

Part of **SPRINGER NATURE**

How chameleons change colour

Career in Science Editing

Paulina Strzyz, PhD

TUD 4th Career Day

17.11.2017



natureresearch

Nature Research Group

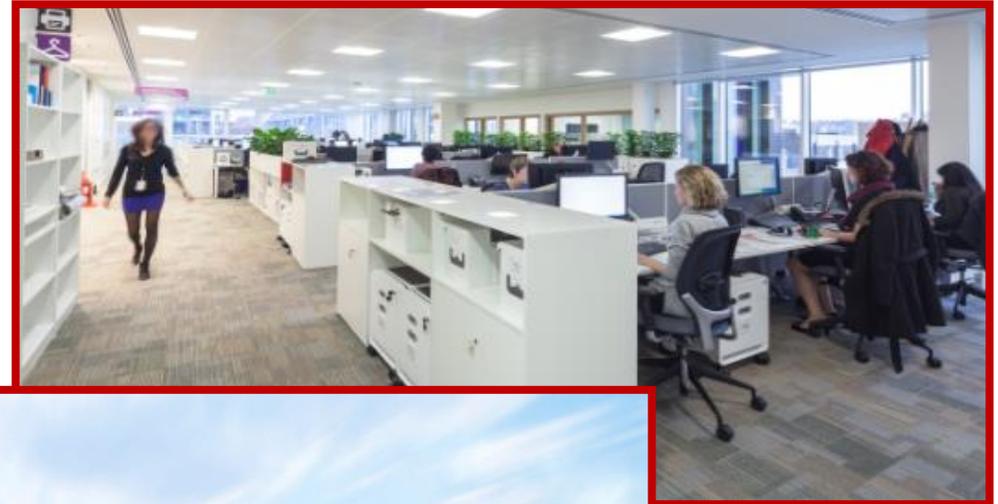
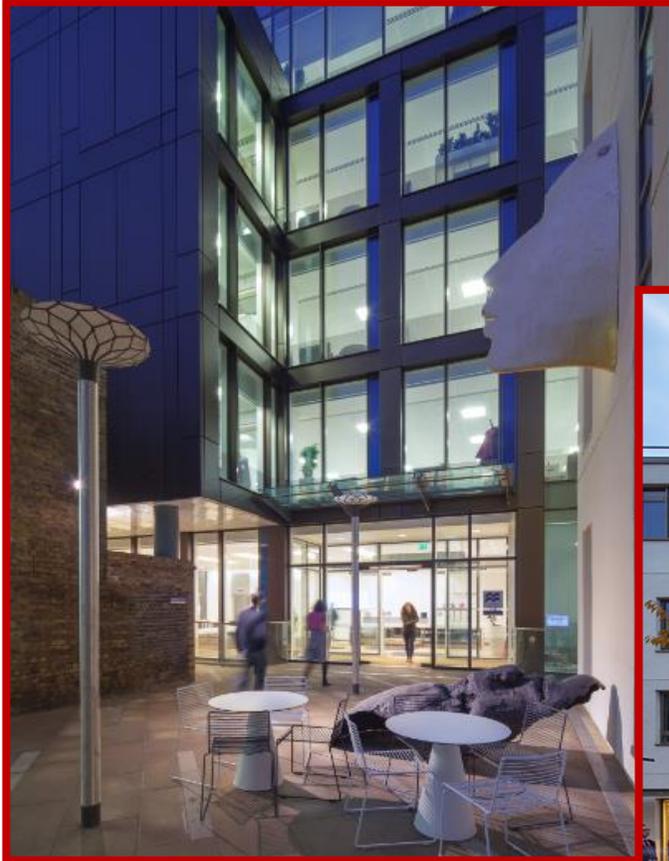
Division of **Springer Nature**, which was formed in 2015 through the merger of **Nature Publishing Group**, Palgrave Macmillan, Macmillan Education and Springer Science+Business Media

Nature Research includes *Nature* (founded in 1869), all *Nature*-branded Research journals, all *Nature*-branded **Reviews** journals (launched in 2000), and *Nature Communications* (Open Access)

Offices in London, Heidelberg, Berlin, New York, Washington DC, San Francisco, Shanghai, Tokyo, Melbourne...



London campus



Journal portfolio at Nature Research

Journal Portfolio	Type	Journal	Launch date
Multidisciplinary	Multidisciplinary	Nature (Life Sciences)	1869
Multidisciplinary	Multidisciplinary	Nature (Physical Sciences)	1870
Multidisciplinary	Multidisciplinary	Nature Communications (Life Sciences)	2009
Multidisciplinary	Multidisciplinary	Nature Communications (Physical Sciences)	2010
Life sciences	Research journals	Nature Cell Biology	1999
Life sciences	Research journals	Nature Ecology & Evolution	2017
Life sciences	Research journals	Nature Genetics	1992
Life sciences	Research journals	Nature Human Behaviour	2017
Life sciences	Research journals	Nature Immunology	2000
Life sciences	Research journals	Nature Medicine	1995
Life sciences	Research journals	Nature Metabolism	2019
Life sciences	Research journals	Nature Microbiology	2016
Life sciences	Research journals	Nature Neuroscience	1998
Life sciences	Research journals	Nature Plants	2015
Life Sciences	Research journals	Nature Structural and Molecular Biology	2004
Applied Sciences	Research journals	Nature Biomedical Engineering	2017
Applied Sciences	Research journals	Nature Biotechnology	1983
Applied Sciences	Research journals	Nature Catalysis	2018
Applied Sciences	Research journals	Nature Chemical Biology	2005
Applied Sciences	Research journals	Nature Chemistry	2009
Applied Sciences	Research journals	Nature Electronics	2018
Applied Sciences	Research journals	Nature Machine Intelligence	2019
Applied Sciences	Research journals	Nature Methods	2004
Applied Sciences	Research journals	Nature Protocols	2006

Journal Portfolio	Type	Journal	Launch date
Physical sciences	Research journals	Nature Astronomy	2017
Physical sciences	Research journals	Nature Climate Change	2011
Physical sciences	Research journals	Nature Energy	2016
Physical sciences	Research journals	Nature Geoscience	2008
Physical sciences	Research journals	Nature Materials	2002
Physical sciences	Research journals	Nature Nanotechnology	2006
Physical sciences	Research journals	Nature Photonics	2007
Physical sciences	Research journals	Nature Physics	2005
Grand Challenges	Research journals	Nature Sustainability	2018
Life sciences	Nature Reviews	Nature Reviews Cancer	2001
Life sciences	Nature Reviews	Nature Reviews Drug Discovery	2002
Life sciences	Nature Reviews	Nature Reviews Genetics	2000
Life sciences	Nature Reviews	Nature Reviews Immunology	2001
Life sciences	Nature Reviews	Nature Reviews Microbiology	2003
Life sciences	Nature Reviews	Nature Reviews Molecular Cell Biology	2000
Life sciences	Nature Reviews	Nature Reviews Neuroscience	2000
Physical sciences	Nature Reviews	Nature Reviews Chemistry	2017
Physical sciences	Nature Reviews	Nature Reviews Materials	2016
Physical sciences	Nature Reviews	Nature Reviews Physics	2019
Clinical sciences	Nature Reviews	Nature Reviews Cardiology	2004
Clinical sciences	Nature Reviews	Nature Reviews Clinical Oncology	2004
Clinical sciences	Nature Reviews	Nature Reviews Disease Primers	2015
Clinical sciences	Nature Reviews	Nature Reviews Endocrinology	2005
Clinical sciences	Nature Reviews	Nature Reviews Gastroenterology and Hepatology	2004
Clinical sciences	Nature Reviews	Nature Reviews Nephrology	2005
Clinical sciences	Nature Reviews	Nature Reviews Neurology	2005
Clinical sciences	Nature Reviews	Nature Reviews Rheumatology	2005
Clinical sciences	Nature Reviews	Nature Reviews Urology	2004

Primary research vs Reviews journals

	<i>Nature</i>	Nature Research	<i>Nat Comms</i>	Nature Reviews
Majority of content	Unsolicited	Unsolicited	Unsolicited	Commissioned
Articles submitted	~185 per week	~30 per week	~400 per week	~1 per week
Rejection rate	High (90-95%)	High (>90%)	High (>85%)	Low (<5%)
Articles published	~800 per year	~150 per year	~3,000 per year	~50-60 per year
Level of editing	Light	Light	Light	Heavy

Nature Reviews journals



LIFE SCIENCES

Nature Reviews Cancer
Nature Reviews Drug Discovery
Nature Reviews Genetics
Nature Reviews Immunology
Nature Reviews Microbiology
Nature Reviews Molecular Cell Biology
Nature Reviews Neuroscience

NEW! PHYSICAL SCIENCES

Nature Reviews Materials
Nature Reviews Chemistry
Nature Reviews Physics

CLINICAL SCIENCES

Nature Reviews Cardiology
Nature Reviews Clinical Oncology
Nature Reviews Disease Primers
Nature Reviews Endocrinology
Nature Reviews Gastroenterology & Hepatology
Nature Reviews Nephrology
Nature Reviews Neurology
Nature Reviews Rheumatology
Nature Reviews Urology

+ CROSS-JOURNAL TEAM



Nature Reviews Molecular Cell Biology: our team



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Impact factor*: 46.602

*2016 Journal Citation Reports (Thomson Reuters, 2017)

Journal content

‘Front half’ – usually not peer-reviewed

Research Highlights: short news pieces on a recent publication of interest, written by the editors

Journal Clubs: Written by external authors

Comments: Invited commentary on a timely topic or event, written by key figures in the field

RESEARCH HIGHLIGHTS

Journal club

REGULATING THE GERM LINE-SOMA BARRIER

August Wilmanns proposed that hereditary information moves only from germline to body cells and never vice versa. The concept proposed by Wilmanns did not support the Lamarckian view of the inheritance of acquired characteristics. However, Wilmanns's idea of a strict germline-soma barrier can now be challenged with research on mammalian germ cells using induced pluripotent stem cells (iPSCs) derived from somatic cells.

Primordial germ cells, which are the immediate precursors of sperm and eggs, are set aside early during human development. Developmental decisions across the germ line from a female to an egg or a male to a sperm cell are of a special category of inheritance, in which the same cells across generations of the germ line is considered normal, as it is germline genetic.

It is possible, in principle, to take adult somatic cells and – via iPSCs – convert them into functional gametes

—and possibly epigenetic— information from one generation to the next. This observation between the germ line and the soma is apparently never breached, which is known as the Weismann barrier. However, under normal circumstances, somatic cells do not migrate back into the germline to contribute to the germ line after the Weismann barrier. This was the new idea if it became possible to reprogramme somatic cells into iPSCs. Using a combination of knowledge from advances in mammalian cell biology, Hasegawa et al. managed to reprogramme mouse cells so that they breached the Weismann barrier, demonstrating that it is possible, in principle, to take adult somatic cells and – via iPSCs – convert them into functional gametes from which live animals can be produced. They showed that iPSCs could be made competent for primordial germ cell fate, and that when these cells are injected to the male reproductive tract of a mouse, they undergo specification into primordial germ cells.

Use of a live recently shown that it is also possible to convert human skin cells into primordial germ cells via iPSCs, which opens the way for epigenetic advances in human germline biology. As well as advances in reproductive biology, this opens up an opportunity to investigate germline factors, such as epigenetic or environmental factors (as envisaged by Lamarck) that are transmitted to the next generation. It will also be possible to explore new gene-editing techniques for germline modifications, and above all, this research will advance our knowledge of early human development.

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COMMENT

THE 3D GENOME

Mapping the 3D genome: Aiming for concision

Job Dekker

Abstract The spatial organization of genomes is studied using microscopy- and chromosome conformation capture (3C)-based methods. The two types of methods produce data that are often consistent, but there are cases where they appear discordant. These cases provide opportunities to derive better models of chromatin folding, which can reconcile the datasets.

A balanced perspective cannot be applied by studying disciplines in situ but through journals of concision among them. From “Conciseness: The Unity of Knowledge” by J.C. Wilson, *Yanagita Books, Boston, Mass., 1988.*

How chromosomes are folded inside the nucleus is a fascinating question in cell biology and genetics. Over the past few decades there has been tremendous progress in our understanding of the 3D organization of chromosomes and its role in gene regulation, chromosome condensation and segregation, and genome stability. Some of the recent progress is discussed in these Review articles in this issue.

The field of 3D genome organization has been driven forward by two different sets of methodological approaches. On the one hand, imaging techniques such as fluorescence in situ hybridization (FISH) and live-cell imaging have provided increasingly dynamic and higher resolution views of chromatin domains and selected loci in single cells. On the other hand, chromosome conformation capture (3C)-based genomic methods such as 3C-seq, circular chromosome conformation capture (4C)-seq, chromosome conformation capture carbon copy (3C_{cc}), genome-wide chromosome conformation capture (Hi-C), and chromosome interaction analysis paired end tag (ChIA-PET) sequencing have begun to provide views of the spatial organization of the genome and entire genomes at kilobase resolution by measuring contact probabilities between loci. The 3C-based methods are mostly performed on large cell populations and provide a population-averaged view, or perhaps more correctly, a probabilistic view of spatial chromosome folding.

Now that large data are being obtained using the diverse array of methods, it is becoming increasingly important to determine whether the different data types that are produced by these technologies can provide coherent insights into chromosome folding and nuclear organization. For instance, generally it is good practice to validate observations that were made using

a method of one type with those made using a method of another type. Indeed, there is often good correspondence between data obtained with genomic methods such as Hi-C and imaging data obtained by FISH. However, considerable discrepancies have also been found (for example, see ref. 1) and the two types of data can produce different models of genome organization. This has led to discussions in the field about whether the methods suffer from false positives and negatives and whether data obtained from either method are correctly interpreted.

However, it is reasonable to assume that FISH- and 3C-based methods are measuring the same features of chromosome structure and hence that they can be used to validate each other's output. It is clear that this validation is usually not straightforward because they capture very different aspects of chromosome folding. Given cell-to-cell and time-dependent variation in chromosome folding, the spatial distance between two loci will display a rather wide distribution in the cell population (see ref. 1). 3C-based methods detect cell events when the two loci are in close spatial proximity, that is, events present in only the small fraction of cells in the left tail of the distribution. FISH, in contrast, can determine the spatial distance between the loci in any cell, and when a relatively small number of cells (for example, several hundred) are analysed, it will mostly detect cells in the middle part of the distribution given that this part represents the majority of cells. These differences illustrate two important points. First, 3C-based and FISH-based methods interrogate different subpopulations of cells. Second, it is unsafe to validate data that was obtained with 3C-based methods by using imaging-based methods, or vice versa, one should restrict the comparison to an analysis of those cells in which the pairs of loci are closely colocalized. In other words, one should compare the contact frequencies that are detected by 3C-based methods with the colocalization frequencies that are detected by FISH. This is often not how FISH data have been used to validate contact frequency data.

the genome, and Sorensen et al. employ imaging with enhanced 3C followed by high-throughput sequencing (Hi-C) to generate 3D structures of whole genomes in single cells.

In the genome architecture mapping (GAM) method developed by Beagrie et al., the nuclear organization profile is extracted from thin cryosections of fixed cells by microdissection, amplified and sequenced, usually using 3C techniques.IGATION is not required to capture interacting portions of DNA. Nuclear profiles contain loci that are in close proximity, even if they are distant on the linear genome, scoring the co-segregation of loci across many chromosomes, using the co-segregation of loci-enriched centromeres (LICE) and histone H3Z3 enrichment (H3Z3) profiles from mouse embryonic stem (ES) cells

RESEARCH HIGHLIGHTS

ANIMATING IN ON NUCLEAR STRUCTURE

Cells are 3D structures that produce 3D genome folding structures at a resolution of 100 kb. Superimposed on the microcopy image of the same cell demonstrated that the 3D structures are consistent with the cell imaging and Hi-C data. Sorensen et al. used the structures to gain insight into the genomic details of individual cells, sometimes by mapping chromosome immunoprecipitation followed by sequencing (ChIP-seq) or RNA sequencing (RNA-seq) data with fine cell population sizes. They determined that, although the structure of TADs and the organization of loops that are generated by the CTCF-binding factor and the cohesion complex (Coh) loops help to stabilize enhancer-promoter interactions, the interaction between the organization of the active and inactive chromatin domains and promoter-protein associated domains and protein-protein interactions between individual cells. Furthermore, the position of distal enhancers and promoters relative to the active chromatin domain is the 3D structure-related but extended contacts data suggesting that Kruppel-like factor 4 (KLF4) and other transcription factors are involved in interactions. The biological relevance of this finding was further highlighted by the novel finding that genes regulated by the downstream modulator and deacetylase (DNMT3) complex cluster.

CONCLUSIONS Sorensen et al. and Beagrie et al. have shown that the 3D structure of the genome is a key determinant of gene expression. Sorensen et al. imaged hybrid ES cells expressing fluorescently labelled CENP-A and histone H3Z3 proteins to show for cells in G1 phase. They then subjected these

using Hi-C and further assessed 400 of the highest quality profiles (the Hi-C 400 dataset). This dataset enabled the study of chromatin contacts as a resolution of 30 kb and could replicate data on chromatin architecture that was previously produced using 3C-based approaches. Beagrie et al. also developed a mathematical model called RECC (Genetic interaction of co-segregation) that determines which chromatin contacts are likely to be specific. RECC revealed that specifically interacting chromatin regions in their Hi-C 400 dataset contained contacts that are, on average, highlighted by the top 2% of right contacts (that is, contacts involving these genomic regions), which were detected at the same organizational level as topologically associated domains (TADs). These right contacts spanned genomic distances of up to 140 Mb and were often found to connect three TADs, at least one of which contained super-enhancers, or to connect highly transcribed TADs.

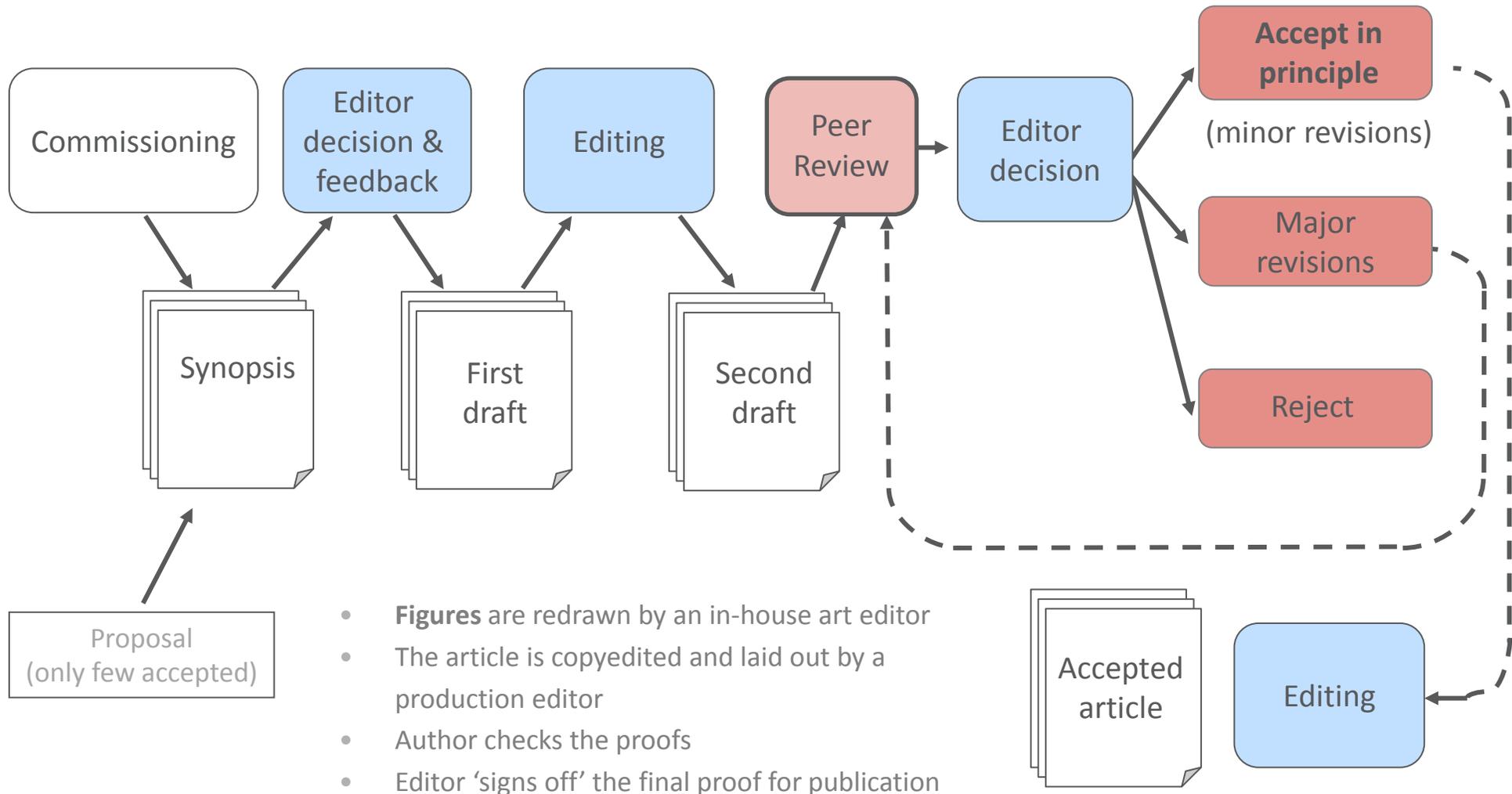
Sorensen et al. imaged hybrid ES cells expressing fluorescently labelled CENP-A and histone H3Z3 proteins to show for cells in G1 phase. They then subjected these

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nature research

The life of a Review: from idea to publication



Article commissioning

A bit like research

- Formulate and research the idea
- Present and defend it in the team
- Find the best possible author
- Convince them to write!

Finalized Review => Satisfaction



Developmental Editing

The classification of the great majority of lncRNAs relies on the empirical attributes originally used to detect them (Table 1, Figure 1), which reflects the short history of lncRNAs relative to protein-coding genes, which are predominately categorized on the basis of function. [Au: OK?]

[Au: I have moved your discussion of TARs and transfrags to the next subsection to improve flow.]

Classification based on transcript length. The length estimate of ncRNAs is the most commonly used attribute for their classification. A somewhat arbitrary cut-off of 200 bases has been adopted to distinguish between short and long ncRNAs. The rationale behind choosing this attribute to classify lncRNAs stems from the fact that information about a given transcript is often limited to a region of transcription rather than to a fully sequenced RNA molecule. As a result, this estimate is often fairly vague. [Au: Can you support this section with a reference, e.g. is there any data on how estimates and actual transcript size differ?] Classification often depends on transcribed regions rather than fully sequenced transcripts. A region of transcription, which is known as a transcribed fragment (TransFrag) [G] or transcriptionally active region (TAR) [G], is usually defined by a tiling array [G] as a run of consecutive positive probes^{44,45}. More recently, researchers have used RNA sequencing (RNA-seq) (Box 1) to generate series of short overlapping reads^{46,47}. [Au: Are these also known as TARs?] that can be used to infer regions of transcription, or artificially assembled transcript molecules. [Au: Please provide a reference for the 'artificially assembled transcript molecules'.] [Au: Edits to avoid repetition OK?] [Au: I have switched the order of the following to paragraphs to improve flow.]

Although intrinsically limited in their information content, tiling array experiments have been important in defining the extent of the transcribed genome, as well as providing an indication of the widespread presence of lncRNAs. [Au: Please reference this statement.] In fact, this approach remains valid in the days of NGS. [Au: Please briefly mention for what] That said, NGS can give accurate evidence of not only transcription but also its relative mass (number of reads from a region), and has thus been instrumental in proving that ncRNA dominates the population of nuclear non-

ribosomal RNAs in a human cell⁴⁸. The limitation of basing classifications on TARs will probably continue for the foreseeable future given that even with imaginable improvements in NGS read length⁴⁹, [Au: Is this what you meant?] transcripts in the ranges of tens or hundreds of thousands of bases will still require mapping and coalescing of different reads.

[Au: I think it would make sense to group those classes/categories that are based on origin/localization and it would be useful to add a figure of a genomic region and depict the various locations (exonic, intronic, overlapping exon and intron, intergenic, promoter/enhancer, sense/antisense...) from which lncRNAs are transcribed. The nonspecialist reader could then refer back to this figure throughout the Review for clarity.]

Classification based on known DNA elements. Perhaps the second most commonly used attribute results from the association of lncRNAs with, or proximity to, a DNA sequence element whose function is known (for example, the promoter of a protein-coding gene) or at least demarcated (such as a space between protein-coding genes or intergenic space) (Table, Figure 1). Notable classes of RNAs using these attributes include enhancer- and promoter-associated long RNAs (Table, Figure 1). These have rapidly established a credible link between the dynamics of nuclear architecture, chromatin signalling plasticity, and transcriptional regulation. [Au: Please reference this statement.] Interestingly, enhancers that give rise to RNA species have greater likelihood of functionality in reporter assays than those that do not²⁵, arguing for a functional, rather than spurious, link between RNA and this type of genomic element. The frequency of overlapping non-coding and coding transcripts at a given locus provides another challenge for the logical and useful classification of lncRNAs. First observed by the FANTOM consortium and called 'transcriptional forests'²⁸, they suggest [Au: Who is 'they'?] that a single transcriptional locus can produce a complex collection of coding and non-coding transcripts from either strand. Targeted rapid amplification of cDNA ends (RACE) experiments⁴⁴ and RNA-seq data⁴⁴ indicate that transcriptional forests represent a general phenomenon in human cells. A prominent category of ncRNAs has emerged from these transcriptional forests composed of sense

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Navigation

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Acknowledgements:

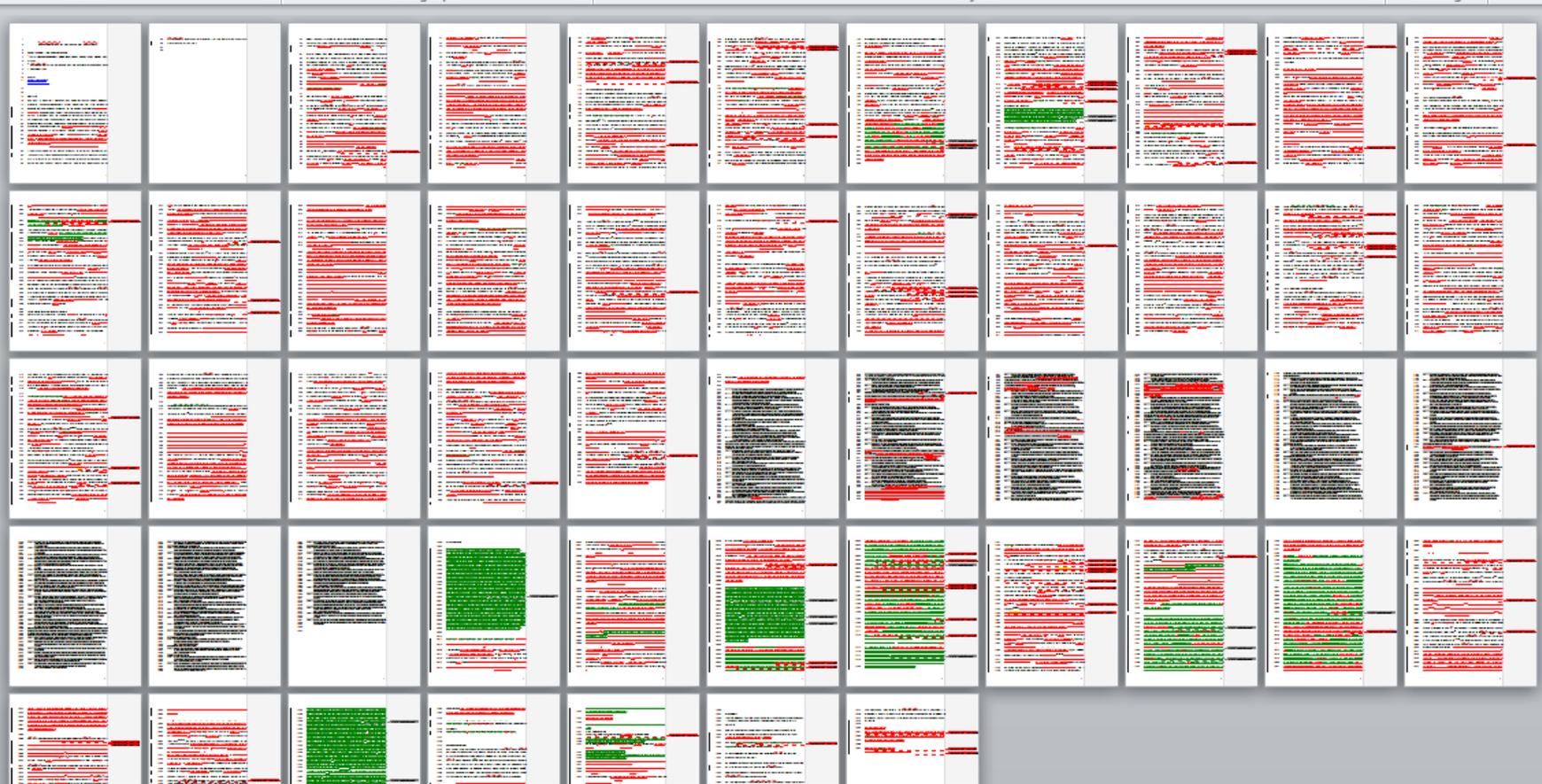
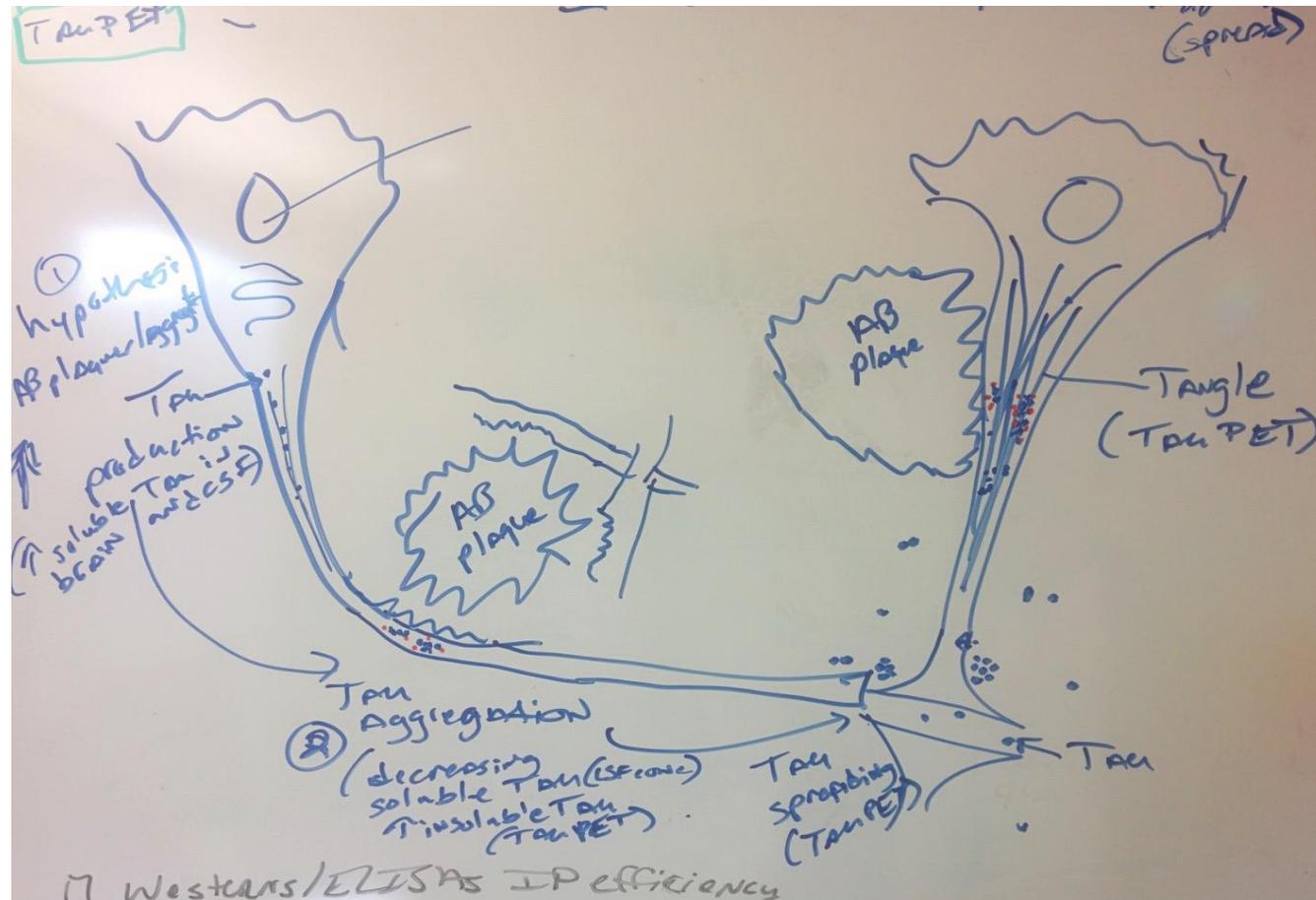
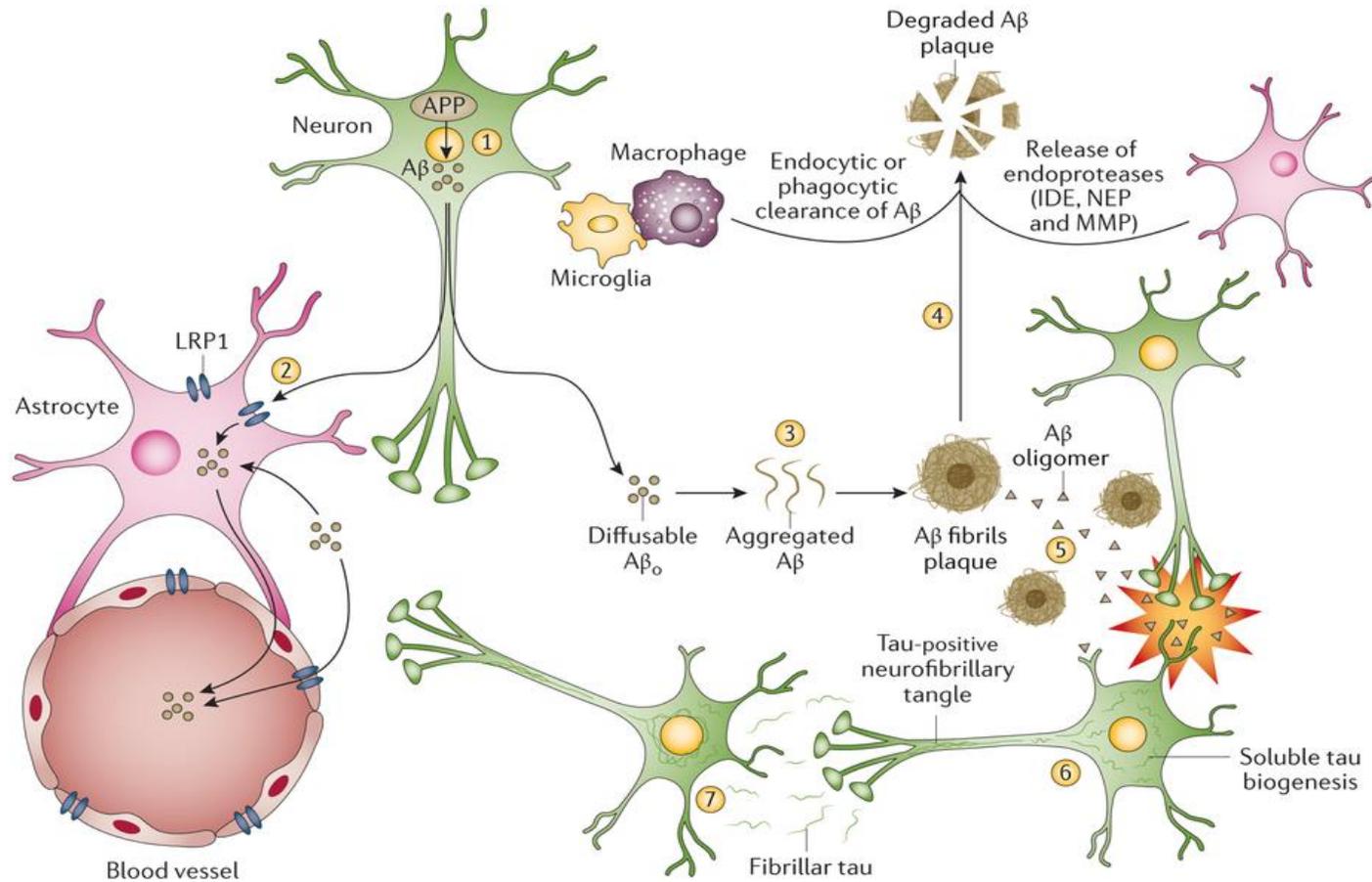


Figure development

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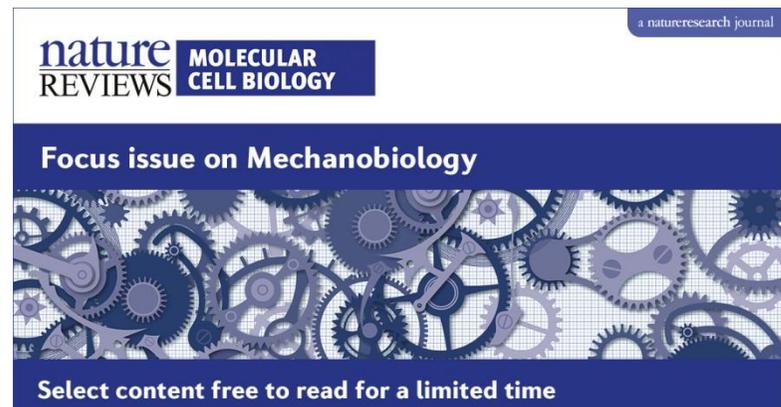
...to this



Nature Reviews | Disease Primers

What else do Reviews editors do?

- Write research highlights
- Read! Scan the literature to select material for research highlights, get commissioning ideas
- Attend conferences/labs (networking, promote the journal, remain updated)
- Design and execute special projects: focus issues, web collections, posters, animations and podcasts



Key skills for the job

- Broad interest in science
- Strong analytical skills
- Strong science writing skills
- Ability to handle multiple tasks simultaneously, to juggle between projects
- Ability to see 'the big picture' (for example emerging themes from individual articles)
- Ability to conceptualize complex problems
- Ability to give and receive feedback
- Confidence in defending your decisions and ideas
- Good eye for detail

Selection process

1. CV + covering letter

- Expert evaluation by the journal team
- Focus on science



2. Editorial test + Interview

In Reviews a two-step process

- Test to complete at home, including all major editorial tasks: editing, commissioning writing => usually to return within 1 week
- Interview with the journal team: your background, interests in science publishing, journal background (focus, scope, recent content, competitors), your test

In primary research journals

- Manuscript test (critical evaluation of real submissions, decision making)
- Interview with the journal team

Career progression

Associate Editor

An Associate Editor is an editor who is still learning aspects of the job and working toward acquiring the skills and experience needed for promotion to Senior editor

Associate Editors undergo a period of initial training of approximately 6 months supervised by a Senior Editor, Team Manager or Chief Editor.

Senior Editor

A Senior Editor is an experienced editor who has mastered all the requirements of the job. Promotion to Senior Editor is merit-based requires formal application. As a guideline, editors should aim to fulfill the promotion criteria within 2 years.

Chief Editor

The Chief Editor is the leader of a journal's editorial team.

Executive Editor

The Executive Editor oversees the editorial direction of multiple titles.

How did I get here?

- **Background**

PhD as a part of DIPP, group of Caren Norden

- **Why publishing?**

I did not feel that I belong in academia (narrow focus, 'luck factor', effort not immediately translated to outcome)

But I did not want to lose contact with research

Interest in science writing, analysing research articles

- **Why Reviews?**

Not planned; opportunity-based

The timeline

- **PhD Thesis**

November 2010-November 2014

- **Graduation**

January 2015

- **Applications**

January 2015-June 2015

One response! *Locum* Assistant Editor at NRMCB (6-month contract; maternity cover)

- **Editorial test and interview**

June 2015

Offer within 24 hrs from the interview

- **Job start**

September 2015

- **Contract extensions....**

- **Application for a permanent position**

October 2016

Permanent contract

- **Promotion to Senior Editor**

October 2017

What worked for me?

- Highly relevant background
- Broad exposure to science and research (regular attendance of seminars, travel to international meetings)
- *Locum* position => typically entry jobs; no guarantee of extension
- Ready to make the next step in my career
- A couple of unsuccessful attempts => improving CV and cover letter with each attempt

What do I particularly enjoy about this role

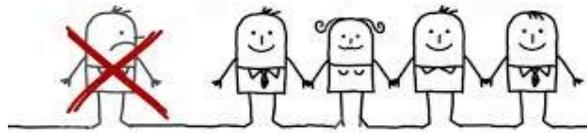
- Very close contact with academia and research
- Work-to-life balance certainly better than in academia
- Highly stimulating job => each day brings something new
- Opportunity to develop many skills
- Direct translation of effort to outcome => you can really see the articles changing and developing!
- Ability to travel
- Rather flexible hours; possibility of working remotely



What are the cons?

“I love deadlines. I love the whooshing noise they make as they go by.”
Douglas Adams

- Tight, sometimes unpredictable deadlines (for which authors have a blatant disregard!)
- Disgruntled authors (e.g. with regard to level of editing), referees (e.g. if we overrule their recommendations) or readers
- High pressure
- No role in discoveries



What else to consider?

- There is no course/internship you could take to prepare for this job=> sink or swim
- Not a 9-5 job!
- Most office locations are in expensive, big cities
- Office job
- Very few job opportunities in general + geographical considerations



My personal tips: how to prepare

- Develop and be prepared to demonstrate the breadth of knowledge in a particular discipline => know what is going on and who is 'on top'
- Engage in writing/proofreading opportunities
- Have a go at writing research highlights and ask others for feedback!
- Try to identify bigger topics, overarching themes emerging from literature => What is 'hot' right now? Where is your field going?
- Analyse papers you read => Is the paper good (on scientific and writing level)? If not, why not? What are the shortcomings?

My personal tips: application process

- Look for opportunities as close to your research area as possible
=> highlight your expertise and knowledge
- Look for *Locum*/temporary positions => less competition! It gives you time to think whether this is really something YOU want to do
- Develop your CV and cover letter => application tailored for a particular position (addressed directly to the chief editor)
- Always have a plan B! => doing a PostDoc* is a good idea

*Although Postdoctoral experience is not mandatory it is often desired (particularly for editorial positions in primary research)

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- physical sciences
- applied sciences
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- mathematics

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Thank you

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Paulina Strzyz

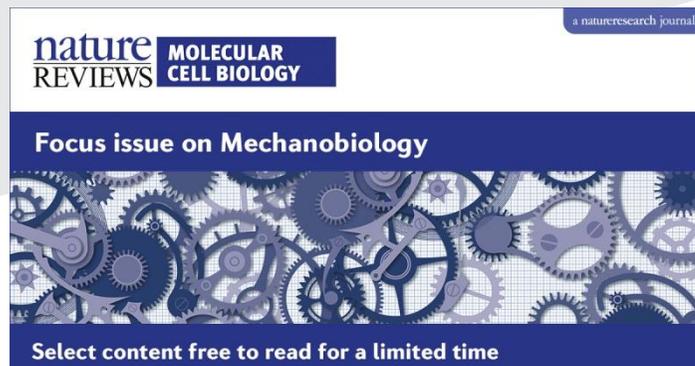
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Focus on Mechanobiology!



The story behind the image



How chameleons change colour

Chameleons are well known for their potential to change colour but recent research on panther chameleons is the first to find two layers of crystal containing cells, each with a potentially different purpose. Researchers from the University of Geneva have speculated that the deeper crystal containing cells may help with the regulation of temperature, whilst the more superficial layer of colour changing cells could be responsible for camouflage or mating displays.

natureresearch

Nature Research Group - Editorial and Publishing Job Family Anchor Roles



Job Family Discipline		Overview of career levels/bands												
		Individual Contributor						Management						
		Business Support		Professional				Management						
		Entry	Competent	Entry	Advanced Beginner	Competent	Specialist	Expert	Supervisor	Manager	Senior Manager	Group Manager	Snr. Group Manager	
Journals Editorial						Associate Editor	Senior Editor		Team Manager/Leader	Chief Editor	Executive Editor			Editorial Director
Editorial Admin		Editorial Assistant	Senior Editorial Assistant						Editorial Assistant Team Leader			Chief Editor, Nature/NComms		
Magazines Editorial						Associate Editor	Senior Editor				Chief Editor	Managing Editor	Executive Editor	Editorial Director
Subediting & Copy Editing				Copy/Sub Editing Assistant	Associate Copy/Sub Editor	Senior Copy/Sub Editor								
Editorial Technical & Support								Head of Editorial Policy				Head of Editorial Services	Head of Researcher Services	
Publishing				Publishing Assistant	Associate Publishing Manager	Publishing Manager	Senior Publishing Manager	Head of Publishing (Specific area)				Head of Publishing, NRG Journals	Publishing Director	
Art & Multimedia														
Art Editing					Assistant Art Editor	Art Editor	Senior Art Editor				Managing Art Editor			
Design					Assistant Designer	Designer	Art Director							
Multimedia				Multimedia Intern		Associate Multimedia Editor	Senior Multimedia Editor				Chief Multimedia Editor	Managing Multimedia Editor		

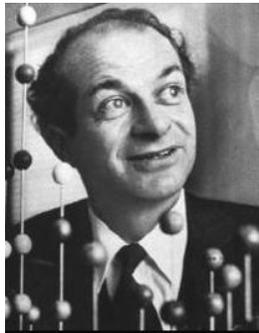
The need for Reviews

- They help to digest and analyse the primary literature
- An invaluable teaching tool
- Useful for grant writing
- They provide an introduction to new fields; can inspire future research; can connect different fields
- Some of the most interesting concepts emerge in Reviews; they provide an opportunity to reflect on the development of a research field

(a service to the research community -- rewarding...)

Commissioning: what do we consider?

- Current hot topics (and likely future hot topics)?
- Are there areas or topics that require an update?
- Current controversies?
- What would be the scope of the proposed article?
- Is now the right time to commission this article?
- Do we have another article in the pipeline that will overlap?
- Who would be a good author?

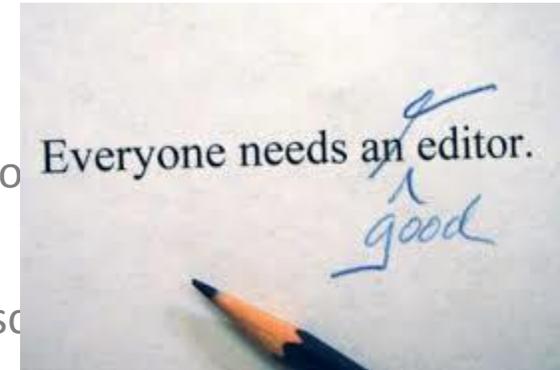


The way to get good ideas is to get lots of ideas,
and throw the bad ones away.

(Linus Pauling)

Editing a Review into shape

- Does the title match the content?
- Does the author give a good introduction?
- Is the article in a logical order, or do sections need to
- Does the text flow well from one section to the next (tell a story)?
- Is the author's meaning clear and do sentences make sense?
- Does the author insightfully synthesize existing data?
- Do the figures work?
- Is the text properly referenced?
- Is the review too long or too short?

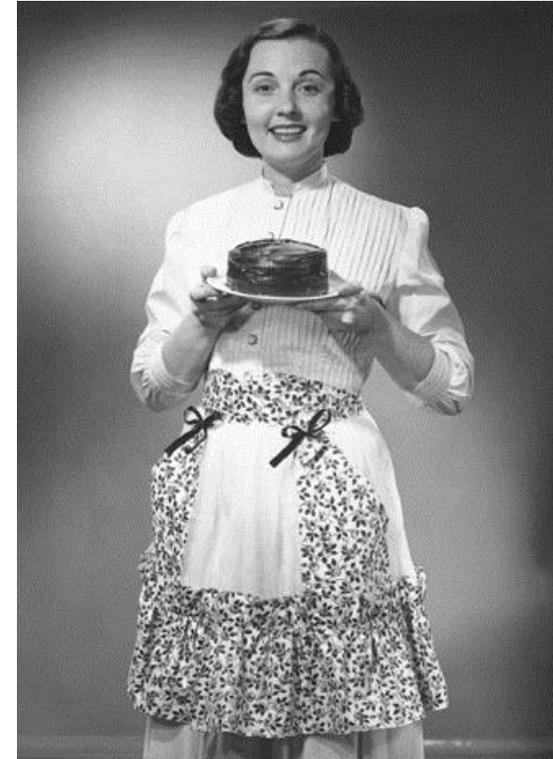


Peer review and decisions

- All back-half content (except Viewpoints) is peer reviewed
- Reviewers (especially if representing different expertise) will often disagree with each other, and some issues are subjective: our job is to guide the author in terms of which comments are (and are not) essential to address
- Editors discuss and make decisions based on arguments; we don't simply count votes
- Editors, not reviewers, ultimately decide what is published in all *Nature*-branded journals, and take full responsibility for decisions
- Rejection is rare but does happen – even for invited reviews



Recognizing what makes a good review



The 'killer' Review: summarizing a field at exactly the right time, with a truly original perspective; an article that generates a shift in perspective.