Broadview
www.broadview.com.cn

R语言

数据可视化之美

专业图表绘制指南

张杰 / 著

中国工信出版集团

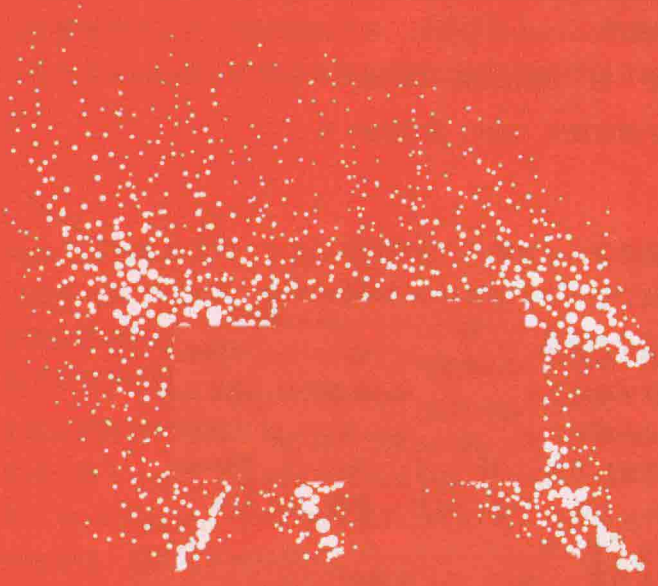
電子工業出版社
PUBLISHING HOUSE OF ELECTRONICS INDUSTRY
http://www.phei.com.cn

R语言

数据可视化之美

专业图表绘制指南

张杰 / 著



電子工業出版社
Publishing House of Electronics Industry
北京•BEIJING

内 容 简 介

本书主要介绍使用 R 中的 ggplot2 包及其拓展包绘制专业图表的方法。本书先介绍了 R 语言编程基础知识，以及使用 dplyr、tidyr、reshape2 等包的数据操作方法；再对比了 base、lattice 和 ggplot2 包的图形语法。本书首次系统性地介绍了使用 ggplot2 包及其拓展包绘制类别对比型、数据关系型、时间序列型、整体局部型等常见的二维图表的方法，以及使用 plot3D 包绘制三维图表（包括三维散点图、柱形图和曲面图等）的方法。另外，本书也首次介绍了论文中学术图表的图表配色、规范格式等相关技能与知识。

图书在版编目（CIP）数据

R 语言数据可视化之美：专业图表绘制指南 / 张杰著. —北京：电子工业出版社，2019.6
ISBN 978-7-121-36366-5

Ⅰ. ①R… Ⅱ. ①张… Ⅲ. ①统计分析—应用软件—指南 Ⅳ. ①C819-62

中国版本图书馆 CIP 数据核字（2019）第 070960 号

责任编辑：石　倩
印　　刷：中国电影出版社印刷厂
装　　订：中国电影出版社印刷厂
出版发行：电子工业出版社
　　北京市海淀区万寿路 173 信箱　邮编 100036
开　　本：787×980　1/16　印张：18.25　字数：461 千字
版　　次：2019 年 6 月第 1 版
印　　次：2019 年 6 月第 1 次印刷
定　　价：109.00 元

凡所购买电子工业出版社图书有缺损问题，请向购买书店调换。若书店售缺，请与本社发行部联系，联系及邮购电话：（010）88254888，88258888。
质量投诉请发邮件至 zlts@phei.com.cn，盗版侵权举报请发邮件至 dbqq@phei.com.cn。
本书咨询联系方式：010-51260888-819，faq@phei.com.cn。

前 言

本书主要介绍使用 R 中的 ggplot2 包及其拓展包绘制专业图表的方法。本书先介绍了 R 语言编程基础知识，以及使用 dplyr、tidyr、reshape2 等包的数据操作方法；再对比了 base、lattice 和 ggplot2 包的图形语法。本书首次系统性地介绍了使用 ggplot2 包及其拓展包绘制类别对比型、数据关系型、时间序列型、整体局部型等常见的二维图表的方法，以及使用 plot3D 包绘制三维图表（包括三维散点图、柱形图和曲面图等）的方法。另外，本书也首次介绍了论文中学术图表的图表配色、规范格式等相关技能与知识。

本书定位

虽然现在 Python 语言越来越流行，尤其是在机器学习与深度学习等领域，但是 R 语言在数据分析与可视化方面仍然具有绝对的优势，其中 ggplot2 包及其拓展包人性化的绘图语法大受用户的喜爱，特别是生物信息与医学研究者。现在 *Nature*、*Science* 和 *Cell* 等期刊上大量的图表都是使用 R 语言绘制的，所以很有必要系统性地介绍 R 语言的绘图方法。

R ggplot2 有两本很经典的教程：*ggplot2 Elegant Graphics for Data Analysis* 和 *R Graphics Cookbook*，两书重点介绍了 ggplot2 包的绘图语法及常见图表的绘制方法，但是其介绍的图表种类并不多。所以本书基于 R 中的 ggplot2 包及其拓展包和 plot3D 包，系统性地介绍了几乎所有常见的二维和三维图表的绘制方法，包括简单的柱形图系列、条形图系列、折线图系列，以及复杂的和弦图、矩形树状图、日历图等。

读者对象

本书适用于想学习数据分析与可视化相关专业课程的高校学生，以及对数据分析与可视化感兴

趣的职场人士阅读，尤其是 R 语言用户。从软件掌握程度而言，本书同样适用于零基础学习 R 语言的用户。

阅读指南

全书内容共有 9 章，其中，第 1 章和第 2 章是后面 7 章的基础，第 3～8 章都是独立章节，可以根据实际需求有选择性地进行学习。

第 1 章　介绍 R 语言编程与数据可视化基础，对比了 base、lattice 和 ggplot2 包的图形语法，重点介绍了 ggplot2 包的图形语法；

第 2 章　介绍 R 语言数据处理基础，重点介绍了使用 dplyr、tidyr、reshape2 等包的数据操作方法；

第 3 章　介绍类别比较型图表，包括柱形图系列、条形图系列、南丁格尔玫瑰图、径向柱图等约 30 种图表；

第 4 章　介绍数据关系型图表，包括二维和三维散点图、气泡图、等高线图、三维曲面图、三元相图、二维和三维瀑布图、相关系数热力图等约 60 种图表；

第 5 章　介绍数据分布型图表，包括一维、二维和三维的统计直方图和核密度估计图、抖动散点图、点阵图、箱形图、小提琴图等约 50 种图表；

第 6 章　介绍时间序列型图表，包括折线图和面积图系列、日历图、螺旋图系列、量化波形图、地平线图等约 20 种图表；

第 7 章　介绍局部整体型图表，包括饼图、散点复合饼图系列、旭日图、矩形树状图、马赛克图、华夫饼图等约 20 种图表；

第 8 章　介绍高维数据的可视化方法，包括分面图系列、矩阵散点图、热力图、平行坐标系图、RadViz 图、图标法等约 20 种图表；

第 9 章　介绍论文中学术图表的常用技能，包括常见的截图与图片处理软件及其功能、矢量图片的修改、论文中学术图表数据的提取与重绘、论文中学术图表的规范与调整等。

应用范围

本书的图表绘制方法都是基于 R 中的 ggplot2 包及其拓展包和其他绘图包实现的，几乎适应于所有常见的二维和三维图表。但是由于依据《地图管理条例》第十五条规定："国家实行地图审核制度。向社会公开的地图，应当报送有审核权的测绘地理信息行政主管部门审核。但是，景区图、街区图、地铁线路图等内容简单的地图除外。"本书本来有专门的章节讲解使用 R 语言如何绘制不同地理坐标

投影下，从世界到不同国家与区域的地图，但是由于地图审核周期等方面的原因忍痛移除。

适用版本

本书所用 R 版本为：3.3.3。R 作为开源免费的软件，数据分析与可视化的包更新迭代很快，这是它的优势。但是有时候有些代码运行可能会由于 R 或者 R 包版本的更新，而出现函数弃用（deprecated）的情况。此时，需要自己更新代码，使用新的函数替代原有的函数等。

源代码

本书配备有几乎所有图表的 R 语言源文件及其.csv 或.txt 格式的数据源文件。但是需要注意的是，如果运行的 R 语言版本没有安装相应的数据分析与可视化的包（package），那么请预先安装相应的包，才能成功运行代码。同时，也请注意运行 R 语言和 R 包的版本是否已经更新。

与我联系

因本人知识与能力所限，书中纰漏之处在所难免，欢迎并恳请读者朋友们给予批评与指正，可以通过邮箱联系笔者本人；如果读者有关于 R 语言学术图表或商业图表绘制的问题，可以联系笔者交流。另外，更多关于 R 语言图表绘制的教程请关注笔者的博客、专栏和微博平台。也可以重点关注我们的微信公众号：EasyCharts，也可以添加笔者微信：EasyCharts。R 语言数据分析与可视化的文章会优先发表在微信公众号平台。


邮　　箱：easycharts@qq.com


知乎专栏：https://zhuanlan.zhihu.com/EasyCharts-R（知乎账号：EasyCharts）


博　　客：http://easychart.github.io/


新浪微博：https://weibo.com/easycharts?source=blog&is_all=1（微博账号：EasyCharts）

致谢

桃李春风一杯酒，江湖夜雨十年灯。笔者的处女作《Excel 数据之美：科学图表与商业图表的绘制》也至今出版逾两年，一直想着要修订这本书的。但是旧书未翻新，新书忙于码字改稿，实在是有愧于读者。其实，在撰写这本新书的时候，数次想放弃。写书实在是一件费力劳神的事情，笔者是凭借着对数据可视化的热爱才坚持至今。

这本书从 2017 年 5 月 25 日开始动笔，断断续续居然也花费了两年的时间。与其说是花费，不如说是陪伴吧。笔者经常对朋友开玩笑说，心情不好的时候码码代码、画画图表，是一件消磨时间、

放松心情的事情。

在断断续续的写稿中，笔者也认识了很多热爱数据分析与可视化的朋友，甚是荣幸，也得益于他们的帮助。很感谢《R 语言游戏数据分析与挖掘》的作者谢佳标老师和先锋信息科技有限公司 CEO 林祯舜老师对笔者的鼓励与帮助，也因此有幸参加 2018 年的 R 语言大会；也非常感谢在码字、写代码时一起交流学习的李誉辉（四川大学高分子学院）、杜雨（美团用户平台—大数据与算法部—商业分组部）、刘钰（河南大学土木建筑学院）、厚缁（深圳中观经济咨询有限公司）等诸多技术大佬。因为有你们的帮助，所以才有今天这本书。

最后，想对大家说，也是对自己说：且将新火试新茶，诗酒趁年华！

作　者

2019 年 3 月 31 日

读 者 服 务

轻松注册成为博文视点社区用户（www.broadview.com.cn），扫码直达本书页面。

- **下载资源**：本书如提供示例代码及资源文件，均可在 下载资源 处下载。
- **提交勘误**：您对书中内容的修改意见可在 提交勘误 处提交，若被采纳，将获赠博文视点社区积分（在您购买电子书时，积分可用来抵扣相应金额）。
- **交流互动**：在页面下方 读者评论 处留下您的疑问或观点，与我们和其他读者一同学习交流。

页面入口：http://www.broadview.com.cn/36366

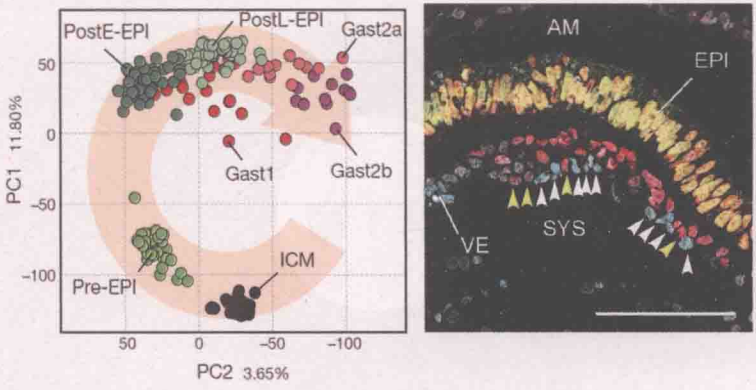
目 录

第1章

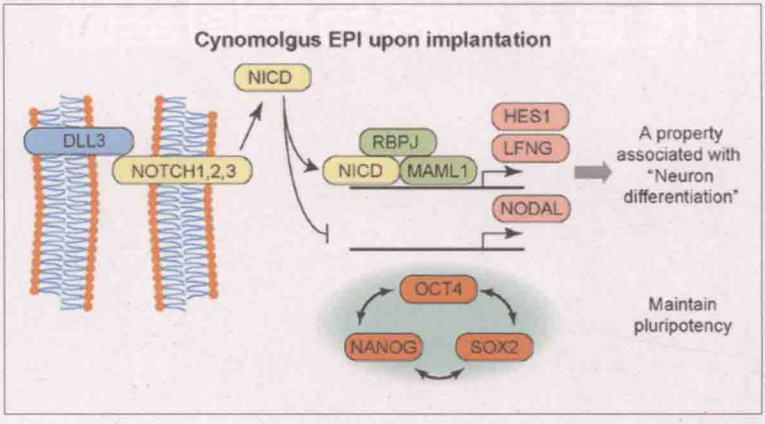
R语言编程与绘图基础

1.1 学术图表的基本概念

学术图表是为论文结论（conclusion）提供证据的视觉方式。所以，论文作者为了产生强烈的视觉效果，应该通过分析实验数据，精心设计可视化图表。本书开篇先跟大家讲讲学术图表的类型。通常学术论文中主要有三类图表，如图 1-1-1 所示。流程示意图和数据展示图都是非常讲究技能的图表，本书重点讲解的是数据展示图。



(a) 数据展示图　　(b) 实验拍摄图



(c) 流程示意图

图 1-1-1　不同类型的图表[1]

1. 数据展示图：先根据数据绘制成图表，再将其导出生成图片，主要包括各种点线图、柱形图、饼图等统计图表，一般使用 Excel、GraphPad Prism、SigmaPlot、Origin、MATLAB、Python、R 等专业绘图软件绘制（Excel 并非如大众所说不能导出高分辨率的图片和矢量图）。注意，保存图片时，

一定要保存成高分辨率的 TIFF 格式和 EPS 矢量格式的图片，因为矢量图片是可以使用图片处理软件进行再编辑的。由数据生成的图表是可重复修改的，因此一定要保存好原始数据，一旦发现图表有任何问题就可以进行修改。

2. 实验拍摄图：使用设备或者仪器拍摄采集的图片，包括显微镜、扫描仪及摄像机等所拍照片。一定要在最刚开始时就拍成高清的（设置成高分辨率），也就是要保证原始图片的高分辨率，接下来处理图片就会比较方便，免得因为图片质量不佳而重复实验。必要的话，把每张图片存储成 TIFF 和 JPG 两种格式（以应对部分期刊的特殊要求）。

3. 流程示意图：使用简明的线条、基本图形和箭头等绘制论文中的重要的实验流程或步骤，用以说明基本原理或解释文字材料，一般使用 PPT、Visio、Illustrator、CorelDRAW、3DMax 等软件绘制。

1.1.1　学术图表的基本作用

图表在学术论文中是很重要的一部分。实验结果通常是论文的核心和主要部分，而实验结果一般以图表的形式呈现。读者经常通过图表来判断这篇文章是否值得阅读，所以每个图表都应该能不依赖正文而独立存在。所谓“一图抵千言”（A picture is worth a thousand words）。图表设计是否精确且合理直接影响数据的完整与准确表达，从而影响论文的质量。图表是期刊评审过程中仅次于摘要的关键一环，准确而美观的图表能促进审稿人和读者对论文表达的快速理解。以 *Nature* 上的文章 *Cotranslational signal-independent SRP preloading during membrane targeting* [2]选取的前两页为例（见图 1-1-2），我们首先关注的是论文的标题（title），其次是第一页最开始的摘要（abstract），接下来我们就被这些包含大量实验数据与信息的图表所吸引。在每页的文章中，包含图名（figure）的图表部分几乎占据整个页面的 1/4~1/3，由此可见图表在论文中的重要性。

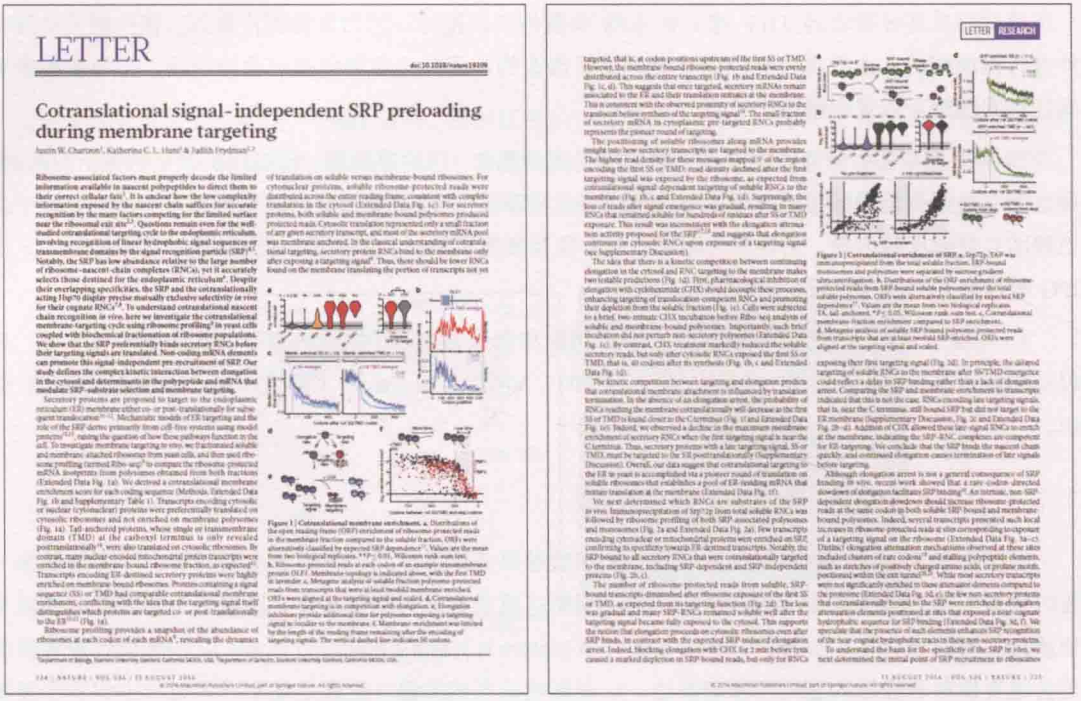
根据 Edward R. Tufte 的 *The Visual Display of Quantitative Information*[3]和 *Visual Explanations*[4]的阐述，图表在论文的作用主要有：

（1）真实、准确、全面地展示数据；

（2）以较小的空间承载较多的信息；

（3）揭示数据的本质、关系、规律。

第三点作用尤为重要，Matthew O. Ward 也提出，可视化的终极目标是洞悉蕴含在数据中的现象和规律，这包括多重含义：发现、决策、解释、分析、探索和学习[5]。表 1-1-1 所示的原始数据是 31 组 *x*-*y* 的二维数据。仅仅只从数据的角度去观察数据，就很难发现 *x* 与 *y* 之间的具体关系。将实际的数据分布情况使用二维可视化的方法呈现，如图 1-1-3 所示，则可以快速地从数据中发现数据内在的模式与规律。所以，有时使用数据可视化的方法也可以很好地帮助我们去分析数据。



LETTER

doi:10.1038/nature19359

Cotranslational signal-independent SRP preloading during membrane targeting

Justin W. Chartron[1], Katherine C. L. Hunt[1] & Judith Frydman[1,2]

Ribosome-associated factors must properly decode the limited information available in nascent polypeptides to direct them to their correct cellular fate[1]. It is unclear how the low complexity information exposed by the nascent chain suffices for accurate recognition by the many factors competing for the limited surface near the ribosomal exit site[2,3]. Questions remain even for the well-studied cotranslational targeting cycle to the endoplasmic reticulum, involving recognition of linear hydrophobic signal sequences or transmembrane domains by the signal recognition particle (SRP)[4,5]. Notably, the SRP has low abundance relative to the large number of ribosome–nascent-chain complexes (RNCs), yet it accurately selects those destined for the endoplasmic reticulum[6]. Despite their overlapping specificities, the SRP and the cotranslationally acting Hsp70 display precise mutually exclusive selectivity in vivo for their cognate RNCs[7,8]. To understand cotranslational nascent chain recognition in vivo, here we investigate the cotranslational membrane-targeting cycle using ribosome profiling[9] in yeast cells coupled with biochemical fractionation of ribosome populations. We show that the SRP preferentially binds secretory RNCs before their targeting signals are translated. Non-coding mRNA elements can promote this signal-independent pre-recruitment of SRP. Our study defines the complex kinetic interaction between elongation in the cytosol and determinants in the polypeptide and mRNA that modulate SRP–substrate selection and membrane targeting.

Secretory proteins are proposed to target to the endoplasmic reticulum (ER) membrane either co- or post-translationally for subsequent translocation[10–12]. Mechanistic models of ER targeting and the role of the SRP derive primarily from cell-free systems using model proteins[13,14], raising the question of how these pathways function in the cell. To investigate membrane targeting in vivo, we fractionated soluble and membrane-attached ribosomes from yeast cells, and then used ribosome profiling (termed Ribo-seq)[9] to compare the ribosome-protected mRNA footprints from polysomes obtained from both fractions (Extended Data Fig. 1a). We derived a cotranslational membrane enrichment score for each coding sequence (Methods, Extended Data Fig. 1b and Supplementary Table 1). Transcripts encoding cytosolic or nuclear (cytonuclear) proteins were preferentially translated on cytosolic ribosomes and not enriched on membrane polysomes (Fig. 1a). Tail-anchored proteins, whose single or transmembrane domain (TMD) at the carboxyl terminus is only revealed posttranslationally[15], were also translated on cytosolic ribosomes. By contrast, many nuclear-encoded mitochondrial protein transcripts were enriched in the membrane bound ribosome fraction, as expected[16]. Transcripts encoding ER-destined secretory proteins were highly enriched on membrane bound ribosomes. Proteins containing a signal sequence (SS) or TMD had comparable cotranslational membrane enrichment, conflicting with the idea that the targeting signal itself distinguishes which proteins are targeted co- or post-translationally to the ER[10,12] (Fig. 1a).

Ribosome profiling provides a snapshot of the abundance of ribosomes at each codon of each mRNA[9], revealing the dynamics of translation on soluble versus membrane-bound ribosomes. For cytonuclear proteins, soluble ribosome-protected reads were distributed across the entire reading frame, consistent with complete translation in the cytosol (Extended Data Fig. 1c). For secretory proteins, both soluble and membrane-bound polysomes produced protected reads. Cytosolic translation represented only a small fraction of any given secretory transcript, and most of the secretory mRNA pool was membrane anchored. In the classical understanding of cotranslational targeting, secretory protein RNCs bind to the membrane only after exposing a targeting signal[17]. Thus, there should be fewer RNCs found on the membrane translating the portion of transcripts not yet

Figure 1 | Cotranslational membrane enrichment. a, Distributions of the open reading frame (ORF) enrichment of ribosome-protected reads in the membrane fraction compared to the soluble fraction. ORFs were alternatively classified by expected SRP dependence[7,8]. Values are the mean from two biological replicates. ***$P < 0.01$, Wilcoxon rank-sum test. **b**, Ribosome-protected reads at each codon of an example transmembrane protein (SLC). Membrane topology is indicated above, with the first TMD in lavender. **c**, Metagene analysis of soluble fraction polysome-protected reads from transcripts that were at least twofold membrane enriched. ORFs were aligned at the targeting signal and scaled. **d**, Cotranslational membrane targeting is in competition with elongation. **c**, Elongation inhibition provides additional time for polysomes exposing a targeting signal to localize to the membrane. **f**, Membrane enrichment was limited by the length of the reading frame remaining after the encoding of targeting signals. The vertical dashed line indicates 50 codons.

[1]Department of Biology, Stanford University, Stanford, California 94305, USA. [2]Department of Genetics, Stanford University, Stanford, California 94305, USA.

targeted, that is, at codon positions upstream of the first SS or TMD. However, the membrane-bound ribosome-protected reads were evenly distributed across the entire transcript (Fig. 1b and Extended Data Fig. 1c, d). This suggests that once targeted, secretory mRNAs remain associated to the ER and their translation initiates at the membrane. This is consistent with the observed proximity of secretory RNCs to the translocon before synthesis of the targeting signal[18]. The small fraction of secretory mRNA in cytoplasmic pre-targeted RNCs probably represents the primary round of targeting.

The positioning of soluble ribosomes along mRNA provides insight into how secretory transcripts are targeted to the membrane. The highest read density for these messages mapped 5′ of the region encoding the first SS or TMD: read density declined after the first targeting signal was exposed by the ribosome, as expected from cotranslational signal-dependent targeting of soluble RNCs to the membrane (Fig. 1b, c and Extended Data Fig. 1d). Surprisingly, the loss of reads after signal emergence was gradual, resulting in many RNCs that remained soluble for hundreds of residues after SS or TMD exposure. This result was inconsistent with the elongation attenuation activity proposed for the SRP[13,19] and suggests that elongation continues on cytosolic RNCs upon exposure of a targeting signal (see Supplementary Discussion).

The idea that there is a kinetic competition between continuing elongation in the cytosol and RNC targeting to the membrane makes two testable predictions (Fig. 1d). First, pharmacological inhibition of elongation with cycloheximide (CHX) should decouple these processes, enhancing targeting of translocation-competent RNCs and promoting their depletion from the soluble fraction (Fig. 1e). Cells were subjected to a brief, two-minute CHX incubation before Ribo-seq analysis of soluble and membrane-bound polysomes. Importantly, such brief incubation did not perturb non-secretory polysomes (Extended Data Fig. 1e). By contrast, CHX treatment markedly reduced the soluble secretory reads, but only after cytosolic RNCs exposed the first SS or TMD, that is, 40 codons after its synthesis (Fig. 1b, c and Extended Data Fig. 1d).

The kinetic competition between targeting and elongation predicts that cotranslational membrane attachment is influenced by translation termination. In the absence of an elongation arrest, the probability of RNCs reaching the membrane cotranslationally will decrease as the first SS or TMD is found closer to the C-terminus (Fig. 1f and Extended Data Fig. 1e). Indeed, we observed a decline in cotranslational membrane enrichment of secretory RNCs when the first targeting signal is near the C-terminus. Thus, secretory proteins with a late targeting signal, SS or TMD, may be targeted to the ER posttranslationally (Supplementary Discussion). Overall, our data suggest that cotranslational targeting to the ER in yeast is accomplished via a primary round of translation on soluble ribosomes that establishes a pool of ER-residing mRNA that initiate translation at the membrane (Extended Data Fig. 1f).

We next determined which RNCs are substrates of the SRP in vivo. Immunoprecipitation of Sec$_{72}$p from total soluble RNCs was followed by ribosome profiling of both SRP-associated polysomes and monosomes (Fig. 2a and Extended Data Fig. 2a). The transcripts encoding cytonuclear or mitochondrial proteins were enriched on SRP, confirming its specificity towards ER-destined transcripts. Notably, the SRP-bound in all secretory RNCs that were cotranslationally targeted to the membrane, including SRP-dependent and SRP-independent proteins (Fig. 2b, c).

The number of ribosome protected reads from soluble, SRP-bound transcripts diminished after ribosome exposure of the first SS or TMD, as expected from its targeting function (Fig. 2d). The loss was gradual and many SRP-RNCs remained soluble well after the targeting signal became fully exposed to the cytosol. This supports the notion that elongation proceeds on cytosolic ribosomes even after SRP binds, in contrast with the expected SRP-induced elongation arrest. Indeed, blocking elongation with CHX for 2 min before lysis caused a marked depletion in SRP bound reads, but only for RNCs

Figure 2 | Cotranslational enrichment of SRP. a, Sec$_{72}$p TAP was immunoprecipitated from the total soluble fraction. SRP-bound monosomes and polysomes were separated by sucrose gradient ultracentrifugation. **b**, Distributions of the ORF enrichment of ribosome-protected reads from SRP-bound soluble polysomes over the total soluble polysomes. ORFs were alternatively classified by expected SRP dependence[7,8]. Values are the mean from two biological replicates. TA, tail-anchored. *$P < 0.05$, Wilcoxon rank-sum test. **c**, Cotranslational membrane-fraction enrichment compared to SRP enrichment. **d**, Metagene analysis of soluble SRP-bound polysome protected reads from transcripts that are at least twofold SRP-enriched. ORFs were aligned at the targeting signal and scaled.

exposing their first targeting signal (Fig. 2d). In principle, the delayed targeting of soluble RNCs to the membrane after SS/TMD emergence could reflect a delay to SRP binding rather than a lack of elongation arrest. Comparing the SRP and membrane enrichment to transcripts indicated that this is not the case. RNCs encoding late targeting signals, that is, near the C-terminus, still bound SRP but did not target to the ER membrane (Supplementary Discussion, Fig. 2c and Extended Data Fig. 2b–d). Addition of CHX allowed these late signal RNCs to enrich at the membrane, indicating the SRP–RNC complexes are competent for ER-targeting. We conclude that the SRP binds the nascent chain quickly, and continued elongation causes termination of late signals before targeting.

Although elongation arrest is not a general consequence of SRP binding in vivo, recent work showed that a rare codon-directed slowdown of elongation facilitates SRP binding[20]. As in vitro, non-SRP-dependent elongation slowdown should increase ribosome protected reads at the same codon in both soluble SRP-bound and membrane-bound polysomes. Indeed, several transcripts protected such local increases in ribosome-protected reads at sites corresponding to exposure of a targeting signal on the ribosome (Extended Data Fig. 3a–c). Diribin elongation attenuation mechanisms observed at these sites included clusters of rare codons[20] and stalling polypeptide elements, such as stretches of positively charged amino acids, or proline motifs, positioned within the exit tunnel[20,21]. While most secretory transcripts were not significantly enriched in these attenuator elements compared to the proteome (Extended Data Fig. 3d, e), the few non-secretory proteins that cotranslationally bound to the SRP were enriched in elongation attenuator elements positioned at sites that exposed a near-cognate hydrophobic sequence for SRP binding (Extended Data Fig. 3d, f). We speculate that the presence of such elements enhances SRP recognition of the near-cognate hydrophobic tracts in these non-secretory proteins.

To understand the basis for the specificity of the SRP in vivo, we next determined the initial point of SRP recruitment to ribosomes

(a) (b)

图 1–1–2　论文摘取的页面案例[21]

表 1-1-1　四组二维数据点集（相同的 *x* 变量，不同的 *y* 变量：*y*1，*y*2，*y*3，*y*4）

x	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
*y*1	4.6	5.4	5.2	6.6	5.9	6.1	5.8	6.8	6.5	6.7	6.9	11.1	8.2	10.3	12.8	13
*y*2	6.1	11.6	16.6	19	22.7	31.8	34	33.7	35.6	34.5	39.6	58.3	57.7	72.9	68.4	82.6
*y*3	5.5	31.1	33.1	51.8	55.7	60.7	63.5	75.5	84.4	84.6	76.3	92.4	81.6	91	88.1	93.8
*y*4	1	3	4.9	7.9	9.8	12	18.9	24.7	28.9	28.6	39.3	33.2	42.1	54.4	43.3	90.2

x	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	-
*y*1	20.8	12.4	15.9	15.3	38.8	35.9	24.3	54.5	62.9	43.8	76.9	91	96.9	51.4	100	-
*y*2	84.5	82	89.1	102.1	68.1	96.3	108.5	76.7	107.6	103.4	116.5	106.4	142.5	115.1	110.5	-
*y*3	101.3	103	107.4	104.3	110.7	103.4	113.6	105.1	112.5	119.3	113.7	109.5	108.7	110.1	118.8	-
*y*4	81.2	90.8	70.9	66.8	67.5	88.6	116.9	141.4	104	161.4	101.8	137.1	175.3	119.5	257.3	-