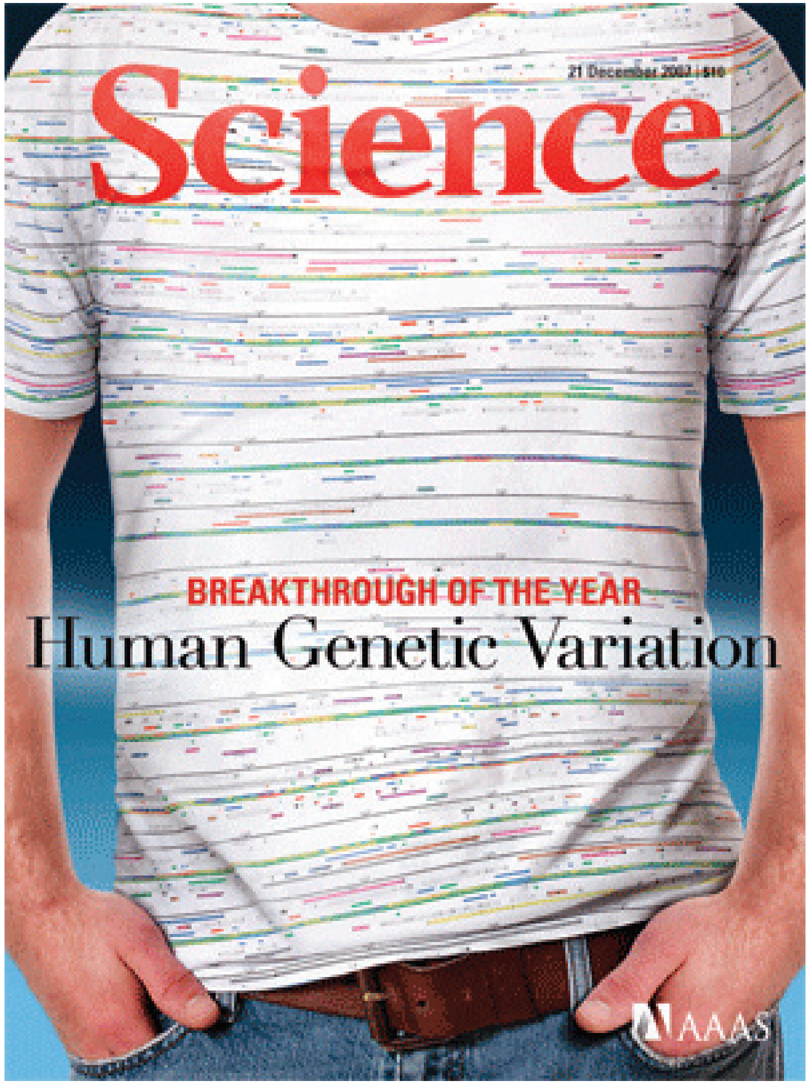
nature

Kelly Krause / Creative director

Part 1

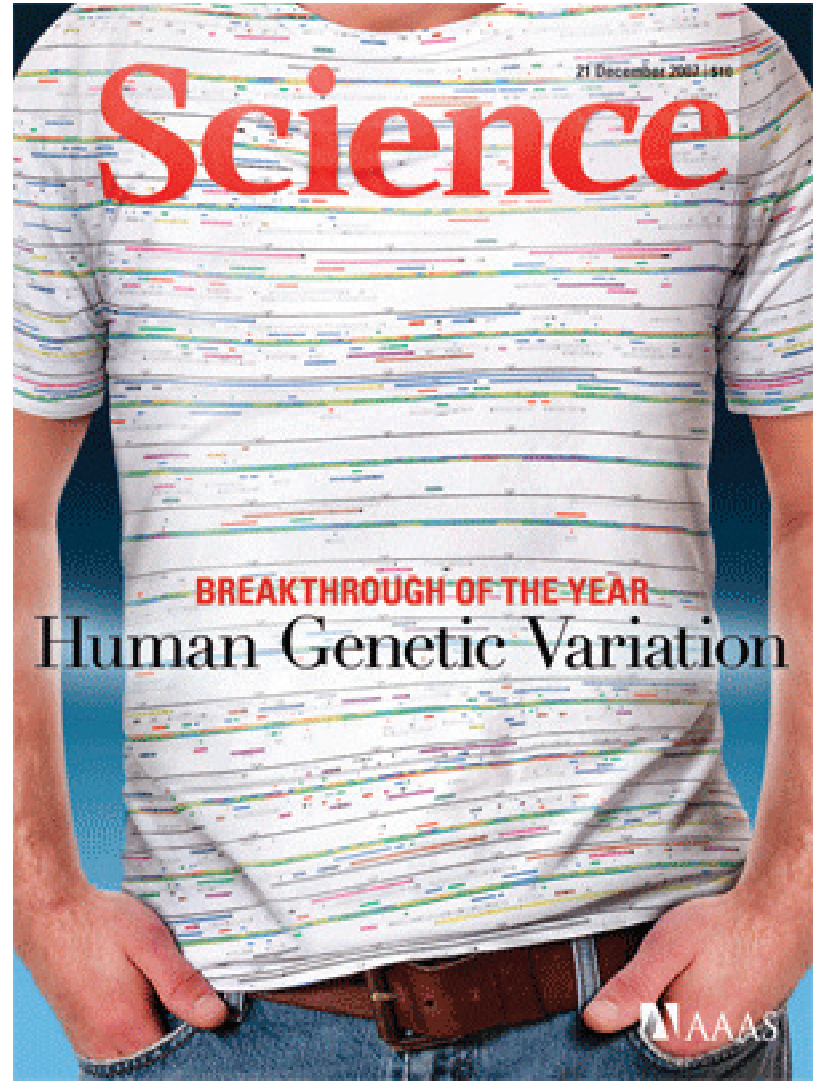
Introduction

since 1869



since 1880

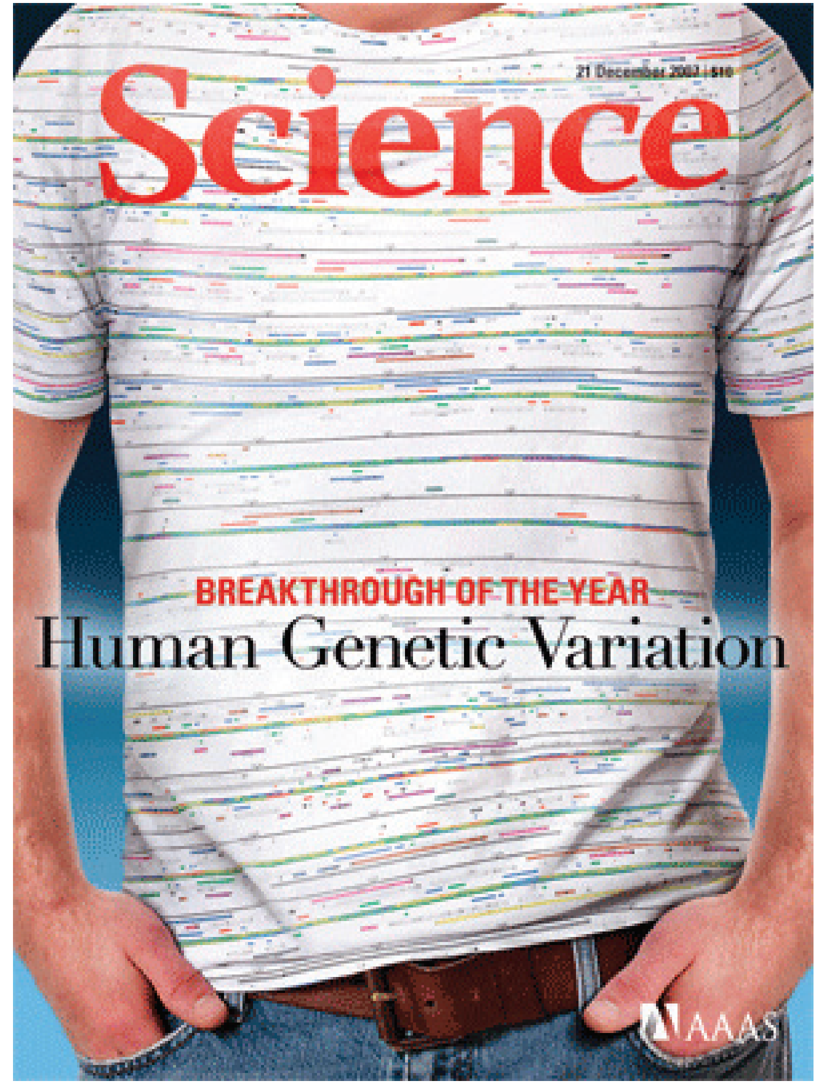
since 1869



since 1880

9 years = more than 450 issues; 90,000+ pages of images

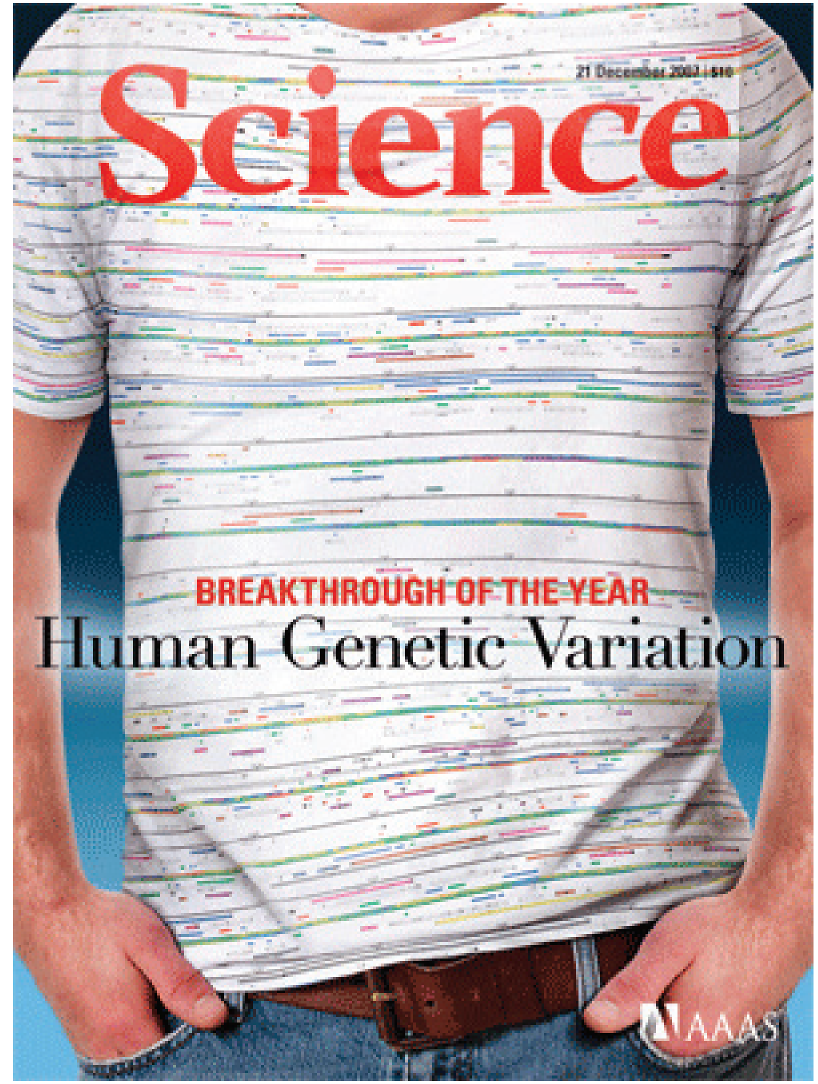
since 1869



since 1880

Multidisciplinary; fundamental breakthroughs

since 1869



since 1880

Half journal, half magazine

the team

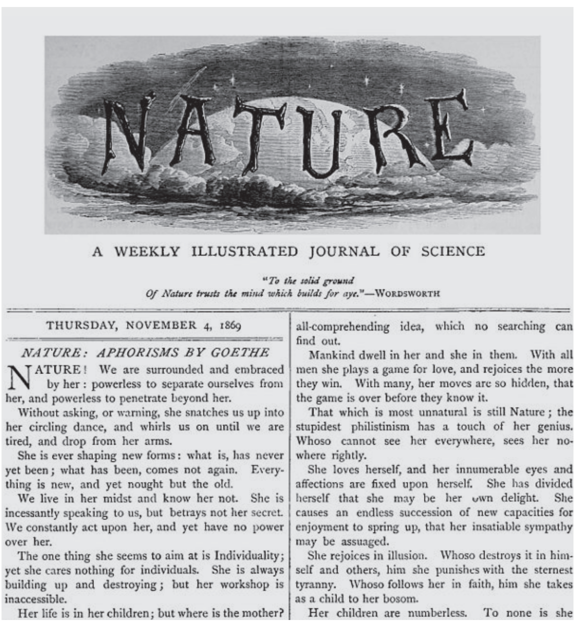
Part 2

Publishing fundamentals

Why do we publish?

Why do we publish?

Archive
knowledge


NATURE

A WEEKLY ILLUSTRATED JOURNAL OF SCIENCE

"To the solid ground
Of Nature trusts the mind which builds for aye."—WORDSWORTH

THURSDAY, NOVEMBER 4, 1869

NATURE: APHORISMS BY GOETHE

NATURE! We are surrounded and embraced by her: powerless to separate ourselves from her, and powerless to penetrate beyond her.

Without asking, or warning, she snatches us up into her circling dance, and whirls us on until we are tired, and drop from her arms.

She is ever shaping new forms: what is, has never yet been; what has been, comes not again. Everything is new, and yet nought but the old.

We live in her midst and know her not. She is incessantly speaking to us, but betrays not her secret. We constantly act upon her, and yet have no power over her.

The one thing she seems to aim at is Individuality; yet she cares nothing for individuals. She is always building up and destroying; but her workshop is inaccessible.

Her life is in her children; but where is the mother? all-comprehending idea, which no searching can find out.

Mankind dwell in her and she in them. With all men she plays a game for love, and rejoices the more they win. With many, her moves are so hidden, that the game is over before they know it.

That which is most unnatural is still Nature; the stupidest philistinism has a touch of her genius. Whoso cannot see her everywhere, sees her nowhere rightly.

She loves herself, and her innumerable eyes and affections are fixed upon herself. She has divided herself that she may be her own delight. She causes an endless succession of new capacities for enjoyment to spring up, that her insatiable sympathy may be assuaged.

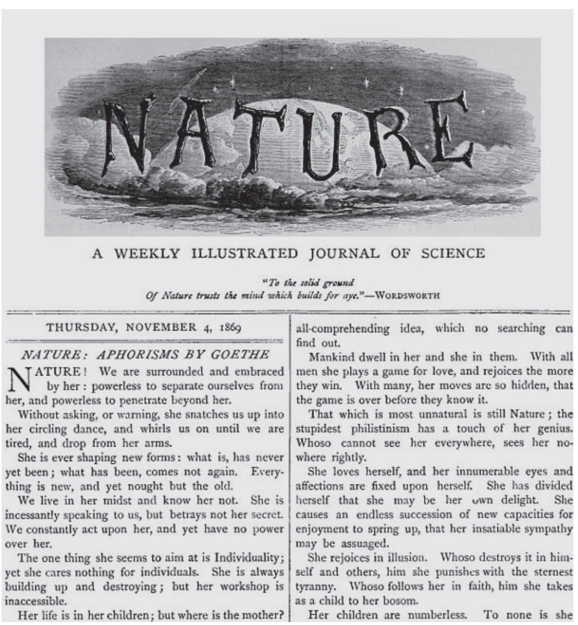
She rejoices in illusion. Whoso destroys it in himself and others, him she punishes with the sternest tyranny. Whoso follows her in faith, him she takes as a child to her bosom.

Her children are numberless. To none is she

Nov 1869

Why do we publish?

Archive knowledge



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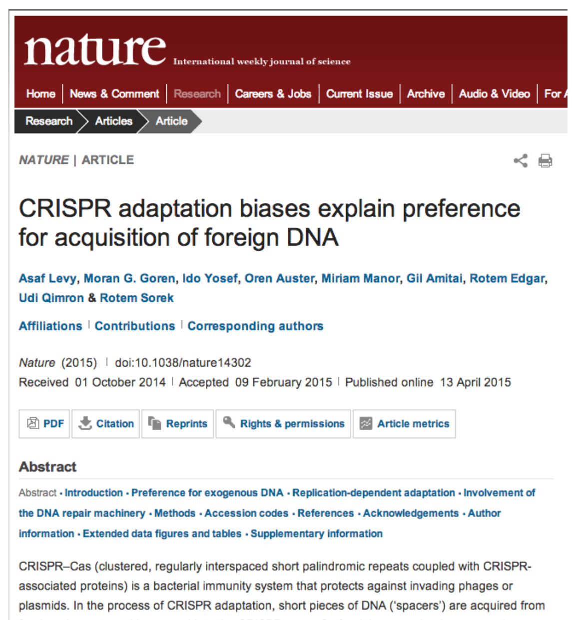
Nov 1869

Communicate ideas quickly



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NATURE | ARTICLE

CRISPR adaptation biases explain preference for acquisition of foreign DNA

Asaf Levy, Moran G. Goren, Ido Yosef, Oren Auster, Miriam Manor, Gil Amitai, Rotem Edgar, Udi Qimron & Rotem Sorek

Affiliations | Contributions | Corresponding authors

Nature (2015) | doi:10.1038/nature14302

Received 01 October 2014 | Accepted 09 February 2015 | Published online 13 April 2015

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Abstract

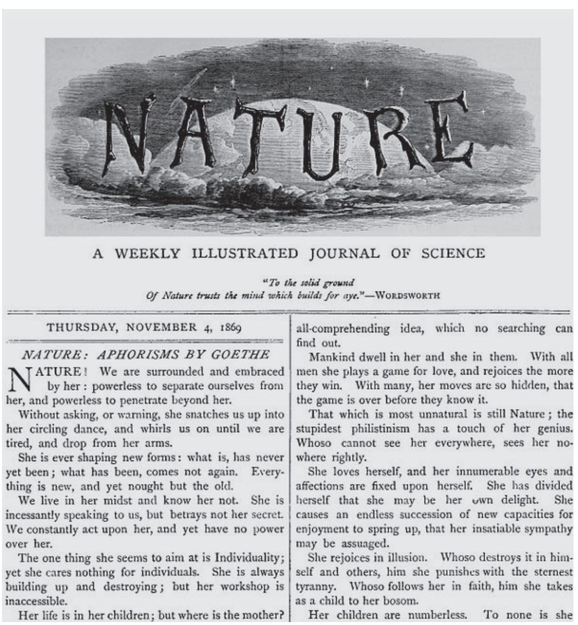
Abstract • Introduction • Preference for exogenous DNA • Replication-dependent adaptation • Involvement of the DNA repair machinery • Methods • Accession codes • References • Acknowledgements • Author information • Extended data figures and tables • Supplementary information

CRISPR–Cas (clustered, regularly interspaced short palindromic repeats coupled with CRISPR-associated proteins) is a bacterial immunity system that protects against invading phages or plasmids. In the process of CRISPR adaptation, short pieces of DNA ('spacers') are acquired from foreign elements and integrated into the CRISPR array. So far, it has remained a mystery how

April 2015

Why do we publish?

Archive knowledge



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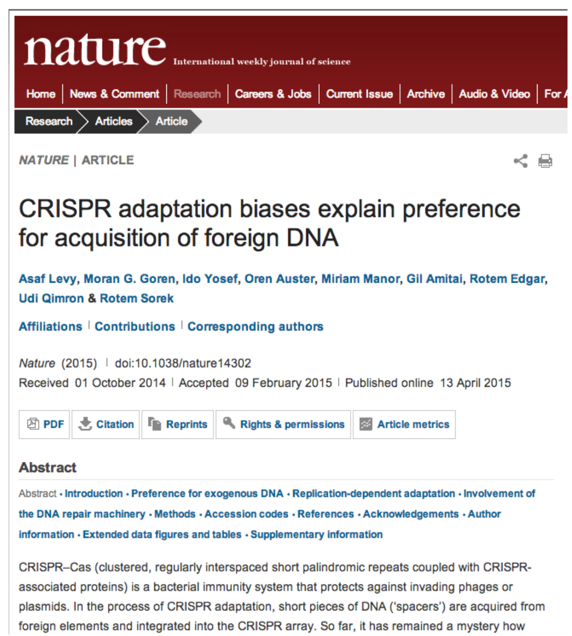

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Research > Articles > Article

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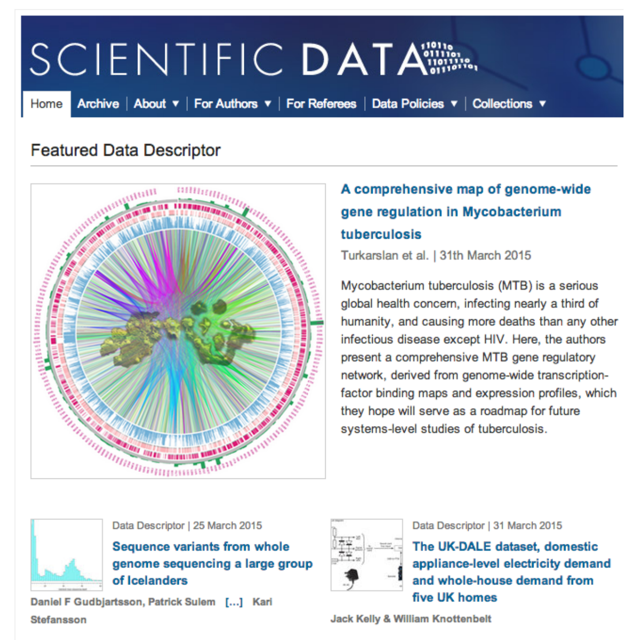
April 2015

Discuss ideas in context



SCIENTIFIC DATA

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Featured Data Descriptor

A comprehensive map of genome-wide gene regulation in Mycobacterium tuberculosis

Turkarslan et al. | 31th March 2015

Mycobacterium tuberculosis (MTB) is a serious global health concern, infecting nearly a third of humanity, and causing more deaths than any other infectious disease except HIV. Here, the authors present a comprehensive MTB gene regulatory network, derived from genome-wide transcription-factor binding maps and expression profiles, which they hope will serve as a roadmap for future systems-level studies of tuberculosis.

Data Descriptor | 25 March 2015

Sequence variants from whole genome sequencing a large group of Icelanders

Daniel F Gudbjartsson, Patrick Sulem [...] Kari Stefansson

Data Descriptor | 31 March 2015

The UK-DALE dataset, domestic appliance-level electricity demand and whole-house demand from five UK homes

Jack Kelly & William Knottenbelt

launched 2014

newsstand at London Stansted airport

Context informs design and aesthetics

newsstand at London Stansted airport

Context informs design and aesthetics

newsstand at London Stansted airport

Context informs design and aesthetics

newsstand at London Stansted airport

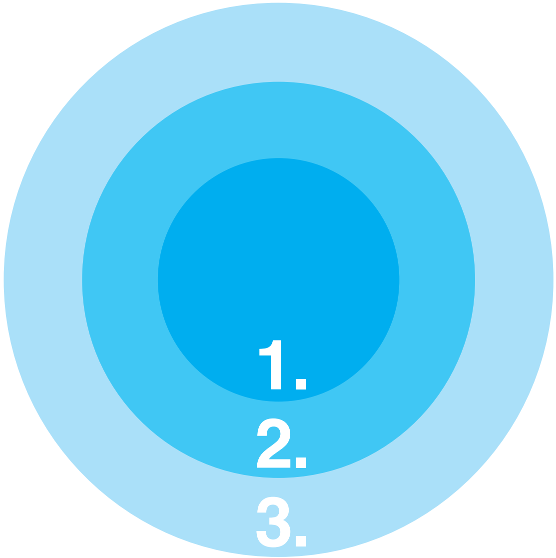
Context:

Who is the audience?

1. Narrow scientific; highly technical

2. Wider scientific

3. Science policy makers, educated science-interested public



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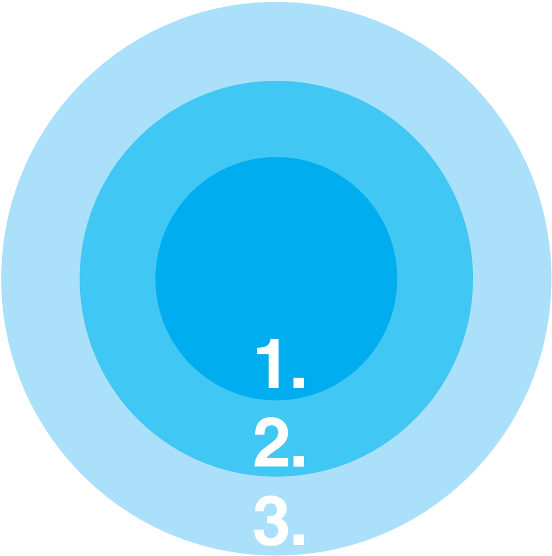


what

What is the appropriate visual language in this case?

how

How do we create this within time and budget constraints?

Part 3

Types of images in context

Research figures

Technical data representation in peer-reviewed research papers

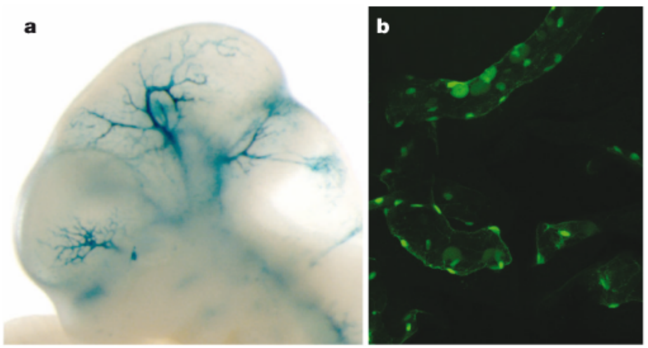
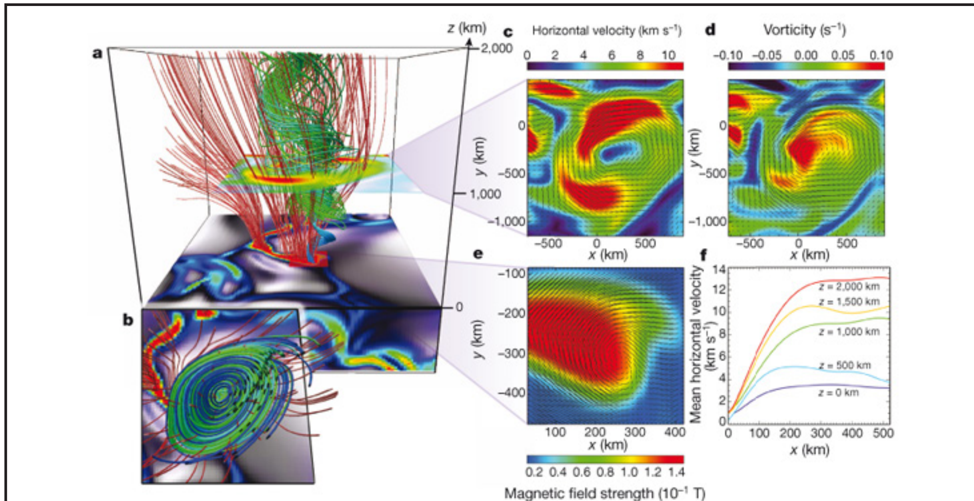


Figure 6 | Experimental characterization of segmentations. Randomly sampled E state segments (see Table 3) from the K562 segmentation were cloned for mouse- and fish-based transgenic enhancer assays. **a**, Representative LacZ-stained transgenic embryonic day (E)11.5 mouse embryo obtained with construct hs2065 (EN167, chr10: 46052882–46055670, GRCh37). Highly reproducible staining in the blood vessels was observed in 9 out of 9 embryos resulting from independent transgenic integration events. **b**, Representative green fluorescent protein reporter transgenic medaka fish obtained from a construct with a basal *hsp70* promoter on meganuclease-based transfection. Reproducible transgenic expression in the circulating nucleated blood cells and the endothelial cell walls was seen in 81 out of 100 transgenic tests of this construct.



3 | **Numerical model of a swirl event produced with CO5BOLD.** displayed close-up region (**a**) is part of the evolved model, which has ll horizontal size of 8,000 km × 8,000 km and extends vertically from below the surface to the top of the chromosphere at an altitude of

co-rotates with the magnetic field, resulting in spiral trajectories (blue– streamlines following the velocity field). The swirl is clearly seen in the horizontal velocity (**c**) and the vorticity (**d**) in horizontal cross-sections height of $z = 1{,}000$ km (middle chromosphere). The arrows map the hori

1.

Research figures

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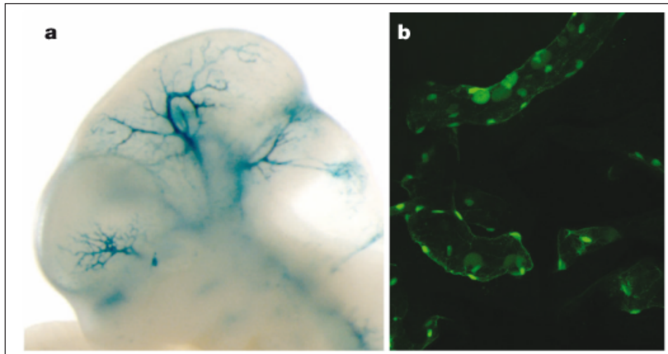

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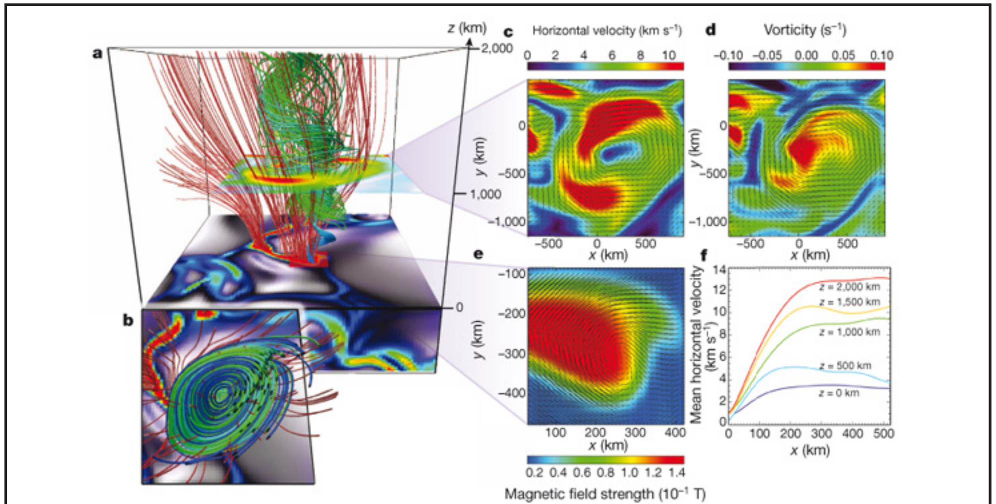

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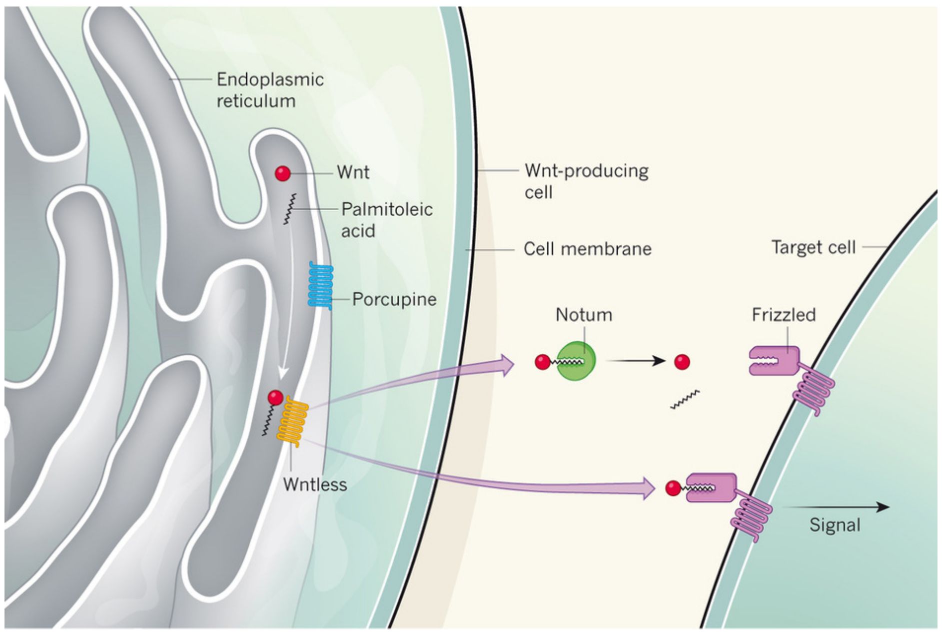
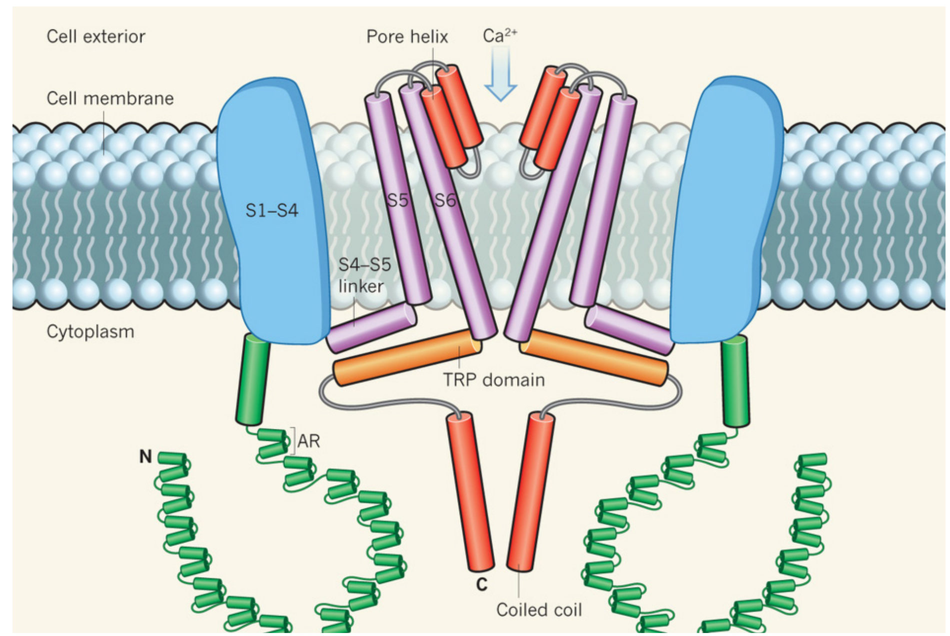
Respect the 'vernacular' of each scientific discipline while urging best practices

1.

Scientific illustration

Illustration that uses a simple visual language to explain a complex process





2.

Scientific illustration

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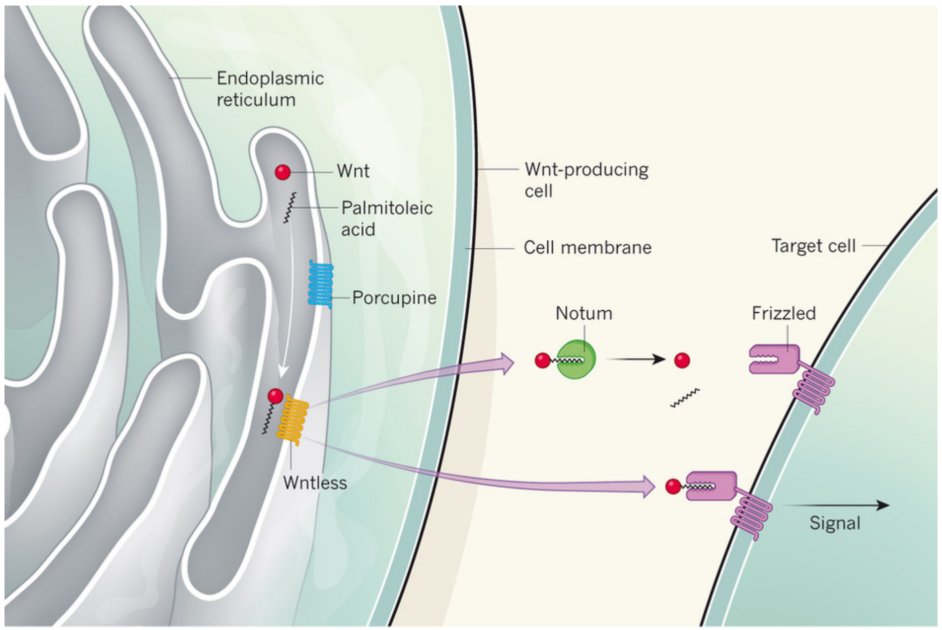
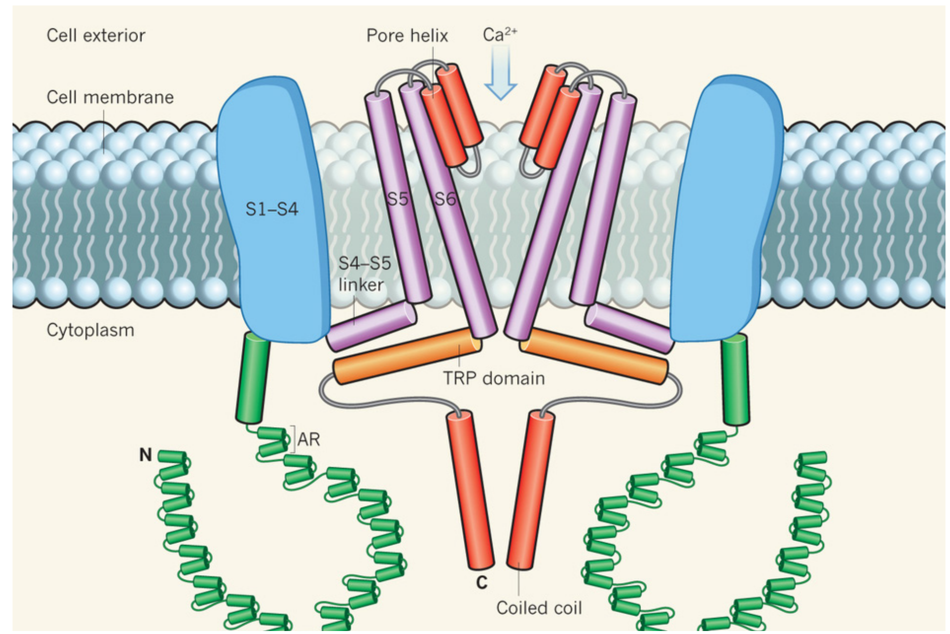
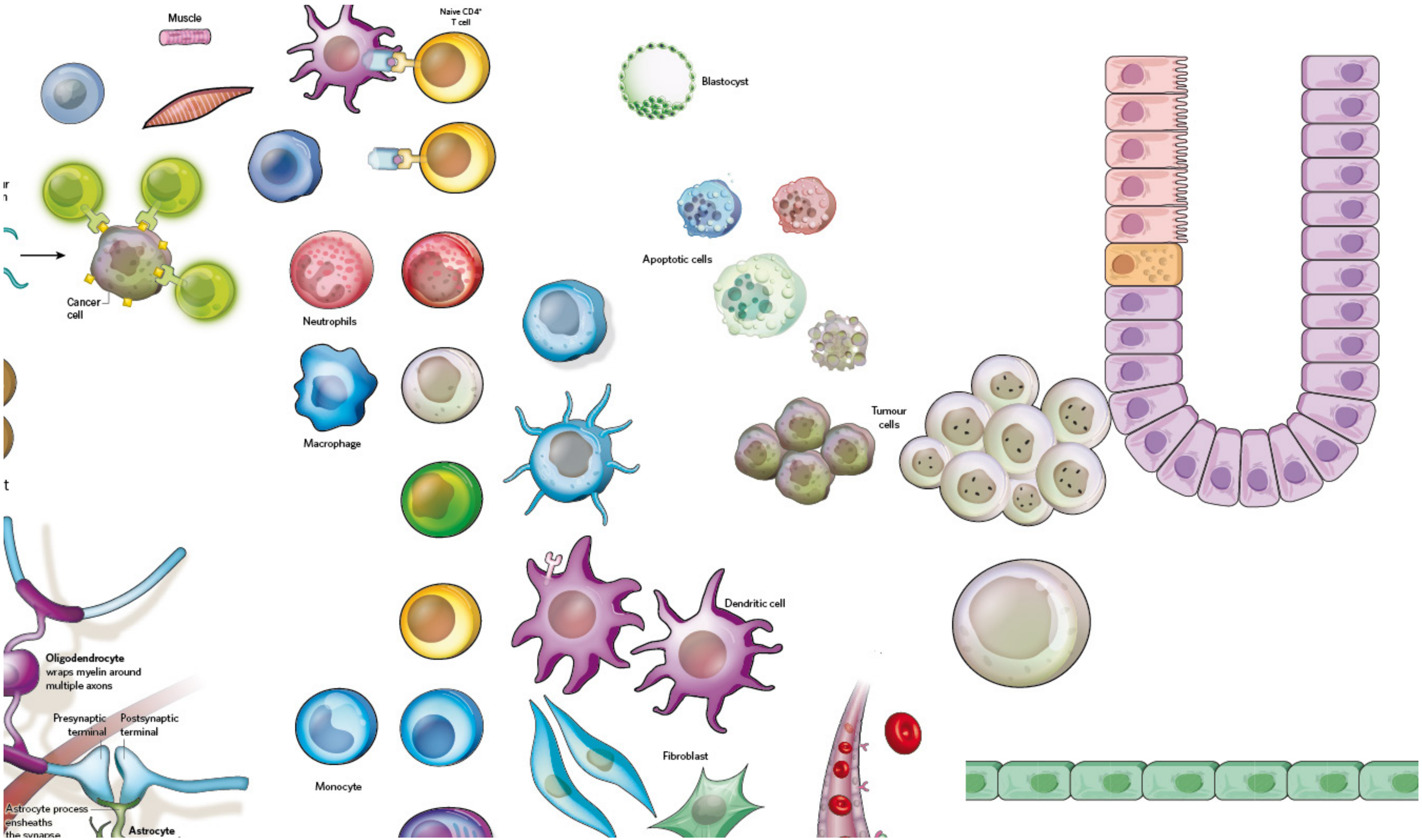




Visual language is a sign system

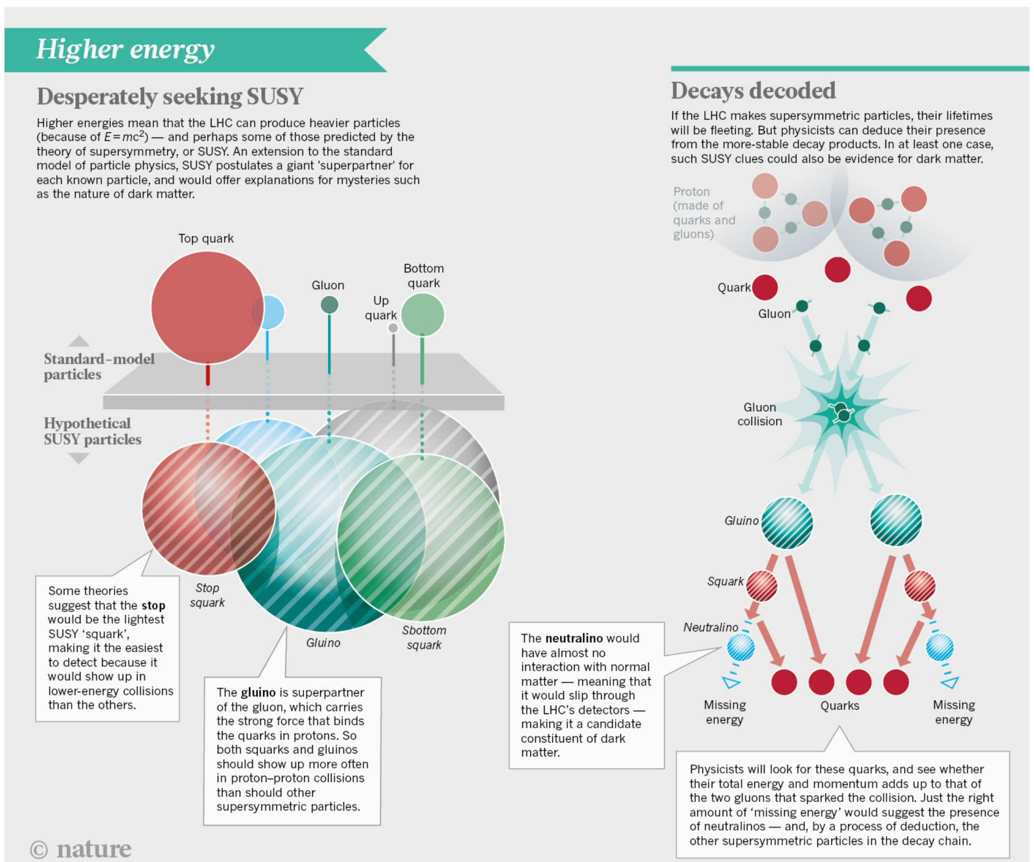
— Jacques Bertin, *Semiologie Graphique (Semiology of Graphics)*, 1967

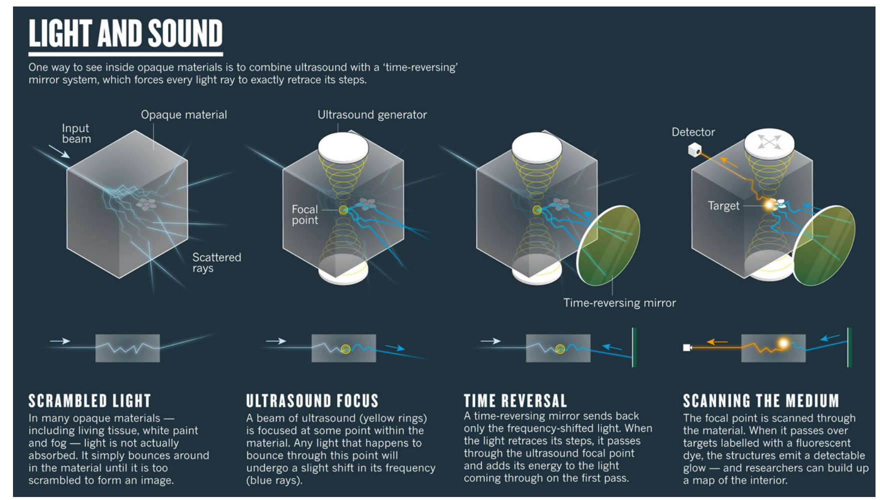
Example: sign system for cells



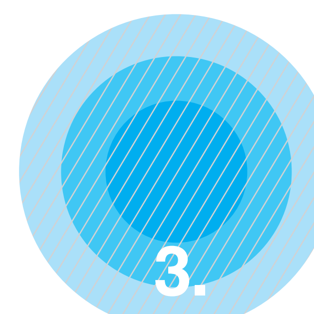
Infographics: Explanatory

Illustrations or diagrams used to explain a phenomenon, event or process



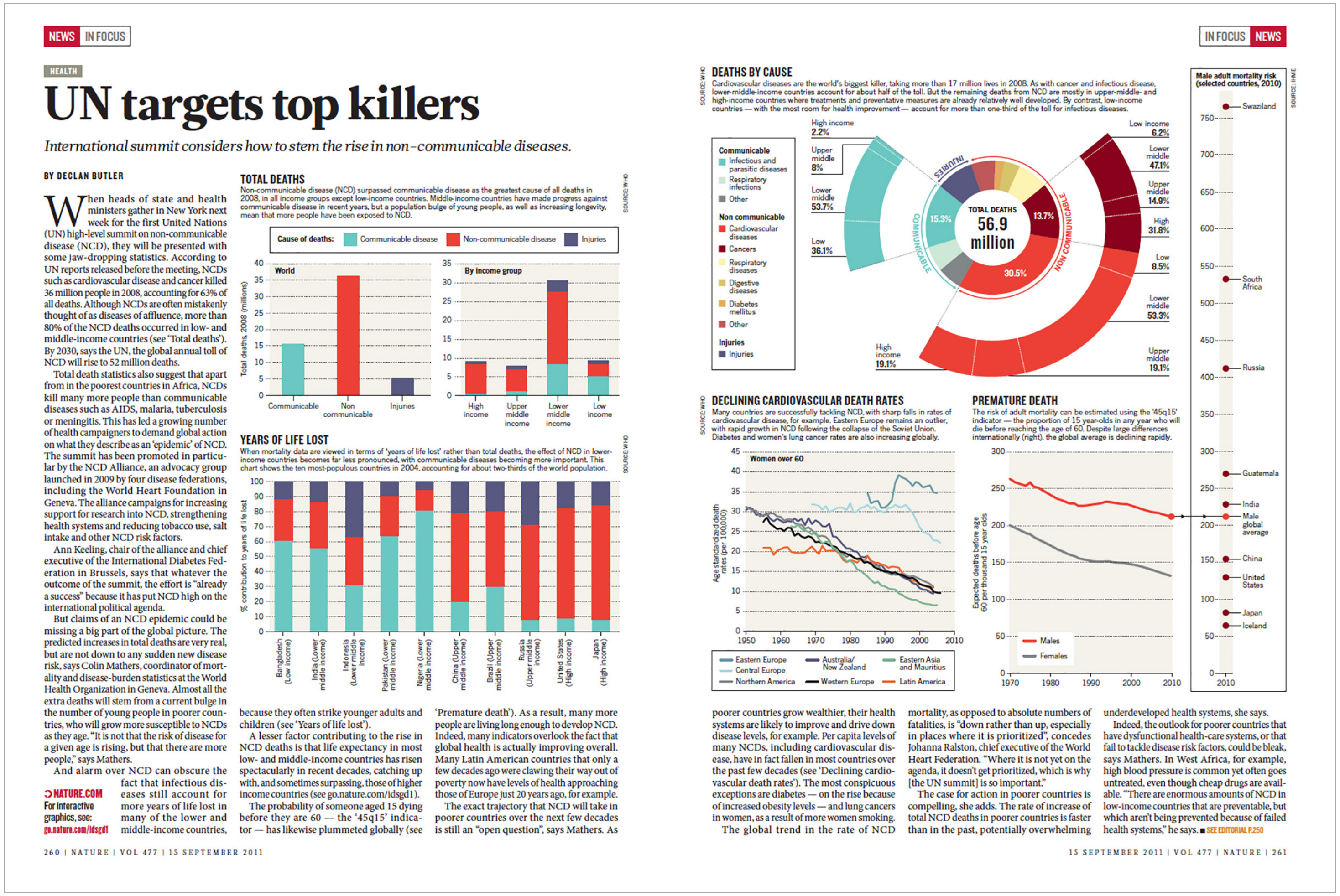


tip: Ask yourself, can this be explained well in words or would it be better visualised?



Infographics: Data display

Graphs and charts created from a set of numbers

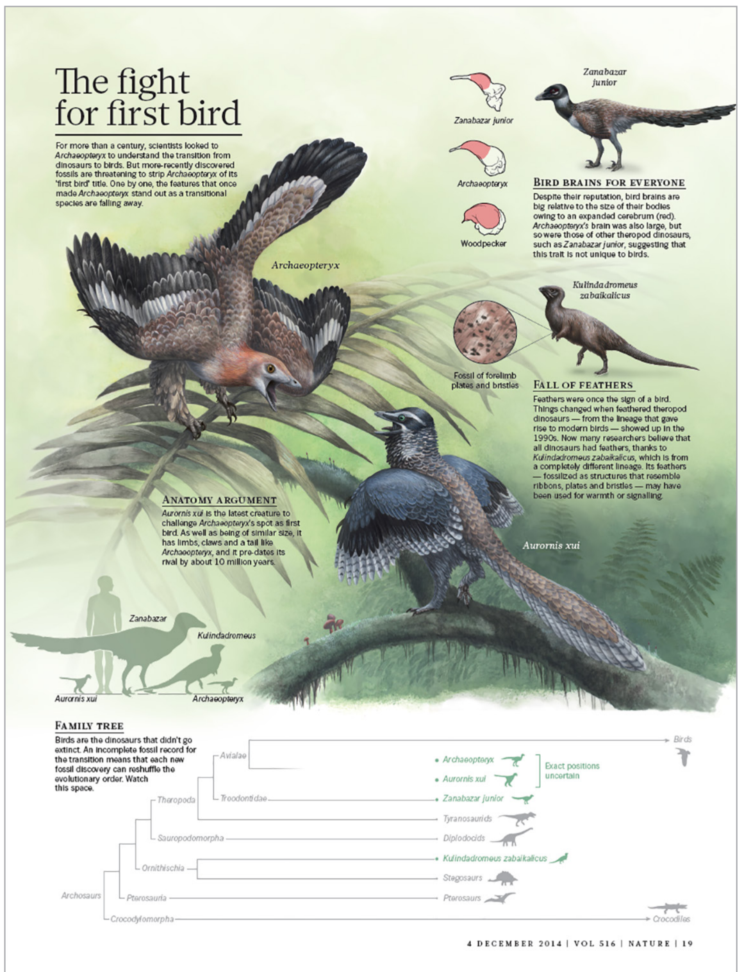


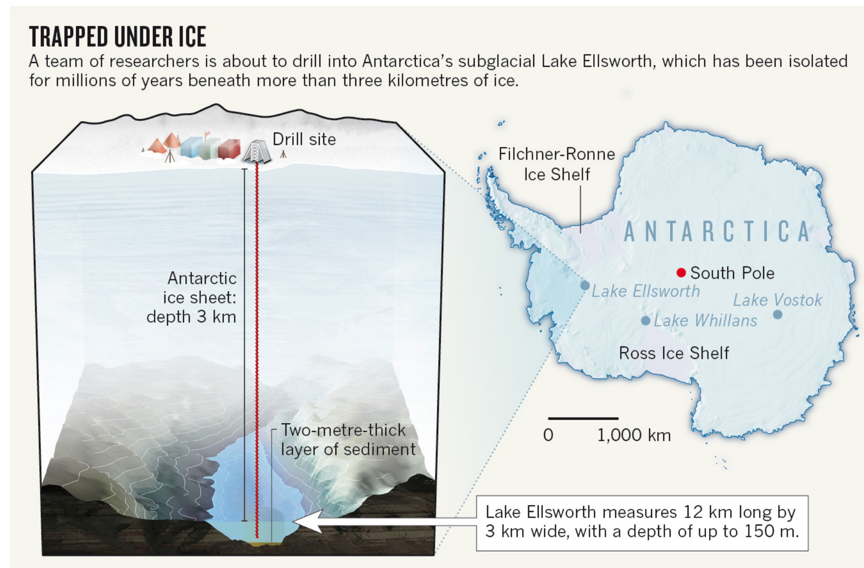
tip: Ask yourself, is the story in the numbers? Would the narrative be enhanced by showing the stats?

3.

Infographics: Contextual aid

Map, timelines and other comparisons that add important context





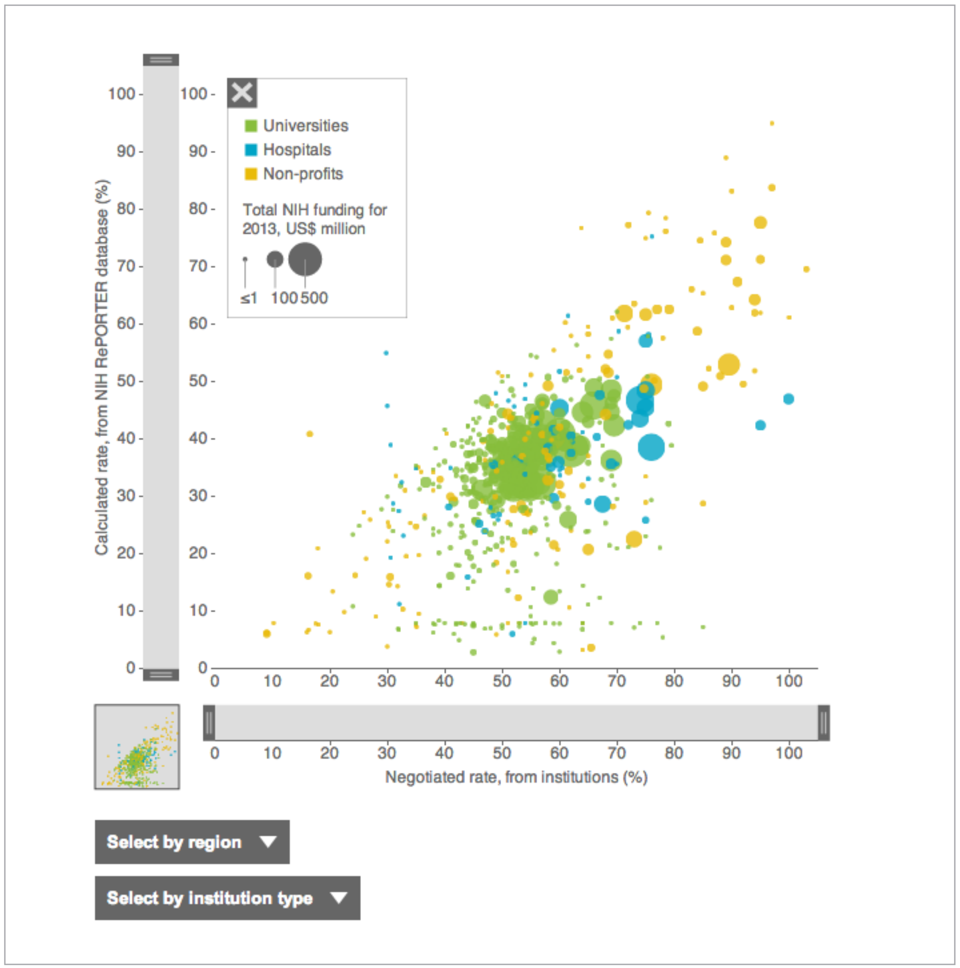
tip: Ask yourself . . .

- Could it be enhanced by context?
- Is this story part of a larger story?
- Will the reader need grounding in other knowledge to appreciate the story?

3.

Graphics: Interactive

Multi-layered graphics that can be interrogated/explored in a digital setting



tip: Interactivity is recommended when there are layers of information. (For example, time, quantity, and location all in one graph.)

Ask yourself . . .

- Is the archival burden low? (Is it news or research?)
- Do I have loads of clean data, and would it be useful to explore many layers of data at once?
- Would our audience would like a non-linear exploration of data? (Rather than an 'edited' static graph.)

Images: Scientific artist conceptions

Artist interpretation based on scientific data

3.

Images: Editorial illustration

Original art created for an editorial piece


ILLUSTRATIONS BY ALESSANDRO GOTTARDO

EVOLUTION

Lies we tell ourselves

Stuart West is inspired by Robert Trivers' evolutionary argument that self-deception is crucial to deceiving others effectively.

Nature is filled with exquisite examples of deception. Fireflies mimic the flashes of others to attract and eat them; birds make fake alarm calls

Trivers starts by making a clear and powerful case that conflict — common

ROBERT TRIVERS
DECEIT

ticated methods for producing and detecting deception. Trivers argues that deception itself may have been an important evolutionary force in selecting the large brains and intel-

tip: Ask yourself, would the piece benefit from original art?

Is the topic itself nuanced or highly original?

Can it bear the weight of being represented by conceptual art, which is by nature open to interpretation?

3.

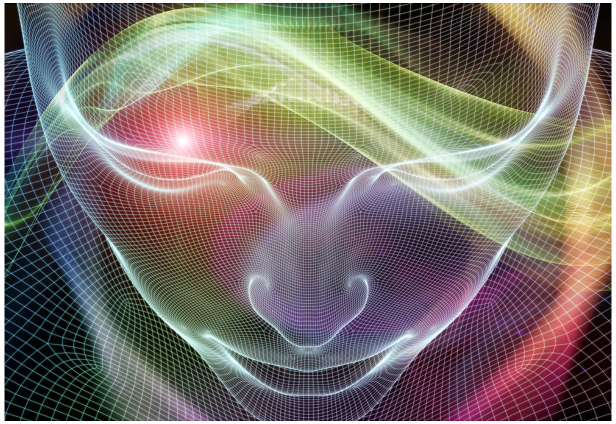
Part 4

A word on aesthetics

What do we mean by aesthetics?

origin:
perception

Mapping sensory attributes (form, color) to data to enable perception



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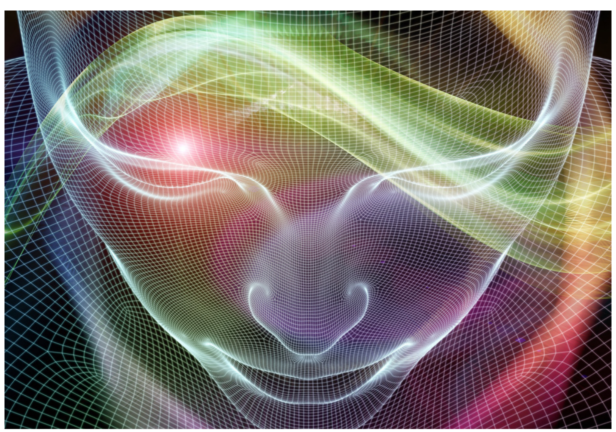

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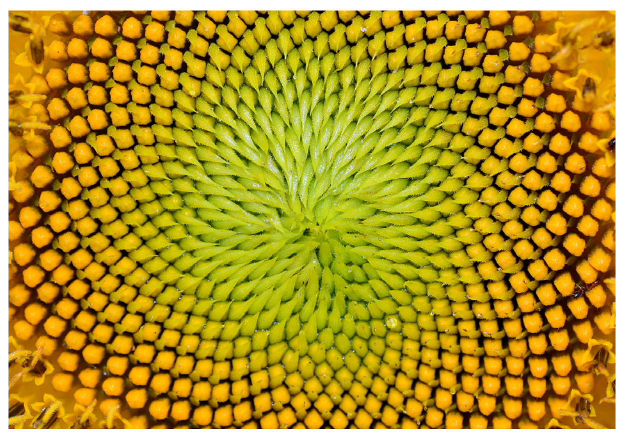
popular meaning:
beauty / taste

Does this appeal to my senses?



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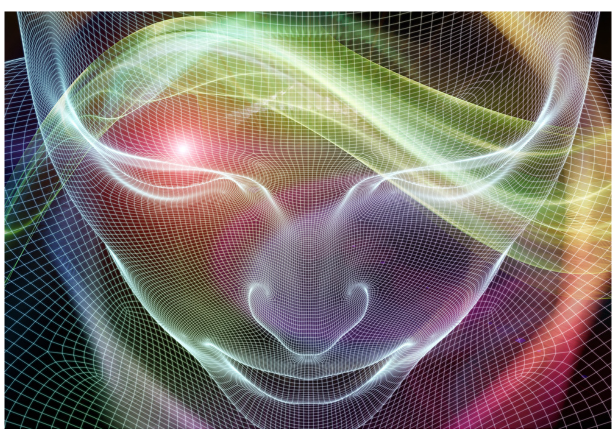

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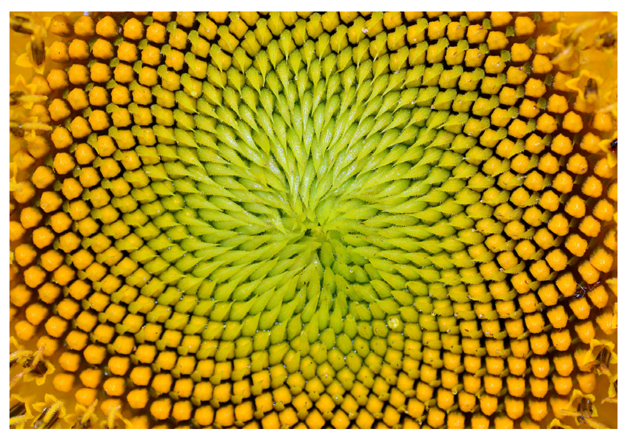

Shutterstock

scholarly:
fine art and philosophy

What is art?

theblogess.com/2012/12/but-is-it-art-no-its-hunter-s-thomcat/

Aesthetic attributes enable perception, which enables comprehension

anscombe's quartet

Statistically similar data sets reveal differences when graphed

I		II		III		IV	
x	*y*	*x*	*y*	*x*	*y*	*x*	*y*
10	8.04	10	9.14	10	7.46	8	6.58
8	6.95	8	8.14	8	6.77	8	5.76
13	7.58	13	8.74	13	12.74	8	7.71
9	8.81	9	8.77	9	7.11	8	8.84
11	8.33	11	9.26	11	7.81	8	8.47
14	9.96	14	8.10	14	8.84	8	7.04
6	7.24	6	6.13	6	6.08	8	5.25
4	4.26	4	3.10	4	5.39	19	12.5
12	10.84	12	9.13	12	8.15	8	5.56
7	4.82	7	7.26	7	6.42	8	7.91
5	5.68	5	4.74	5	5.73	8	6.89

Aesthetic attributes enable perception, which enables comprehension

anscombe's quartet

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x	*y*	*x*	*y*	*x*	*y*	*x*	*y*
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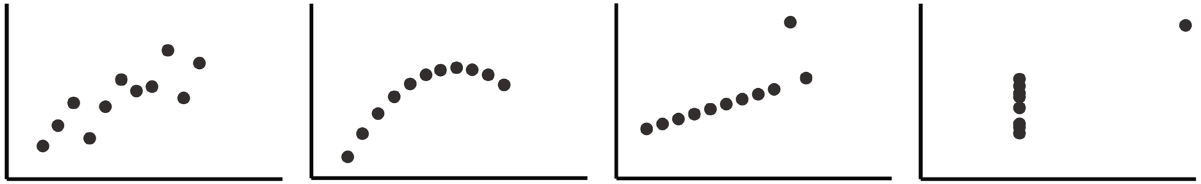
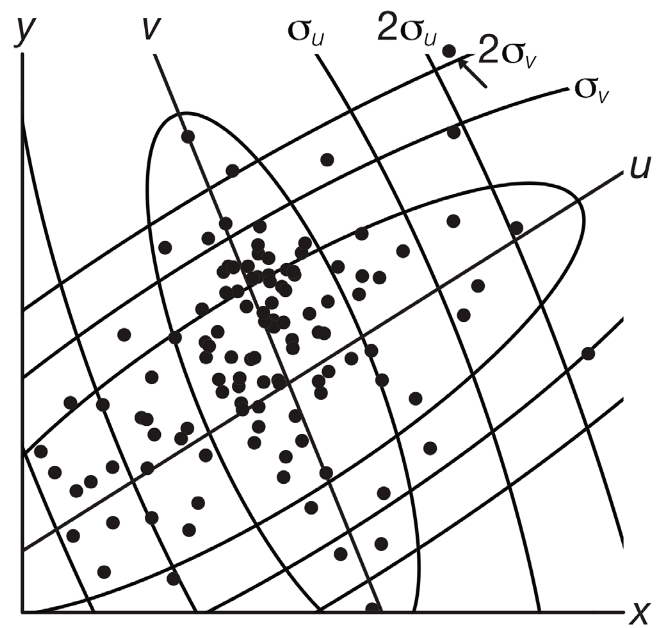
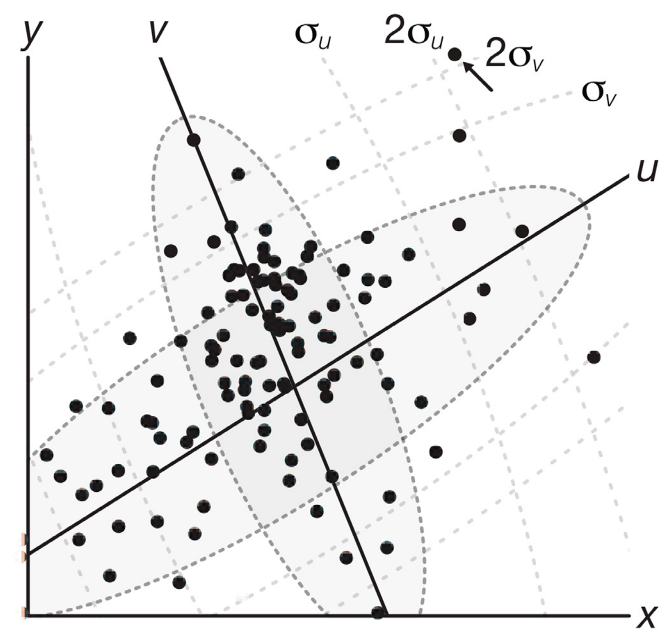
8	6.95	8	8.14	8	6.77	8	5.76
13	7.58	13	8.74	13	12.74	8	7.71
9	8.81	9	8.77	9	7.11	8	8.84
11	8.33	11	9.26	11	7.81	8	8.47
14	9.96	14	8.10	14	8.84	8	7.04
6	7.24	6	6.13	6	6.08	8	5.25
4	4.26	4	3.10	4	5.39	19	12.5
12	10.84	12	9.13	12	8.15	8	5.56
7	4.82	7	7.26	7	6.42	8	7.91
5	5.68	5	4.74	5	5.73	8	6.89



Small changes to aesthetic attributes can make a big difference



Same line style used for different purposes



Visual distinctions are made by assigning different styles to axes, contours and cluster boundaries

Part 4

Case studies

LETTER

doi:10.1038/nature13674

The Laniakea supercluster of galaxies

R. Brent Tully[1], Hélène Courtois[2], Yehuda Hoffman[3] & Daniel Pomarède[4]

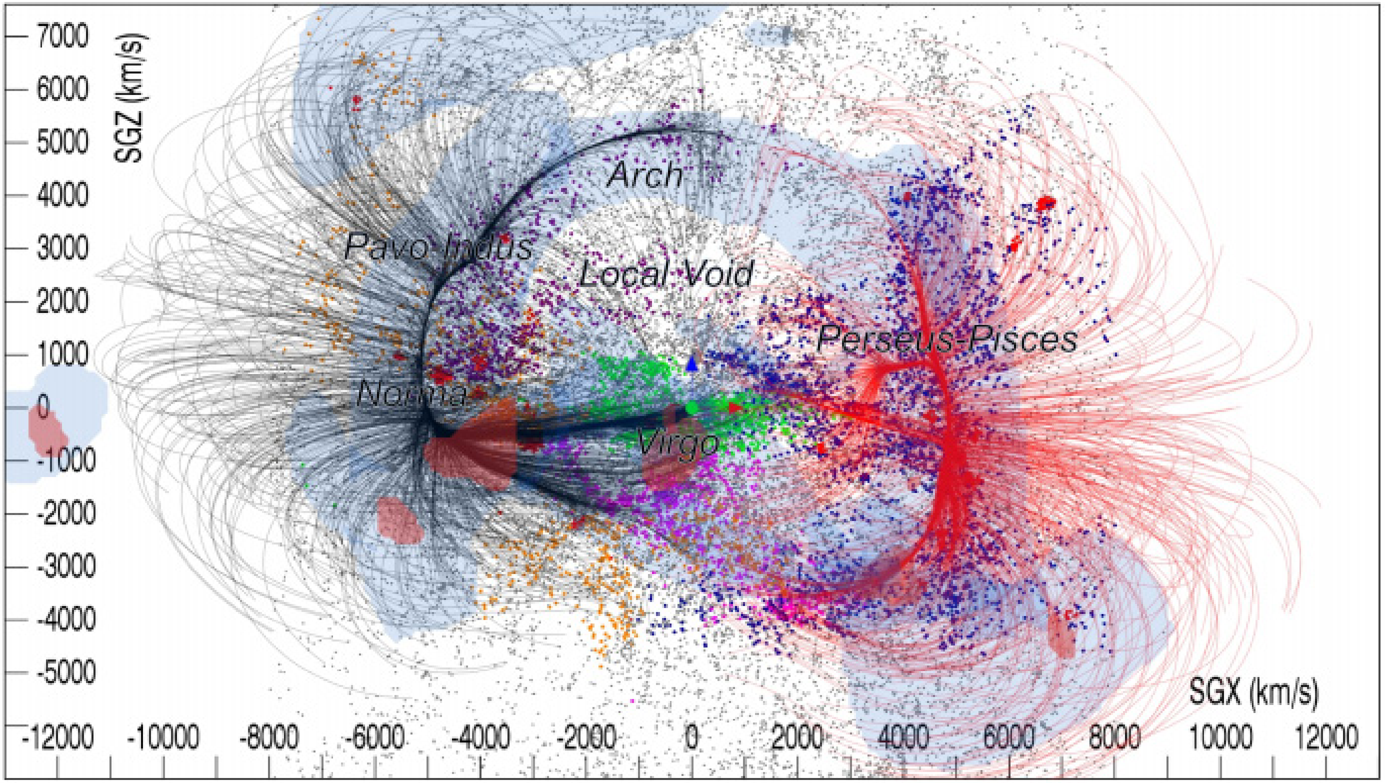
Galaxies congregate in clusters and along filaments, and are missing from large regions referred to as voids. These structures are seen in maps derived from spectroscopic surveys[1,2] that reveal networks of structure that are interconnected with no clear boundaries. Extended regions with a high concentration of galaxies are called 'superclusters', although this term is not precise. There is, however, another way to analyse the structure. If the distance to each galaxy from Earth is directly measured, then the peculiar velocity can be derived from the subtraction of the mean cosmic expansion, the product of distance times the Hubble constant, from observed velocity. The peculiar velocity is the line-of-sight departure from the cosmic expansion and arises from gravitational perturbations; a map of peculiar velocities can be translated into a map of the distribution of matter[3]. Here we report a map of structure made using a catalogue of peculiar velocities. We find locations where peculiar velocity flows diverge, as water does at watershed divides, and we trace the surface of divergent points that surrounds us. Within the volume enclosed by this surface, the motions of galaxies are inward after removal of the mean cosmic expansion and long range flows. We define a supercluster to be the volume within such a surface, and so we are defining the extent of our home supercluster, which we call Laniakea.

The distribution of matter can be determined by two independent methods: either based on surveys of the distribution of galaxies in projection and redshift, or from the motions of galaxies. With the former, using galaxy redshift surveys, the assumption is required that the galaxy

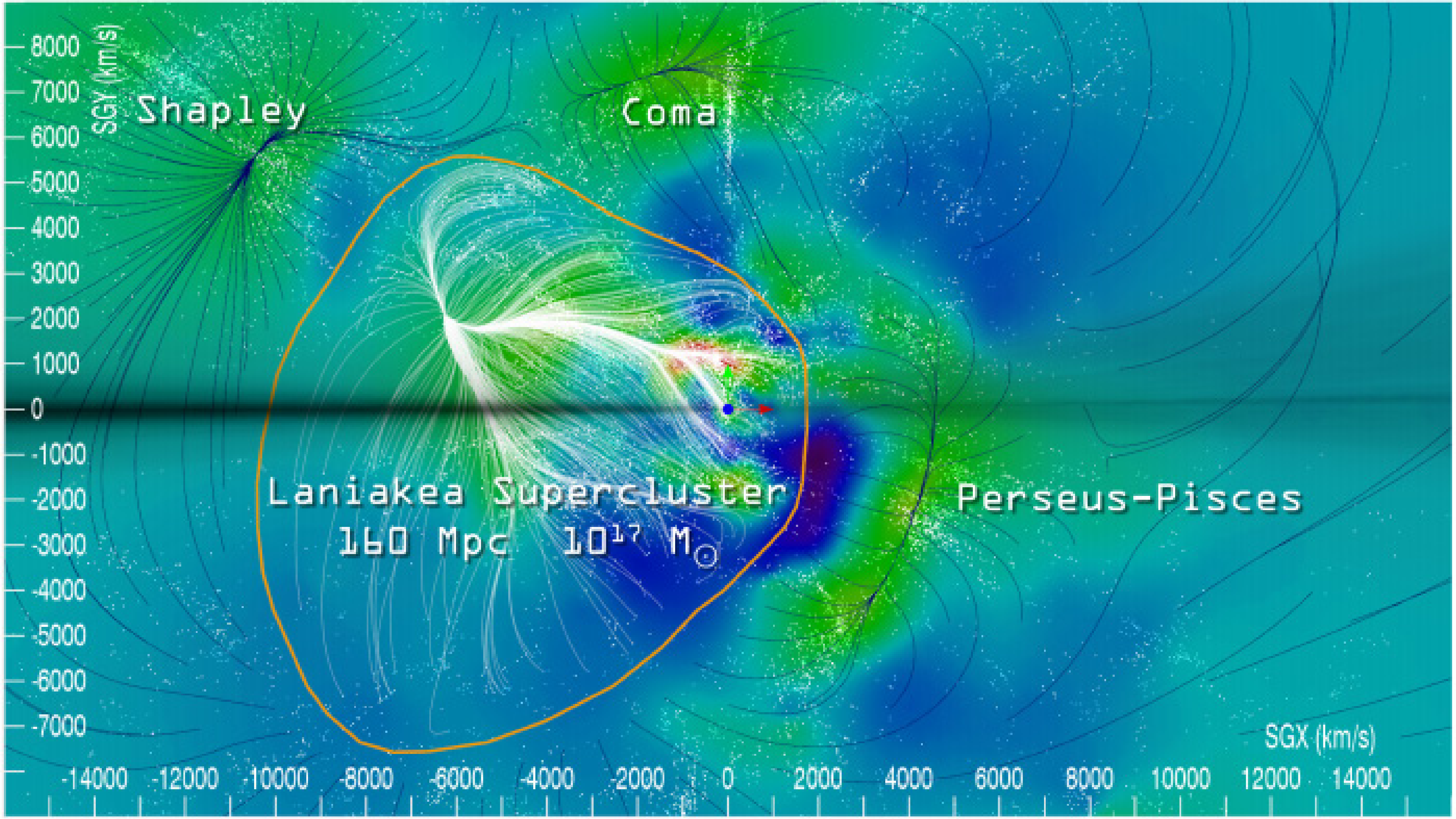
We obtain the underlying three-dimensional velocity and density fields by the Wiener filter algorithm[8,9], assuming the standard model of cosmology as a Bayesian prior. Large-scale structure is assumed to develop from gravitational instabilities out of primordial random Gaussian fluctuations. The developing density and velocity fields retain their Gaussian properties as long as the growth is in the linear regime. It has been shown[8] that with a random Gaussian field, the optimal Bayesian estimator of the field given the data is the Wiener filter minimal variance estimator. At the present epoch, large-scale structure has become nonlinear on small scales. However, it is an attractive feature of the velocity field that the break from linearity is only on scales of a few megaparsecs, an order of magnitude smaller in scale than the deviations from linearity for the density field. In any event, the present discussion concerns structure on scales of tens to hundreds of megaparsecs, comfortably in the linear regime.

The Wiener filter result is determined by the ratio of power to power + noise. Hence, the large-scale structure is strongly constrained nearby, where uncertainties are small and the coverage is extensive. At large distances, where the data become more sparse and noisy, the Wiener filter attenuates the recovered density and velocity fields to the null field that is expected in the absence of data. However in the linear regime there is coherence in galaxy flows on much larger scales than seen in density fluctuations. Tidal influences from beyond the surveyed regions can be manifested in cosmic flows on scales that exceed the coverage in measured distances by a factor of two (ref. 10).

The Laniakea supercluster of galaxies

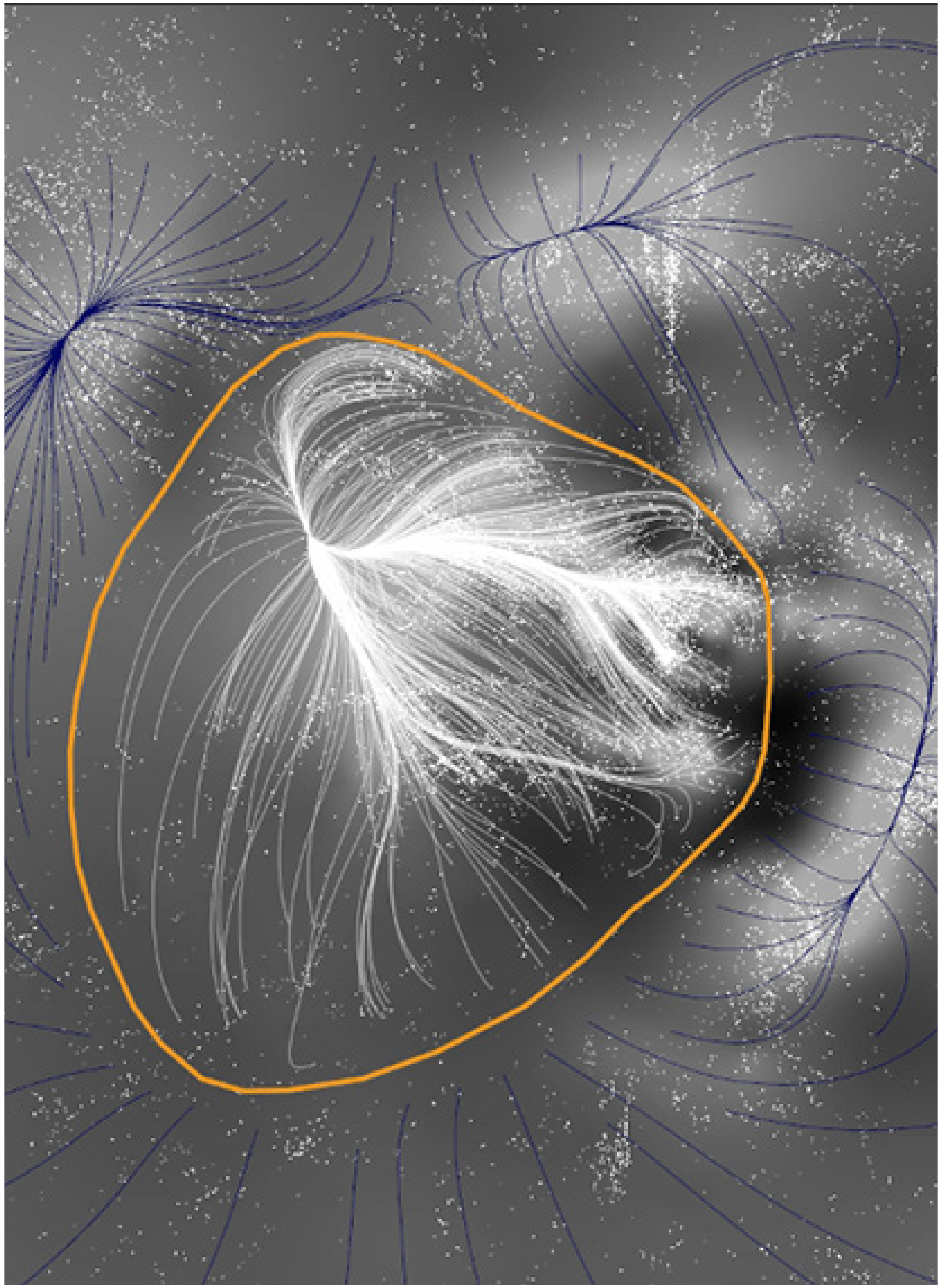


The Laniakea supercluster of galaxies

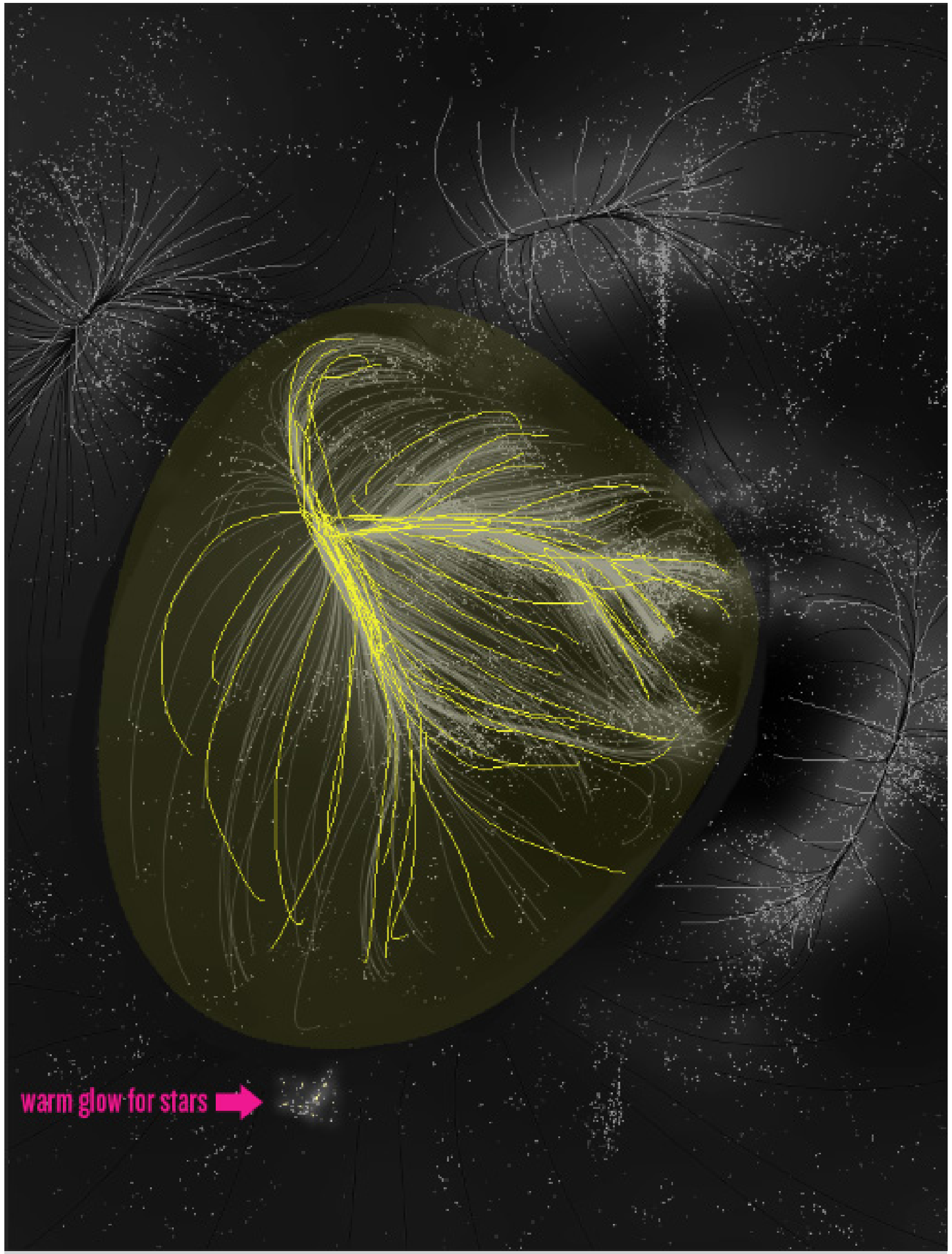


The Laniakea supercluster of galaxies

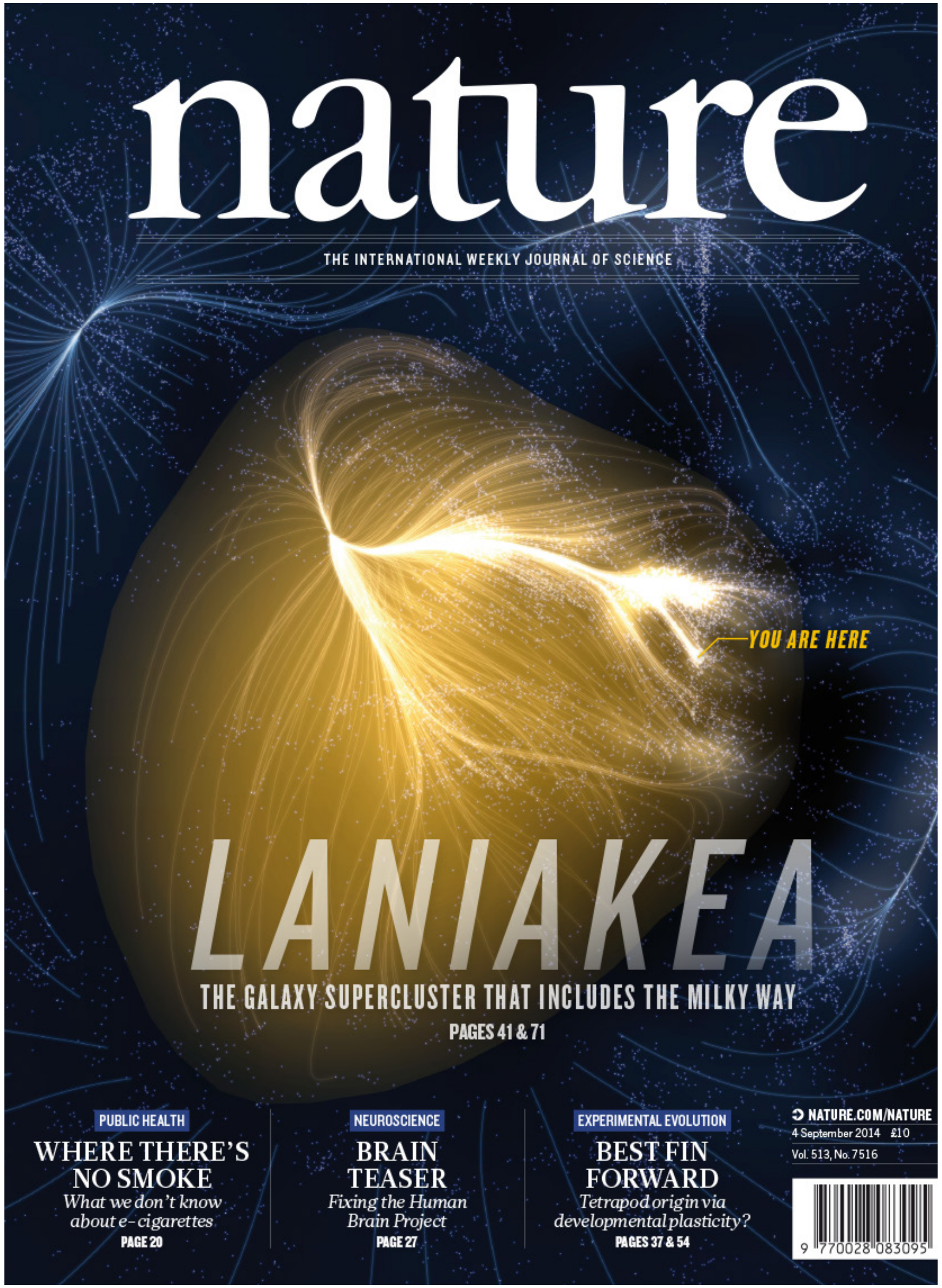
The Laniakea supercluster of galaxies

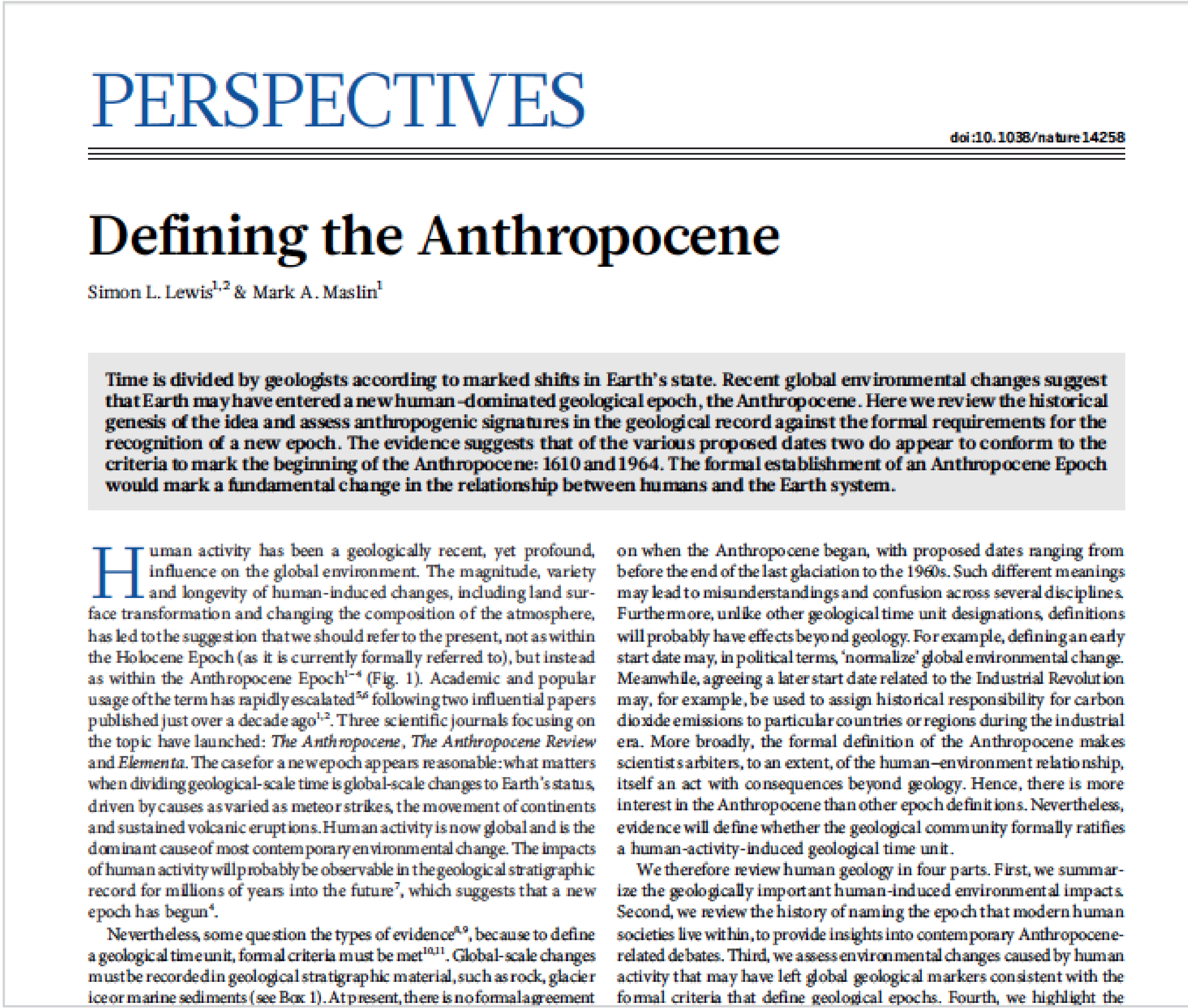


The Laniakea supercluster of galaxies



The Laniakea supercluster of galaxies





PERSPECTIVES

doi:10.1038/nature14258

Defining the Anthropocene

Simon L. Lewis[1,2] & Mark A. Maslin[1]

Time is divided by geologists according to marked shifts in Earth's state. Recent global environmental changes suggest that Earth may have entered a new human-dominated geological epoch, the Anthropocene. Here we review the historical genesis of the idea and assess anthropogenic signatures in the geological record against the formal requirements for the recognition of a new epoch. The evidence suggests that of the various proposed dates two do appear to conform to the criteria to mark the beginning of the Anthropocene: 1610 and 1964. The formal establishment of an Anthropocene Epoch would mark a fundamental change in the relationship between humans and the Earth system.

Human activity has been a geologically recent, yet profound, influence on the global environment. The magnitude, variety and longevity of human-induced changes, including land surface transformation and changing the composition of the atmosphere, has led to the suggestion that we should refer to the present, not as within the Holocene Epoch (as it is currently formally referred to), but instead as within the Anthropocene Epoch[1–4] (Fig. 1). Academic and popular usage of the term has rapidly escalated[5,6] following two influential papers published just over a decade ago[1,2]. Three scientific journals focusing on the topic have launched: *The Anthropocene*, *The Anthropocene Review* and *Elementa*. The case for a new epoch appears reasonable: what matters when dividing geological-scale time is global-scale changes to Earth's status, driven by causes as varied as meteor strikes, the movement of continents and sustained volcanic eruptions. Human activity is now global and is the dominant cause of most contemporary environmental change. The impacts of human activity will probably be observable in the geological stratigraphic record for millions of years into the future[7], which suggests that a new epoch has begun[4].

Nevertheless, some question the types of evidence[8,9], because to define a geological time unit, formal criteria must be met[10,11]. Global-scale changes must be recorded in geological stratigraphic material, such as rock, glacier ice or marine sediments (see Box 1). At present, there is no formal agreement on when the Anthropocene began, with proposed dates ranging from before the end of the last glaciation to the 1960s. Such different meanings may lead to misunderstandings and confusion across several disciplines. Furthermore, unlike other geological time unit designations, definitions will probably have effects beyond geology. For example, defining an early start date may, in political terms, 'normalize' global environmental change. Meanwhile, agreeing a later start date related to the Industrial Revolution may, for example, be used to assign historical responsibility for carbon dioxide emissions to particular countries or regions during the industrial era. More broadly, the formal definition of the Anthropocene makes scientists arbiters, to an extent, of the human–environment relationship, itself an act with consequences beyond geology. Hence, there is more interest in the Anthropocene than other epoch definitions. Nevertheless, evidence will define whether the geological community formally ratifies a human-activity-induced geological time unit.

We therefore review human geology in four parts. First, we summarize the geologically important human-induced environmental impacts. Second, we review the history of naming the epoch that modern human societies live within, to provide insights into contemporary Anthropocene-related debates. Third, we assess environmental changes caused by human activity that may have left global geological markers consistent with the formal criteria that define geological epochs. Fourth, we highlight the

Defining the Anthropocene

Defining the Anthropocene

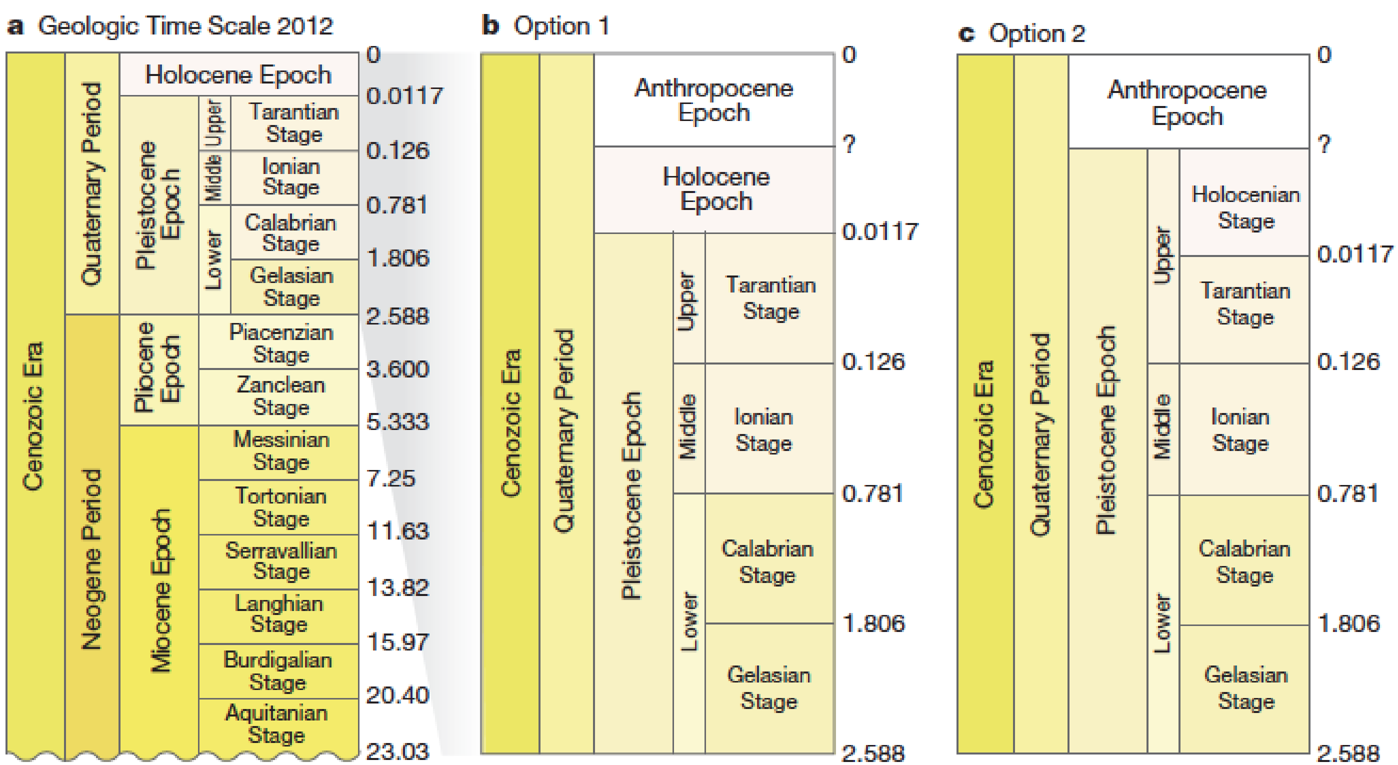


Figure 1 | Comparison of the current Geologic Time Scale[10] (GTS2012), with two alternatives. **a**, GTS2012, with boundaries marked in millions of years (ref. 10). **b**, **c**, The alternatives include a defined Anthropocene Epoch following either the Holocene (**b**) or directly following the Pleistocene (**c**). Defining the Anthropocene as an epoch requires a decision as to whether the Holocene is as distinct as the Anthropocene and Pleistocene; retaining it or not distinguishes between **b** and **c**. The question mark represents the current debate over the start of the Anthropocene, assuming it is formally accepted as an epoch (see Box 1, Fig. 2). Colour coding is used according to the Commission for the Geological Map of the World[10], except for the Anthropocene.

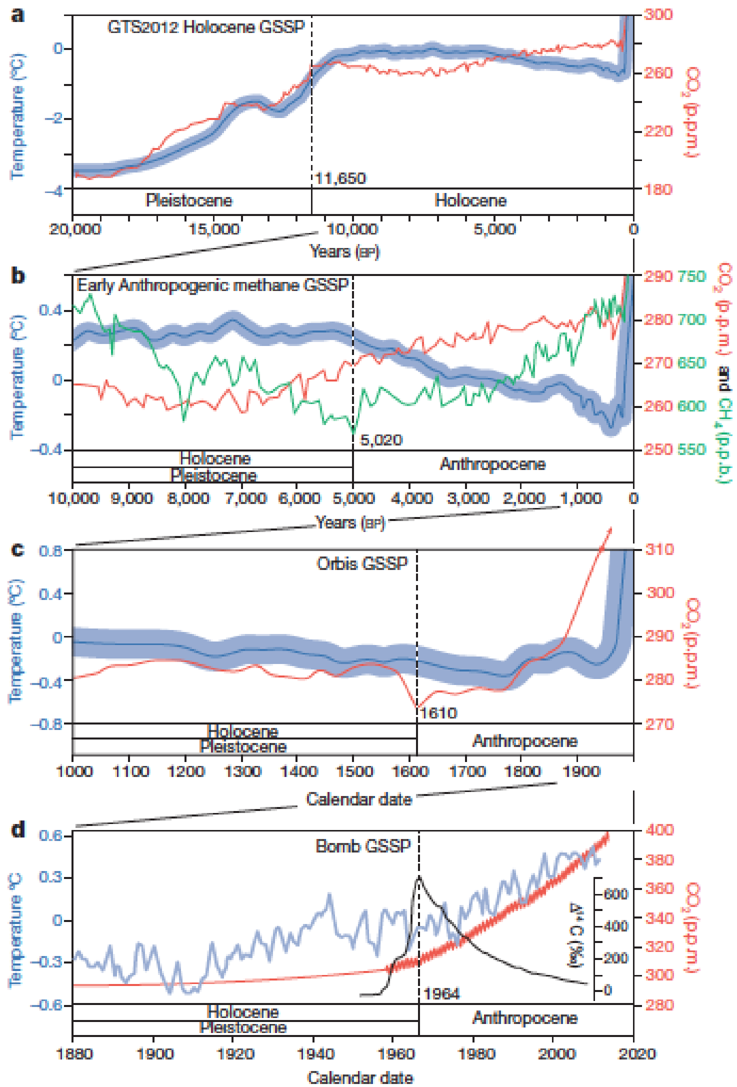
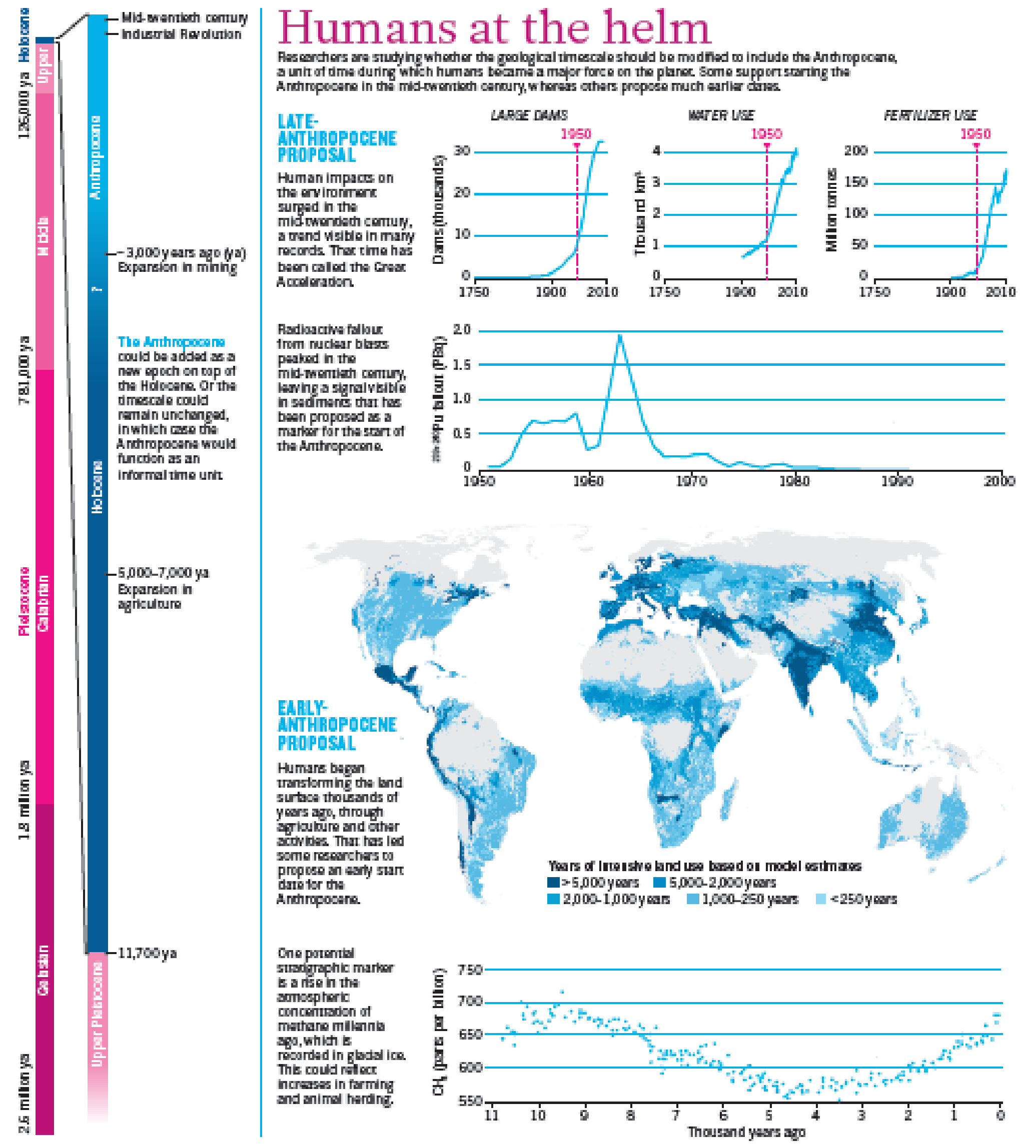


Figure 2 | Defining the beginning of the Anthropocene. **a**, Current GTS2012 GSSP boundary between the Pleistocene and Holocene[38] (dashed line), with global temperature anomalies (relative to the early Holocene average over the



Defining the Anthropocene

Table 1 | Potential start dates for a formal Anthropocene Epoch

Event	Date	Geographical extent	Primary stratigraphic marker	Potential GSSP date*	Potential auxiliary stratotypes
Megafauna extinction	50,000–10,000 yr BP	Near-global	Fossil megafauna	None, diachronous over ~40,000 yr	Charcoal in lacustrine deposits
Origin of farming	~11,000 yr BP	Southwest Asia, becoming global	Fossil pollen or phytoliths	None, diachronous over ~5,000 yr	Fossil crop pollen, phytoliths, charcoal
Extensive farming	~8,000 yr BP to present	Eurasian event, global impact	CO_2 inflection in glacier ice	None, inflection too diffuse	Fossil crop pollen, phytoliths, charcoal, ceramic minerals
Rice production	6,500 yr BP to present	Southeast Asian event, global impact	CH_4 inflection in glacier ice	5,020 yr BP CH_4 minima	Stone axes, fossil domesticated ruminant remains
Anthropogenic soils	~3,000–500 yr BP	Local event, local impact, but widespread	Dark high organic matter soil	None, diachronous, not well preserved	Fossil crop pollen
New–Old World collision	1492–1800	Eurasian–Americas event, global impact	Low point of CO_2 in glacier ice	1610 CO_2 minima	Fossil pollen, phytoliths, charcoal, CH_4, speleothem $\delta^{18}O$, tephra†
Industrial Revolution	1760 to present	Northwest Europe event, local impact, becoming global	Fly ash from coal burning	~1900 (ref. 94); diachronous over ~200 yr	^{14}N:^{15}N ratio and diatom composition in lake sediments
Nuclear weapon detonation	1945 to present	Local events, global impact	Radionuclides (^{14}C) in tree-rings	1964 ^{14}C peak§	^{240}Pu: ^{239}Pu ratio, compounds from cement, plastic, lead and other metals
Persistent industrial chemicals	~1950 to present	Local events, global impact	For example, SF_6 peak in glacier ice	Peaks often very recent so difficult to accurately date§	Compounds from cement, plastic, lead and other metals

For compliance with a Global Stratotype Section and Point (GSSP) definition, a clearly dated global marker is required, backed by correlated auxiliary markers that collectively indicate global and other widespread and long-term changes to the Earth system. BP, before present, where present is defined as calendar date 1950.

* Requires a specific date for a GSSP primary marker. †From Huaynaputina eruption in 1600 (refs 78, 79).

§ Peak, rather than earliest date of detection selected, because earliest dates reflect available detection technology, are more likely influenced by natural background geochemical levels[101], and will be more affected by the future decay of the signal, than peak values.

Defining the anthropocene

ARTICLE

doi:10.1038/nature11234

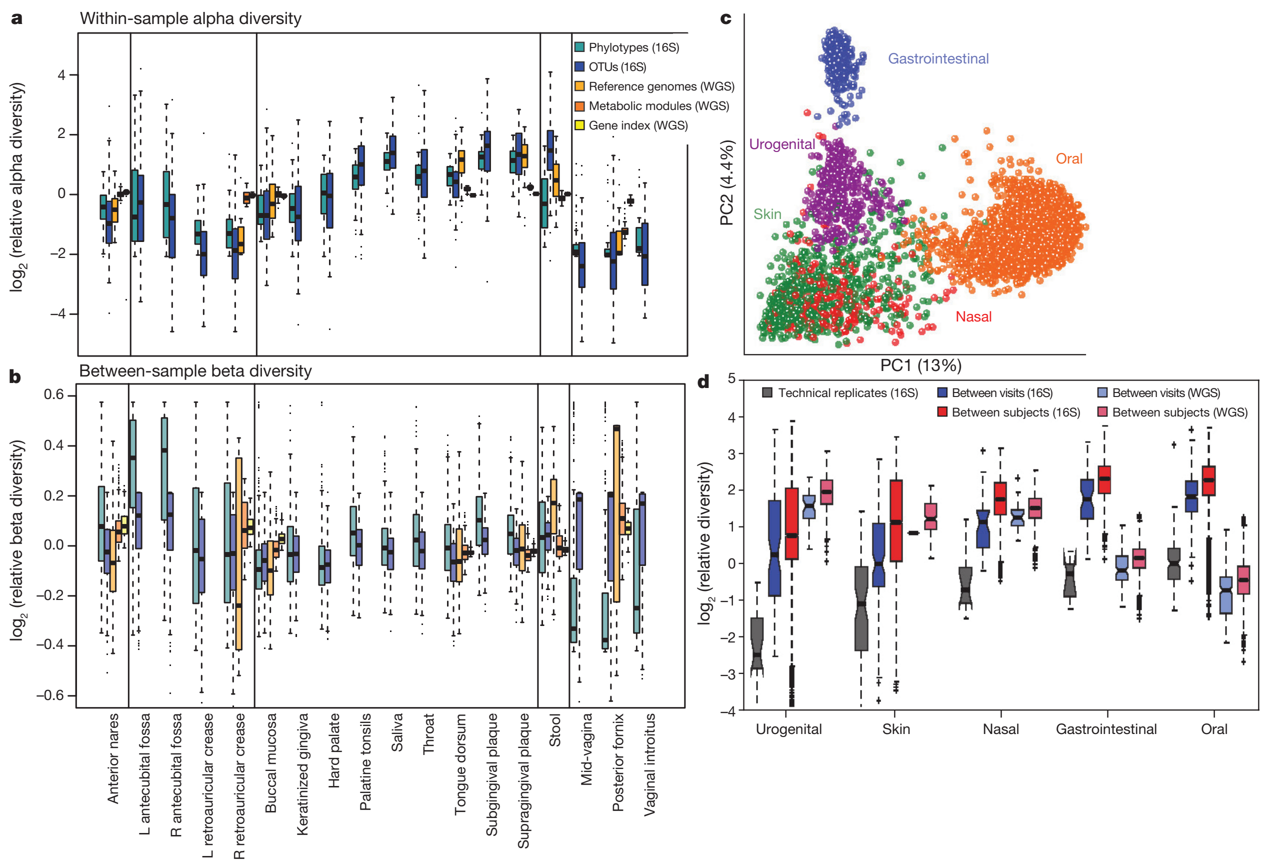
Structure, function and diversity of the healthy human microbiome

The Human Microbiome Project Consortium*

Studies of the human microbiome have revealed that even healthy individuals differ remarkably in the microbes that occupy habitats such as the gut, skin and vagina. Much of this diversity remains unexplained, although diet, environment, host genetics and early microbial exposure have all been implicated. Accordingly, to characterize the ecology of human-associated microbial communities, the Human Microbiome Project has analysed the largest cohort and set of distinct, clinically relevant body habitats so far. We found the diversity and abundance of each habitat's signature microbes to vary widely even among healthy subjects, with strong niche specialization both within and among individuals. The project encountered an estimated 81–99% of the genera, enzyme families and community configurations occupied by the healthy Western microbiome. Metagenomic carriage of metabolic pathways was stable among individuals despite variation in community structure, and ethnic/racial background proved to be one of the strongest associations of both pathways and microbes with clinical metadata. These results thus delineate the range of structural and functional configurations normal in the microbial communities of a healthy population, enabling future characterization of the epidemiology, ecology and translational applications of the human microbiome.

A total of 4,788 specimens from 242 screened and phenotyped adults[1] (129 males, 113 females) were available for this study, representing the majority of the target Human Microbiome Project (HMP) cohort of 300 individuals. Adult subjects lacking evidence of disease were recruited based on a lengthy list of exclusion criteria; we will refer to them here as 'healthy', as defined by the consortium clinical sampling criteria (K. Aagaard *et al.*, manuscript submitted). Women were sampled at 18 body habitats, men at 15 (excluding three vaginal sites), distributed among five major body areas. Nine specimens involving microbiome samples collected from healthy volunteers at two distinct geographic locations in the United States, we have defined the microbial communities at each body habitat, encountering 81–99% of predicted genera and saturating the range of overall community configurations (Fig. 1, Supplementary Fig. 1 and Supplementary Table 1; see also Fig. 4). Oral and stool communities were especially diverse in terms of community membership, expanding prior observations[5], and vaginal sites harboured particularly simple communities (Fig. 1a). This study established that these patterns of alpha diversity

Structure, function and diversity of the healthy human microbiome



Structure, function and diversity of the healthy human microbiome

Structure, function and diversity of the healthy human microbiome

NEWS & VIEWS

MICROBIOLOGY

Learning about who we are

Microbial inhabitants outnumber our body's own cells by about ten to one. These residents have becon intensive research, which is beginning to elucidate their roles in health and disease. SEE ARTICLES P.20

DAVID A. RELMAN

The dawn of the twenty-first century has seen the emergence of a major theme in biomedical research: the molecular and genetic basis of what it is to be human. Surprisingly, it turns out that we owe much of our biology and our individuality to the microbes that live on and in our bodies — a realization that promises to radically alter the principles and practice of medicine, public health and basic science. It is therefore appropriate that ever more research is focused on these microbes and their genes, which together are known as the human microbiome[1]. In this issue, the Human Microbiome Project Consortium[2,3] publishes the most extensive catalogue yet of organisms and genes pertaining to our microbiomes.

The first observations of indigenous human microbiota were published more than 300 years ago, soon after the invention of the microscope. Today's view of the microbial world has been radically improved by DNA-sequencing technology. In the wake of the Human Genome Project, calls were issued[1,4] for enhanced efforts to be made to characterize the 'second human genome' — the human microbiome. At the

Figure 1 | Variation in diversity. Researchers of the Human Microbiome Project are studying the microbial inhabitants of the human body, using samples taken from 242 healthy adults at 15 (for males) or 18 (for females) body sites — from the skin (four sites), mouth and throat (nine sites), vagina (three sites), nostrils and faeces (to represent

used to infer the gene organisms. The resea genomes of the micro using a shotgun sequ generates random s complex pool of DN are then assembled ping sequence simila to identify genes and of the proteins that t

The investigators all available micro sequences to assess — the different type relative abundance — The researchers also genome sequences strains isolated from total of 3,000); thes placed in public data reference genomes fo The consortium auth have identified the microbial taxa and th 242 healthy humans.

One of the great that samples were c from multiple body

Structure, function and diversity of the healthy human microbiome

ARTICLE

doi:10.1038/nature14967

Mapping tree density at a global scale

T. W. Crowther[1], H. B. Glick[1], K. R. Covey[1], C. Bettigole[1], D. S. Maynard[1], S. M. Thomas[2], J. R. Smith[1], G. Hintler[1], M. C. Duguid[1], G. Amatulli[3], M.-N. Tuanmu[3], W. Jetz[1,3,4], C. Salas[5], C. Stam[6], D. Piotto[7], R. Tavani[8], S. Green[9,10], G. Bruce[9], S. J. Williams[11], S. K. Wiser[12], M. O. Huber[13], G. M. Hengeveld[14], G.-J. Nabuurs[14], E. Tikhonova[15], P. Borchardt[16], C.-F. Li[17], L. W. Powrie[18], M. Fischer[19,20], A. Hemp[21], J. Homeier[22], P. Cho[23], A. C. Vibrans[24], P. M. Umunay[1], S. L. Piao[25], C. W. Rowe[1], M. S. Ashton[1], P. R. Crane[1] & M. A. Bradford[1]

The global extent and distribution of forest trees is central to our understanding of the terrestrial biosphere. We provide the first spatially continuous map of forest tree density at a global scale. This map reveals that the global number of trees is approximately 3.04 trillion, an order of magnitude higher than the previous estimate. Of these trees, approximately 1.30 trillion exist in tropical and subtropical forests, with 0.74 trillion in boreal regions and 0.66 trillion in temperate regions. Biome-level trends in tree density demonstrate the importance of climate and topography in controlling local tree densities at finer scales, as well as the overwhelming effect of humans across most of the world. Based on our projected tree densities, we estimate that over 15 billion trees are cut down each year, and the global number of trees has fallen by approximately 46% since the start of human civilization.

Forest ecosystems harbour a large proportion of global biodiversity, contribute extensively to biogeochemical cycles, and provide countless ecosystem services, including water quality control, timber stocks and carbon sequestration[1–4]. Our current understanding of the global forest extent has been generated using remote sensing approaches that provide spatially explicit values relating to forest area and canopy cover[3,5,6]. Used in a wide variety of global models, these maps have enhanced our understanding of the Earth system[3,5,6], but they do not currently address population numbers, densities or timber stocks. These variables are valuable for the modelling of broad-scale biological and biogeochemical processes[7–9] because tree density is a prominent component of ecosystem structure, governing elemental processing and retention rates[7,9,10], as well as competitive dynamics and habitat suitability for many plant and animal species[11–13].

The current estimate of global tree number is approximately 400.25 billion[18]. Generated using satellite imagery and scaled based on global forest area, this estimate engaged policy makers and environmental practitioners worldwide by suggesting that the ratio of trees-to-people is 61:1. This has, however, been thrown into doubt by a recent broad-scale inventory that used 1,170 ground-truthed measurements of tree density to estimate that there are 390 billion trees in the Amazon basin alone[19].

Mapping tree density

Here, we use 429,775 ground-sourced measurements of tree density from every continent on Earth except Antarctica to generate a global map of forest trees. Forested areas are found in most of Earth's biomes, even those as counterintuitive as desert, tundra, and grassland (Fig. 1a, b). We generated predictive regression models for the

Mapping tree density at global scale

Mapping tree density at global scale

a

Terrestrial biome (number of ground-sourced density estimates)	Total trees (billions) ± 95% CI
Boreal forests (*n* = 8,688)	749.3 (± 50.1)
Deserts (*n* = 14,637)	53.0 (± 2.9)
Flooded grasslands (*n* = 271)	64.6 (± 14.2)
Mangroves (*n* = 21)	8.2 (± 0.3)
Mediterranean forests (*n* = 16,727)	53.4 (± 1.2)
Montane grasslands (*n* = 138)	60.3 (± 24.0)
Temperate broadleaf (*n* = 278,395)	362.6 (± 2.9)
Temperate conifer (*n* = 85,144)	150.6 (± 1.3)
Temperate grasslands (*n* = 17,051)	148.3 (± 4.9)
Tropical coniferous (*n* = 0)	22.2 (± 0.4)
Tropical dry (*n* = 115)	156.4 (± 63.4)
Tropical grasslands (*n* = 999)	318.0 (± 35.5)
Tropical moist (*n* = 5,321)	799.4 (± 24.0)
Tundra (*n* = 2,268)	94.9 (± 6.3)
***n* = 429,775**	**3,041.2 (± 96.1)**

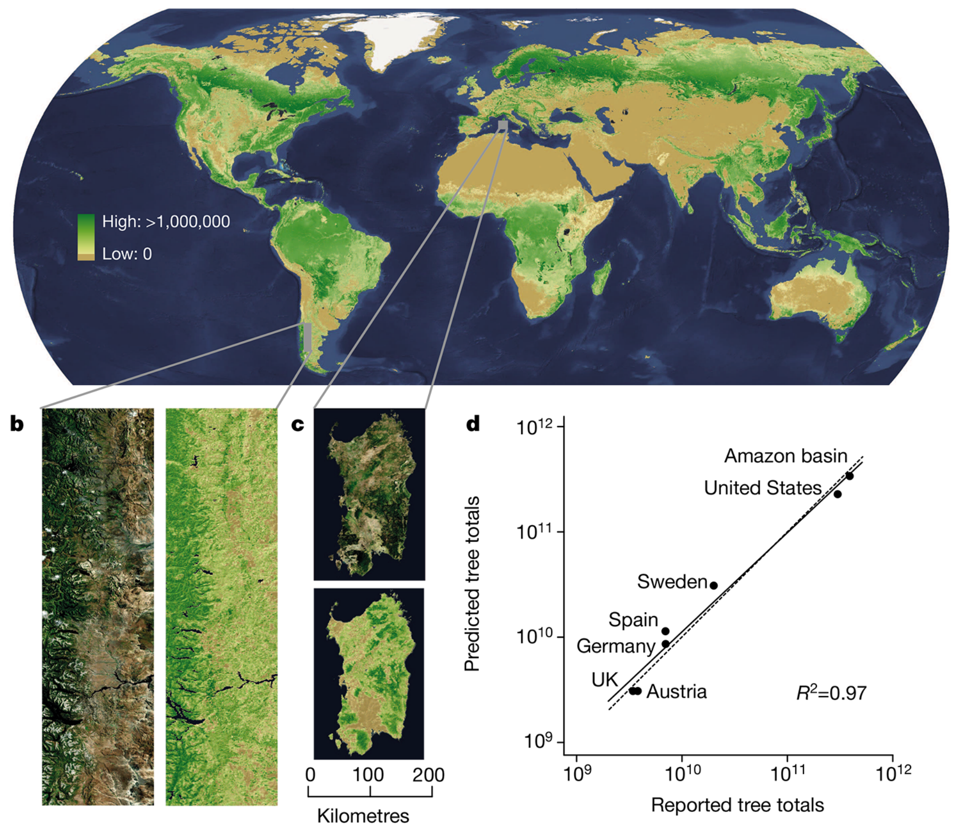
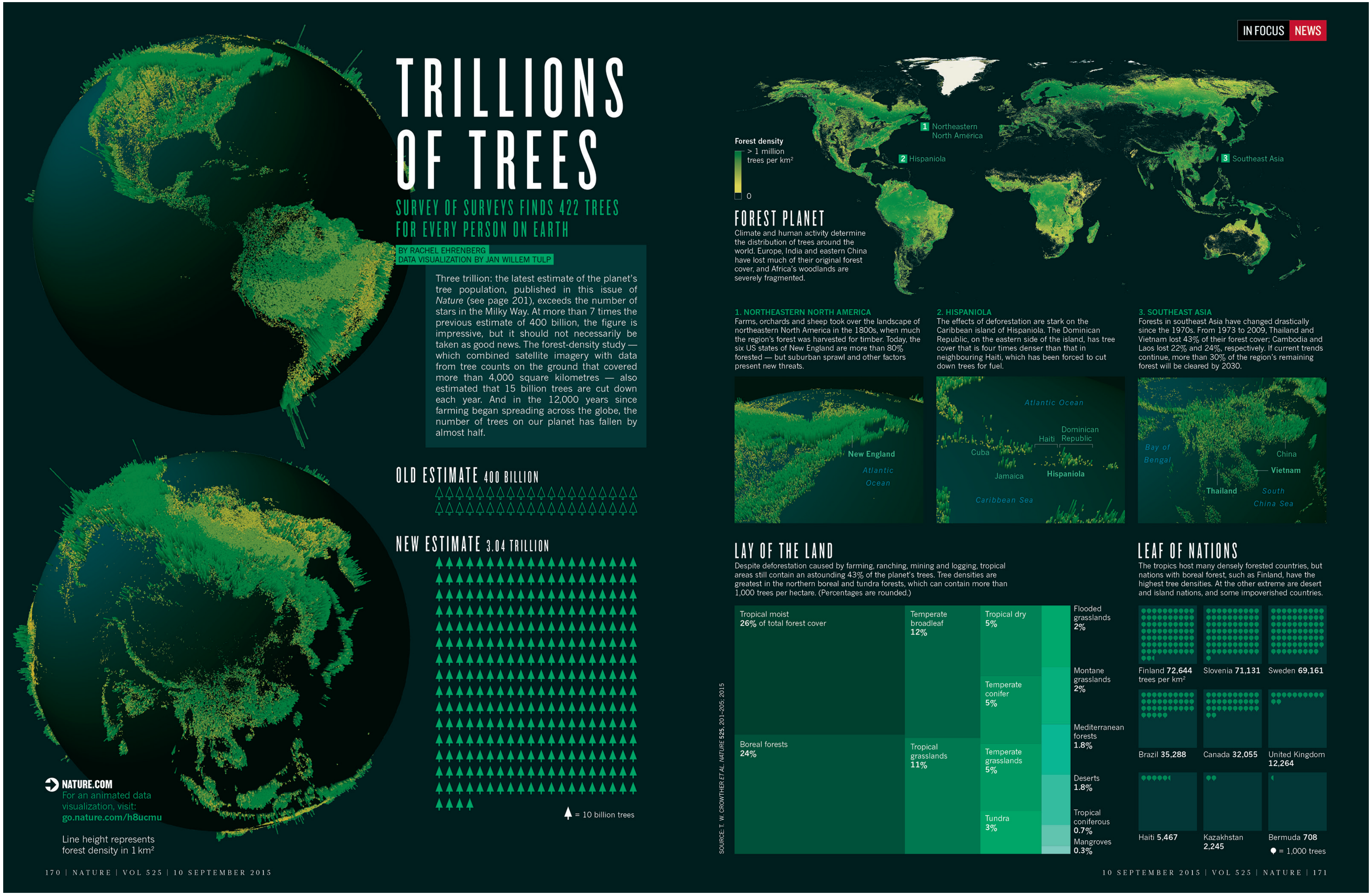


Figure 4 | The global map of tree density at the 1-km^2 pixel (30 arc-seconds) scale. **a**, The scale refers to the number of trees in each pixel. **b**, **c**, We highlight the map predictions for two areas (South American Andes (**b**) and Sardinia (**c**)) and include the corresponding images for visual comparison. All maps and images were generated using ESRI basemap imagery. **d**, A scatterplot as validation for our broad-scale estimates of total tree number. This shows the relationship between our predicted tree estimates and reported totals for regions with previous broad-scale tree inventories (see Methods for details). The straight line and the dotted line are the predicted best fit line and the 1:1 line, respectively.



Mapping tree density at global scale

Mapping tree density at global scale

Thank you

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