

尊敬的侯建国院长、科学院领导、姚期智院士、科学道德建设委员会院士、信息学部院士和相关专家：

你们好！

中国科学院于2021年8月1日公布了院士初步候选人名单，并接着在相关单位公示了初步候选人的院士申报材料。本人在认真分析北京大学许进教授的材料后，发现**关键内容严重造假并有意掩饰其有本质错误的学术论文**，今天通过这个邮件正式举报。由于担心被打击报复，我不得不用匿名方式举报，但是我今天提供的佐证材料都是**国外著名科学家的实名回复，有邮件佐证**，任何疑问欢迎中国科学院正式向下面这些国外教授发信确认：

- Jeannette M. Wing (周以真) 教授：哥伦比亚大学副校长（首位华裔），美国科学与艺术院院士。
主页：<https://datascience.columbia.edu/people/jeannette-m-wing/>
邮件：wing@columbia.edu 或 jw3585@columbia.edu
- Wing Hung Wong (王永雄) 教授：美国国家科学院院士、中央研究院院士、香港科学院创院院士、斯坦福大学统计系教授。
主页：<https://statistics.stanford.edu/people/wing-hung-wong>
邮件：whwong@stanford.edu
- Eric Winfree 教授：加州理工大学教授。2000年MacArthur Fellowship、美国总统奖PECASE得主。DNA计算国际权威和顶尖学者。
主页：<https://www.dna.caltech.edu/~winfree/>
邮件：winfree@caltech.edu
- Scott Aaronson 教授：德州大学奥斯汀分校教授，曾任麻省理工大学副教授。美国自然科学基金委最高奖Alan T. Waterman奖、美国总统奖PECASE、Tomassoni-Chisesi奖、

ACM Prize in Computing得主。理论计算机、计算复杂性和量子计算国际权威和顶尖学者。

主页：<https://www.scottaaronson.com>

邮件：scott@scottaaronson.com 或 aaronson@cs.utexas.edu

- Richard Beigel教授：天普（Temple）大学教授。算法和复杂性，理论计算机和生物信息学专家。

主页：<https://cis.temple.edu/~beigel/long.html>

邮件：richard.beigel@temple.edu

需要说明的是，在查证过程中，除了给Scott Aaronson教授的邮件用的不是匿名以外，别的邮件本人也均以匿名方式和其他四位教授联系。令人尊敬的是，他们没有因为匿名邮件而不回复，而选择本着科学和实事求是的原则明确澄清，其中Eric Winfree教授还对许进教授的工作进行了点评。从这个角度，我深切体会到**科学真理不容践踏和肆意捏造**，也希望中国科学院对此事严肃处理。

在下面对具体内容的查证和分析前，先总结一下许进材料问题性质和严重性。主要包括三个方面：

1. **肆无忌惮的自行捏造国际专家对其工作的评价**。事实上在院士申报材料 and 北京大学网页报道中出现的专家大多根本就不认识许进教授，也不知道他的工作。这个问题的严重性在于：**许进教授是明明知道是假的，还有意这么写，想蒙混过关，违反了最基本的实事求是的科学精神和学术道德**。这些应该是所有的科研工作者都应该准守的底线，而许进教授竟然在中国最高学术称号的申报材料中屡次跨越红线，是不可原谅的。在调查中发现，**许进教授的惯用伎俩是，在材料中故意只写出外国教授的姓（而不是全名），修改或隐去对方的学校，含糊其辞，以达掩人耳目防止联系对方调查的目的**。我注意到大多数这些评价都有附件支持，但是公示材料中没有展示，我有理由相信附件都是伪造的。可以想象，如果当选，这些问题势必成为国际科学界的丑闻，严重影响中国科学工作者的声誉。

2. 试图掩盖其科学研究的本质错误，并用无关痛痒的所谓特色论文等“称号”试图蒙混过关。这一点可以从Scott Aaronson的回信清楚的看到：许进教授提出的所谓“探针机”是没有实用价值的，论文中生成超过图灵机的论点是完全错误的。这也是国际上做计算机理论研究的严肃学者从来没有引用许进论文的原因，同时论文也没有发表在公认的计算机理论的会议和期刊上。

3. 掩盖自己提出的错误猜想。别人证明了其猜想的错误，许进企图通过“解决了”他的猜想蒙混过关。

这三个问题中前两个及其严重，无论许进是否当选，都已经对中国计算机研究的声誉造成了损害。为避免进一步的国际科研丑闻和对中国科学院的影响，本人认为许进教授应该立即撤回院士申报（或由中科院停止其院士申报流程），并接受相关的责任和调查。这样做的理由是不难理解的：发表在学术期刊的论文如果造假，需要撤稿，而许进这种伪造专家评价的明知故犯的行为，因为直接牵扯到造假人当选科学院院士以后可能的利益，只会性质更加恶劣，期望中国科学院严肃处理。

本人并不认识许进教授，也和他没有瓜葛，我作为一名计算机研究者，我举报许进是因为：

第一，对客观真理的尊重：关于图灵机的计算能力，以及P和NP问题的讨论全世界理论计算机学术界有基本的认识，许进通过发表在一个非理论计算机的刊物上的论文想说自己找到了比图灵机还强的计算模型，这是对真理广大严肃的研究者的不尊重。

第二，对祖国的热爱：许进肆无忌惮的用国外著名学者的名字捏造对自己工作的评价的行为，会严重影响中国科学研究在国际上的声誉，造成国际丑闻。近年来论文撤稿、造假的事情已经层出不穷，如果许进成为院士后果不堪设想。

下面我对许进的问题根据确凿证据进行分析。

问题一：“Your recent breakthrough in DNA computing”，“This is very exciting”的专家评价造假。

许进公示材料的论文2和评价情况如下：

论文：作者：Xu Jin, Qiang Xiaoli, Zhang Kai, Zhang Cheng, Yang Jing； 题目：A DNA computing model for the graph vertex coloring problem based on a probe graph； 期刊名称：Engineering； 卷(期)(年)：4(1) (2018)； 起止页码：第61页至第77页

主要贡献及引用评价情况：

提出并行DNA计算模型，建立相应硬件实现系统，利用该模型成功求解出61-阶图的所有48个3-着色，是迄今国际上最大规模生物计算实验，美国科学院院士Wing及著名DNA计算专家Richard教授评价为：“Your recent breakthrough in DNA computing”，“This is very exciting”。一位论文评审专家称：是继Adleman开创生物计算后最重要成果。[附5-5,6]

针对以上材料，本人不能确认“美国科学院院士Wing”和“著名DNA专家Richard”的身份，但是我在如下网页发现了对许进教授相同研究成果的报道：

<https://hcst.pku.edu.cn/info/1029/1412.htm> （网页见附件1）。

网页面包括下页开始的截图信息：

可以清楚的看到，院士申报材料中的话（被翻译成中文）在这里被说成是“美国科学院院士Eric Winfree”和“美国加利福尼亚大学教授Richard Beigel”的评价。这里的人物和院士材料中不完全一样，不同的人给出一样的评价，有这么巧合的事情吗？这难免让人怀疑这些“评价”就是许进自己杜撰的。请注意上述网页虽然不是院士申报材料，但是是北京大学的新闻，许进在提供新闻稿的时候完全有责任保证信息的真实和准确性。由于

上述两个方面均取得了突破性进展。在DNA计算机领域，课题组针对典型的NP-完全问题——图着色问题的求解，相继提出了非枚举、并行、大规模DNA计算模型后，从理论上对并行DNA计算模型给予系统研究，研究成果《A DNA Computing Model for the Graph Vertex Coloring Problem Based on a Probe Graph》发表在领袖级期刊《Engineering》上。该成果包括在实验方面，实现人类非传统计算机最大规模问题的求解，其算法复杂度到达 3^{59} ；在理论方面，有机将DNA特性与数学模型相结合，整个计算模型中含4个并行部分。美国科学院院士Erik Winfree和美国加利福尼亚大学教授Richard Beigel评价为“你们突破性的成果振奋人心”。审稿专家称该成果是“继Adleman开创生物计算后最重要的突破”。

网页给出了国外教授的名字，我以匿名方式发电子邮件给他们看了网页，要求确认。网页虽然是中文的，但是大概意思可以很容易通过谷歌翻译得到，而且他们的英文名字可以直接看到。另外Eric Winfree不是美国科学院院士，Richard Beigel也不是加利福尼亚大学教授（见开头介绍），也许许进是有意而为之，意在掩人耳目，万一出了问题了可以抵赖。

下页置顶是Eric Winfree的回复，我给对方邮件以及对方邮件回复的包括信箱的完整信息见附件2，中科院可以发信确认。Eric Winfree的邮件明确证明了几点事实：

1. Eric Winfree教授不认识许进，没有看过他的这篇发表在Engineering上的论文；

2. 他对这篇论文的评价不高，认为如果发表在20年前，他也许会有兴趣读。许进这篇论文研究的问题已经不是当前的重要问题，他在今天不会去读它；

3. 他对许进论文所描述的一般计算机用完全穷举搜索方法解决这类问题的不可能性不认同，因为没有人会真的想这么做。他同时指出了基于当前计算机的标准方法能够在1秒之内解决这个问题。换句话说，许进的结果没有实际意义。

4. 他同时查找了他的邮件，但没有发现任何和许进的通信。他虽然说在开会的时候也许和许进见过并说一些客气话，但是他对次深表怀疑。特别强调对这个论文做出breakthrough之类的评价是不可能的。

Dear anonymous Chinese computer researcher,

I am uncomfortable replying to an anonymous account and to someone who is themselves not willing to reveal their name. But I can understand your concern, as this appears to involve academic dishonesty. So I will reply nonetheless. Although, there must be a better way.

It is disconcerting to see my name in these two news links (which I read via translate.google.com to get the gist). I do not recall seeing this paper before; certainly, I have not read it. Just now, I read the abstract — it sounds like the kind of thing I would have been interested to read about 20 years ago, and the theoretical results sound in line with what I would expect to be possible with the theoretical frameworks and techniques of that time. From a superficial skim of the paper, the experimental results appear quite impressive, conceivably comparable to Adleman's 2002 Science paper, although I can't say anything with confidence unless I read the paper carefully. Alas, today, using DNA to compete with electronic computers on NP-complete problems is not something I have much hope for, so I would not be motivated to read a paper with this abstract, at this time. (Further, the claim about how long an electronic computer would take is misleading hype, since no one would seriously program an electronic computer to use exhaustive search. Standard techniques for graph coloring easily solve hard 60-vertex problems in under a second.)

Since my memory is not as good as I might wish, I searched my email but did not find any correspondence with or about Jin Xu or this specific paper. Could I have met Jin Xu at a conference, and said something nice in person? Not impossible, though I doubt it. I do tend to try to see the best in others and compliment them on what they've done well. However, according to translate.google.com, the news articles quote me saying "your breakthrough results are inspiring" and I would not have used the words "breakthrough" or "inspiring" to a journalist about this paper.

I have no idea what Jin Xu's greater ambitions are, and perhaps that's for the best. I have no desire to get involved.

Best regards, whomever you are,
Erik

下面是Richard Beigel教授的回复，我给对方的邮件以及对对方邮件回复的包括信箱的完整信息见附件3，中科院可以发信确认。我们有理由相信Richard Beigel就是许进院士申报材料中的“美国加利福尼亚大学教授Richard Beigel”。

My interests have changed. I have not read any recent papers on DNA computing or graph coloring.

Sincerely,
Richard Beigel

上面的邮件明确说明他没有看过许进的关于DNA computing和graph coloring的论文。

对于“美国科学院院士Wing”，从许进材料中不能判断具体是什么人，但是美国科学院院士是很少的，特别是和许进研究方向相关的院士。通过搜索发现仅有两个可能：Jeannette M. Wing（她是计算机，特别是计算模型专家，虽然不是科学院院士，但她是美国艺术科学院院士，不排除是许进材料中的笔误）和Wing Hung Wong（他确实是科学院院士，而且近年还到过中国访问，在清华北大做过报告，而且他在香港任教的时间和许进材料里面他在香港访问的时间重合）。我分别给这两位教授发了匿名邮件询问，得到回复如下。我给对方邮件以及对方邮件回复的包括信箱的完整信息见附件4和附件5，中科院可以发信确认。

Jeannette M. Wing的回信：

I do not know this person or his work.

I am not a member of the National Academy of Sciences.

Executive Vice President for Research

Professor of Computer Science

Columbia University

Wing Hung Wong的回信：

Dear Academic.clarity.

Thank you for your message. I am not aware of the work "A DNA Computing Model for the Graph Vertex Coloring Problem Based on a Probe Graph" and had not made comments on it.

Sincerely,

Wing H Wong

上面的邮件明确说明他们都不知道许进的这篇论文，没有读过，没有评价过。Jeannette M. Wing说她不认识许进，Wing Hung Wong是否认识许进不得而知。

通过上面和附件里提供的实名邮件证据可以确凿的证明，无论许进如何可以对别人的评价含糊其辞，考虑所有的可能，许进院士申报材料以及前述北大报道里面的评价彻底是伪造的。希望中科院可以拿出材料中的“附件5-5, 6”进行彻查，如果许进能出示相关评论的证据，那么请中科院发信联系这几位教授对证。我认为如果许进能拿得出证据，那么这个证据也是他伪造的。

问题2：探针机 (Probe Machine) 存在本质错误。

许进公示材料的论文³和评价情况如下：

论文：作者: Xu Jin; 题目: Probe machine; 期刊名称: IEEE Transactions on Neural Networks and Learning Systems: 卷(期)(年): 27(7) (2016): 起止页码: 第1406页至第1416页

主要贡献及引用评价情况：

提出了一种完全并行的计算模型—探针机，它可以同时处理多对数据，而不是顺序处理每对线性相邻数据。对于图着色，汉密尔顿圈问题，可以通过一次探针运算求出这些问题的所有正确解。。。作为期刊首发至今，SCI他引52次，入选IEEE计算智能学会(CIS)年度三片特色论文之一，并被《IEEE CIM》列为2016年第4季度CIS首篇亮点论文。[附5-5,6]

上述材料有两个问题，首先许进说的特色论文这些并不是什么值得炫耀的荣誉，是网站为了宣传最近发表的论文的做法。这一点不是对错问题，所以不再深究。

第二个问题是，**探针机不能解决NP完全问题，他比图灵机强的结论是错误的**。许进自己知道写这个的严重性，所以并没有把这些放在院士申报材料中，避重就轻的强调不值得一提的“荣誉”。但是我们可以看到在北京大学的宣传网页中有相关评述，见下面截图，网址：<https://eecs.pku.edu.cn/info/1086/3266.htm>（网页见附件6）。

许进对计算机做出形如“计算机=数学计算模型+实现该模型的材料研制的机器”的分解性定义，即“电子计算机=图灵机+电子器件”，提出人类首次超越电子计算机的图灵机 (Turing machine) 模型——探针机 (生物神经网络就是一种稀疏的固定通道型探针机)，并指出图灵机是探针机的特例。对于当今电子计算机无法处理的NP完全问题，利用探针机，只需一次探针运算，即可求出问题的全部解；由于基于图灵机的所有NP完全问题在多项式时间内是等价的，这就意味着在探针机模型下不再有困惑人类的NP完全问题。文中还讨论了探针机的硬件实现等。2016年11月，该论文还被《IEEE计算智能期刊》(IEEE Computational Intelligence Magazine) 作为当期首个出版亮点 (publication spotlight) 推介。

我们可以看到，**许进声称“这就意味着在探针机模型下不再有困惑人类的NP完全问题”**。关于这个问题，我发信给**Scott Aaronson**教授询问，他是**计算理论和计算复杂性的国际顶尖学**

者，姚期智院士可以证明。我给对方的邮件以及对方邮件回复的包括信箱的完整信息见附件7，中科院可以发信确认。他的回信如下：

Hi [REDACTED],

The obvious problem with the “probe model” in this paper is that the amount of DNA that’s needed will grow exponentially with the size n of the problem to be solved — becoming more than the size of the known universe even for $n=1000$ or so. That’s why the model isn’t scalable in our actual universe, and why there’s no serious challenge here to the Extended (Polynomial-Time) Church-Turing Thesis. A word of advice: don’t take so seriously every obscure random paper you find that makes a shocking claim — in $>99\%$ of cases, the resolution is just that the author doesn’t understand the relevant issues and the paper is wrong! :-)

Hope that helps and best regards,
Scott

Scott Aaronson教授认为：

1. Probe model（探针机）的明显问题是完成计算需要的DNA的总量需要根据问题的规模 n 指数级增长，当 n 为1000左右的时候，就会比已经知道的宇宙还大；
2. 基于上述原因，许进的探针机模型在实际我们生活的宇宙中是不具有可扩展性的，因此也不会对邱奇-图灵论题（Church-Turing Thesis）有任何挑战；
3. 同时给出了建议：如果随便遇到的一篇晦涩的论文宣称一些令人震惊的结论，不要太当回事，因为大于99%的情况，作者并不理解相关的问题，论文本身就是错误的。

上述邮件清楚的表明了许进的探针机是有本质问题的，没有实际的意义。这种论文为什么能发表？我认为这是因为这并不是发表在专门的理论计算机会议和期刊上，隔行如隔山，这也

表明了评价一个科研工作者的成果，特别是院士评选，需要看关于研究问题本身的权威期刊和会议的成果。如果这样的研究成果也能作为院士申报材料的一部分，许进也因此当选院士的话，我认为一定会造成国内外的丑闻。

问题三：1995年的错误猜想

许进公示材料的论文⁹和评价情况如下：

论文：作者：Xu Jin, Liu Zhenhong； 题目：The chromatic polynomial between graph and its complement—About Akiyama and Hararys' open problem； 期刊名称：Graphs and Combinatorics； 卷(期)(年)：11(4) (1995)； 起止页码：第337页至第345页

主要贡献及引用评价情况：

解决了著名的Akiyama—Hararys猜想：存在图与它的补图不同构，但有相同色多项式，给出了猜想的充要条件，并提出另一个猜想。此猜想证明及新猜想提出均为许进工作。2015年Azarija解决了许进的猜想，发表在《Graphs and Combinatorics》。著名图论专家马耳他大学Stanley教授将该成果作为指导学生研究方向，在其学生毕业论文中对该成果进行详细评述和研究。[附5-40,41]

本文发表于1995年，到现在引用10次。26年引用10次的情况不得不说是个非常尴尬的事实，所以我看到许教授也并没有列出具体数字。对于这篇论文，许教授首先声称解决了“著名”的Akiyama-Harary猜想，本人对这个猜想一无所知，所以无法评价，但是作为科研工作者，如果一个猜想真是著名的，那么他的解决一定会引起人们的广泛关注，应该不会有26年引用10次的尴尬情况。

许教授还声称1995年这篇文章“。。给出了猜想的充要条件，并提出另一个猜想。此猜想的证明及新猜想提出均为许进工作。2015年Azarija解决了许进的猜想。”通过这段引用一般读者想的应该是许进教授提出了新的猜想，然后在20年以后（距离1995年），被另外一个数学工作者证明了。但是我查看材料中提到的于2015年在《Graphs and Combinatorics》上发表的文章（见附件8），摘要和引言有如下段落：

Can a non self-complementary graph have the same chromatic polynomial as its complement? The answer to this question of Akiyama and Harary is positive and was given by J. Xu and Z. Liu. They conjectured that every such graph has the same degree sequence as its complement. In this paper we show that there are infinitely many graphs for which this conjecture does not hold. We then solve a more general variant of the Akiyama-Harary problem by showing that there exists infinitely many non self-complementary graphs having the same Tutte polynomial as their complements.

以上是摘要，概括了许进的工作和猜想，说他们提出了更一般的问题。接下来引言部分：

The question received little attention until 1995 when J. Xu and Z. Liu [4] showed that such a graph indeed exists. They have shown that for any $n \geq 8$ congruent to 0 or 1 modulo 4 there exists a graph G of order n such that G is not self-complementary and $p_G(k) = p_{\overline{G}}(k)$. In their paper they constructed graphs with a specific degree sequence and then used the degree sequence to compute the chromatic polynomial of the corresponding graph. Given the nature of their construction they posed

Conjecture 1 (J. Xu, Z. Liu). *If a graph G has the property that $p_G(k) = p_{\overline{G}}(k)$ then G has the same degree sequence as \overline{G} .*

As it turns out, their conjecture is false. In this paper we present an infinite family of graphs not adhering to this condition.

从上面最后一句来看，Azarija等人证明了许进的猜想是错误的”As it turns out, their conjecture is false”。许进教授当然不会在申报材料里面写出他的猜想是错误的，（否则这是对他院士申报加分还是减分？）但是也不能直接写“证明”了他的猜想，于是煞费苦心的用了”解决了许进的猜想“的说法。这一段实在让人忍俊不禁。

许进申报的虽然是信息学部，不是数学学部，但是各位专家院士对于基本的理论研究的过程和评价应该是非常清楚的。我想，这里不能怪各位专家没有看出来，只是百忙中可能被许进教授煞费苦心准备的材料所迷惑。

和这封举报信一起发给大家的还有我近期写的关于许进材料其他的一些自我拔高的问题，我没有将他们放到这里是因为那些没有确凿证据证明。但是相信广大院士专家会有明确的判断。

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首页 (.././index.htm) >> 新闻动态 (.././xwdt1.htm) >> 正文

许进教授团队生物计算机取得突破成果

生命体是一个以生物大分子为材料构成的人类已知的最智慧的信息处理“机器”。所以，人类近几十年来，意在用生物材料研发信息处理的计算机，称为生物计算机。当前的生物计算机主要集中于DNA计算机的理论、实现技术与方法展开研发。

DNA计算机目前的研究方向有两个：一个是以DNA分子作为“数据”，以生物酶或生化操作为信息处理的“工具”来研发DNA计算机，其功能类似于当今的电子计算机；另一类是以DNA为纳米材料，以DNA自组装技术为主要技术手段来构建纳米机器。例如构建纳米机器人来实现疾病诊断和治疗，快速实现纳米电路。近些年，北京大学计算机科学技术系高可信软件教育部重点实验室的许进团队在DNA计算机的上述两个方面均取得了突破性进展。在DNA计算机领域，课题组针对典型的NP-完全问题——图着色问题的求解，相继提出了非枚举、并行、大规模DNA计算模型后，从理论上对并行DNA计算模型给予系统研究，研究成果《A DNA Computing Model for the Graph Vertex Coloring Problem Based on a Probe Graph》发表在领袖级期刊《Engineering》上。该成果包括在实验方面，实现人类非传统计算机最大规模问题的求解，其算法复杂度到达 3^{59} ；在理论方面，有机将DNA特性与数学模型相结合，整个计算模型中含4个并行部分。美国科学院院士Erik Winfree和美国加利福尼亚大学教授Richard Beigel评价为“你们突破性的成果振奋人心”。审稿专家称该成果是“继Adleman开创生物计算后最重要的突破”。

在DNA自组装方面，课题组设计了一种可复用的十字形DNA瓦片结构。DNA瓦片两两之间能任意拼接，构成大小可控的逻辑阵列。折纸结构上的沟道，为纳米电路的排布留下了布线空间。该方法大幅减少了所需DNA瓦片的数量，且降低了连接复杂度。相关成果以封面论文发表在2020年7月的国际著名期刊《Nanoscale》上，该成果的第一作者为许进的博士生陈从周，许进为通讯作者。

另外，许进团队课题组聚焦DNA计算理论和DNA分子机器，围绕生物计算、自组装等领域开展研究。设计了非枚举型的计算模型，可控DNA环阵列，相关成果在IEEE Trans等杂志上发表，受到英国化学皇家学会的专题报道。

系列研究得到了科技部国家重点研发计划、国家自然科学基金重点项目、国家自然科学基金多项面上项目资助。

上一条: [刘讓哲副教授获首个中国计算机学会服务计算“杰出成就奖” \(1413.htm\)](#)

下一条: [王腾蛟教授团队研发多源大数据疫情防控研判系统 \(1402.htm\)](#)

高可信软件技术教育部重点实验室(北京大学) , Key Lab of High Confidence Software Technologies(PKU), Ministry of Education

----- Original Message -----

On Thursday, September 9th, 2021 at 3:45 PM, Erik Winfree <winfree@caltech.edu> wrote:

Dear anonymous Chinese computer researcher,

I am uncomfortable replying to an anonymous account and to someone who is themselves not willing to reveal their name. But I can understand your concern, as this appears to involve academic dishonesty. So I will reply nonetheless. Although, there must be a better way.

It is disconcerting to see my name in these two news links (which I read via translate.google.com to get the gist). I do not recall seeing this paper before; certainly, I have not read it. Just now, I read the abstract — it sounds like the kind of thing I would have been interested to read about 20 years ago, and the theoretical results sound in line with what I would expect to be possible with the theoretical frameworks and techniques of that time. From a superficial skim of the paper, the experimental result appears quite impressive, conceivably comparable to Adleman's 2002 Science paper, although I can't say anything with confidence unless I read the paper carefully. Alas, today, using DNA to compete with electronic computers on NP-complete problems is not something I have much hope for, so I would not be motivated to read a paper with this abstract, at this time. (Further, the claim about how long an electronic computer would take is misleading hype, since no one would seriously program an electronic computer to use exhaustive search. Standard techniques for graph coloring easily solve hard 60-vertex problems in under a second.)

Since my memory is not as good as I might wish, I searched my email but did not find any correspondence with or about Jin Xu or this specific paper. Could I have met Jin Xu at a conference, and said something nice in person? Not impossible, though I doubt it. I do tend to try to see the best in others and compliment them on what they've done well. However, according to translate.google.com, the news articles quote me saying "your breakthrough results are inspiring" and I would not have used the words "breakthrough" or "inspiring" to a journalist about this paper.

I have no idea what Jin Xu's greater ambitions are, and perhaps that's for the best. I have no desire to get involved.

Best regards, whomever you are,
Erik

Dear Erik,

I am a computer science researcher in China. Recently, I read from the news articles in Chinese (links below) that you commented on some research results on DNA computing from Prof. Jin Xu's group in Peking University as "Recent breakthrough in DNA computing". It appears to refer to the paper "A DNA Computing Model for the Graph Vertex Coloring Problem Based on a Probe Graph" published in "Engineering" (<https://www.sciencedirect.com/science/article/pii/S2095809917308019>). Based on this paper, Prof. Xu seems to have solved the graph vertex coloring problem using DNA computing, which has been applied for various other problems. The citation of this article is not high and it is not cited by any well-known authors like you. It is hard to imagine you mentioned it as a breakthrough in this field. I recently read your paper in Nature "Diverse and robust molecular algorithms using reprogrammable DNA self-assembly", which is truly fascinating. Thus, any comment from a leader like you should be taken seriously, can you comment whether you are aware of and have given Prof. Xu's work (above paper) such comments?

The Chinese news links are as follows:

<https://hcst.pku.edu.cn/info/1029/1412.htm> (this is from Peking University)

<https://www.kjcxun.com/m/view.php?aid=24821> (this is a general piece of news article)

I am not quite sure whether you can read Chinese, but you can search your name in these articles. In addition, you may consult some Chinese colleagues in your department. I am sending this email anonymously due to the sensitivity of the matter. As you may not know, Prof. Xu is recently using this comment for other far greater ambitions. I think it is better to let you know, and clarify.

Thank you so much!

A Chinese computer researcher

----- Original Message -----

On Friday, September 10th, 2021 at 2:48 PM, Richard Beigel <richard.beigel@temple.edu> wrote:

My interests have changed. I have not read any recent papers on DNA computing or graph coloring.

Sincerely,
Richard Beigel

Dear Richard,

I am a computer science researcher in China. Recently, I read from the news articles in Chinese (links below) that you commented on some research results on DNA computing from Prof. Jin Xu's group in Peking University as "Recent breakthrough in DNA computing". It appears to refer to the paper "A DNA Computing Model for the Graph Vertex Coloring Problem Based on a Probe Graph" published in "Engineering" (<https://www.sciencedirect.com/science/article/pii/S2095809917308019>). Based on this paper, Prof. Xu seems to have solved the graph vertex coloring problem using DNA computing, which has been applied for various other problems. The citation of this article is not high and it is not cited by any well-known authors like you. It is hard to imagine you mentioned it as a breakthrough in this field. Any comment from a leader like you should be taken seriously, can you comment whether you are aware of and have given Prof. Xu's work (above paper) such comments?

The Chinese news links are as follows:

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<https://www.kjcxun.com/m/view.php?aid=24821> (this is a general piece of news article)

I am not quite sure whether you can read Chinese, but you can search your name in these articles. In addition, you may consult some Chinese colleagues in your department. I am sending this email anonymously due to the sensitivity of the matter. As you may not know, Prof. Xu is recently using this comment for other far greater ambitions. I think it is better to let you know, and clarify.

Thank you so much!

A Chinese computer researcher

----- Original Message -----

On Thursday, September 9th, 2021 at 1:17 PM, Jeannette Wing <jw3585@columbia.edu> wrote:

I do not know this person or his work.

I am not a member of the National Academy of Sciences.

Executive Vice President for Research

Professor of Computer Science

Columbia University

Dear Jeannette,

I am a computer science researcher in China. Recently, I read the supporting documents (publicly posted in several leading universities in China) for Prof. Jin Xu's election to a member of Chinese Academy of Sciences. Regarding one of this papers "A DNA Computing Model for the Graph Vertex Coloring Problem Based on a Probe Graph" published in "Engineering (<https://www.sciencedirect.com/science/article/pii/S2095809917308019>), he claimed that "the NAS member Wing" commented on this paper as "Your recent breakthrough in DNA computing". I am attaching the picture of this part in Prof. Xu's material, sorry for the low image quality because I moved when I took the picture and didn't check until later.

I have the following two key questions:

1. Do you know Prof. Jin Xu and his work, does the "NAS member Wing" refer to you? As far as I know, you are not (yet) an NAS member, but you are a member of National Academy of Arts and Sciences. Perhaps he made a small mistake in the material? There is only one NAS member with the last name Wing and she is not in computer field and has been retired for a number of years.
2. Suppose the question to 1 is affirmative, do you have the comment? As a leader in computer science, your comment should be taken seriously and precisely. This is the reason that Prof. Xu is using it to show the significance of his work. However, my personal opinion is that, using such comments without a context in such serious, formal and publicly accessible document is not quite professional.

Thank you for reading the email and look forward to your response.

A Chinese computer researcher

----- Original Message -----

On Friday, September 10th, 2021 at 9:32 AM, Wing H Wong <whwong@stanford.edu> wrote:

Dear Academic.clarity.

Thank you for your message. I am not aware of the work "A DNA Computing Model for the Graph Vertex Coloring Problem Based on a Probe Graph" and had not made comments on it.

Sincerely,

Wing H Wong

Sent from my iPhone

Dear Prof. Wong,

I wanted to send a follow-up email to explain why I need to maintain the anonymity for such inquiry. I noticed that you visited China several times and you should understand the importance of CAS member in China. Many people want to be elected with different means. Thus, it is very important to ensure the integrity of the application material. The quoted information I provided yesterday is publicly available and since the comments such as "your recent breakthrough" are claimed to be from you with specific name, the clarification also protects your reputation. On the other side, due to the seriousness of the matter, I need to keep the anonymity to protect myself from retaliation.

My impression is that such claim is fake and the matter involves academic dishonesty. Since you can read Chinese, please check the following links:

<https://hcst.pku.edu.cn/info/1029/1412.htm> (this is from Peking University)

<https://www.kjxun.com/m/view.php?aid=24821> (this is a general piece of news article)

You can see the same comments are indicated as from different people. Specifically, "NAS member Wing" is changed to Eric Winfree and "Professor Richard in University of California" is indicated as Richard Beigel (who is not from University of California). This is why I think the claims are forged. Sadly, such information is used in the supporting document for Prof. Xu's attempted election to CAS.

I also sent the inquiry to Winfree and he denied he knew this person and his work. With the above additional information provided, I appreciate you can confirm your comment ("the recent breakthrough") or provide some contexts to make sure the clarity.

Thank you.

A Chinese computer researcher

Dear Prof. Wing Hung Wong,

I am a computer science researcher in China. Recently, I read the supporting documents (publicly posted in several leading universities in China) for Prof. Jin Xu's election to a member of Chinese Academy of Sciences. Regarding one of this papers "A DNA Computing Model for the Graph Vertex Coloring Problem Based on a Probe Graph" published in "Engineering (<https://www.sciencedirect.com/science/article/pii/S2095809917308019>), he claimed that "the NAS member Wing" commented on this paper as "Your recent breakthrough in DNA computing". I am attaching the picture of this part in Prof. Xu's material, sorry for the low image quality because I moved when I took the picture and didn't check until later.

You can also access the similar information in the following page:

<https://eecs.pku.edu.cn/info/1502/6719.htm>

"1) Biological computing models and implementation: In 2010, Dr. XU proposed a parallel DNA computing model. With this model, all 48 3-colorings of a graph of order 61 are successfully worked out, which is by far the largest international bio-computing experiment. Professor B?awicz, winner of the European Journal of Operational Research, said: The proposed DNA algorithm solves the coloring problem. Professor Wing, member of the US National Academy of Sciences, and Professor Richard in University of California, the world's leading DNA computing experts, commented: "Your recent breakthrough in DNA computing" "This is very exciting"."

I have the following two key questions:

1. Do you know Prof. Jin Xu and his work, does the "NAS member Wing" refer to you?
2. Suppose the question to 1 is affirmative, do you have the comment? As a leader in computer science, your comment should be taken seriously and precisely. This is the reason that Prof. Xu is using it to show the significance of his work. However, my personal opinion is that, using such comments without a context in such serious, formal and publicly accessible document is not quite professional.

Thank you for reading the email and look forward to your response.

A Chinese computer researcher

软件研究所许进教授所撰写论文入选美国电气电子工程师学会计算智能分会 2016年度特色论文

附件6

近日，北京大学信息科学技术学院软件研究所、高可信软件技术教育部重点实验室许进教授所撰写的《探针机》（Probe machine）一文被选为美国电气电子工程师学会（the Institute of Electrical and Electronics Engineers, IEEE）计算智能分会（Computational Intelligence Society, CIS）2016年度特色论文（feature paper; 见<http://cis.ieee.org/>）。

IEEE计算智能分会专注于生物和语言驱动计算模式中的理论、设计、应用与开发，特别是神经网络、连接系统、遗传算法、进化编程、模糊系统和混合智能系统及其相关领域。按照惯例，分会每年度从已出版的旗下期刊遴选特色论文，2016年度选出三篇，其中包括许进于7月发表于《IEEE神经网络与学习系统汇刊》（IEEE Transactions on Neural Networks and Learning Systems, 27(7): 1405-1416; <http://ieeexplore.ieee.org/xpl/articleDetails.jsp?arnumber=7466831&newsearch=true&queryText=probe%20machine>) 的上述论文。

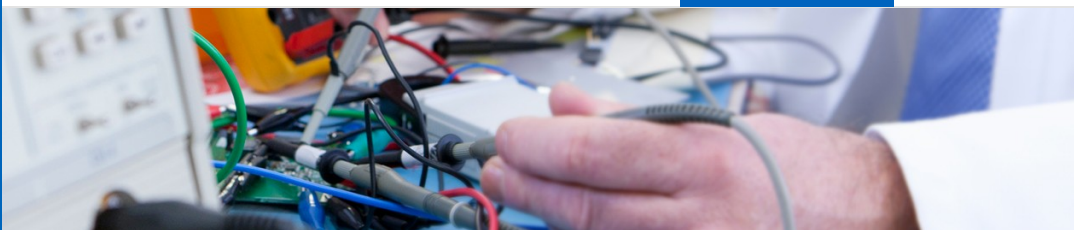
许进对计算机做出形如“计算机=数学计算模型+实现该模型的材料研制的机器”的分解性定义，即“电子计算机=图灵机+电子器件”，提出人类首次超越电子计算机的图灵机（Turing machine）模型——探针机（生物神经网络就是一种稀疏的固定通道型探针机），并指出图灵机是探针机的特例。对于当今电子计算机无法处理的NP完全问题，利用探针机，只需一次探针运算，即可求出问题的全部解；由于基于图灵机的所有NP完全问题在多项式时间内是等价的，这就意味着在探针机模型下不再有困惑人类的NP完全问题。文中还讨论了探针机的硬件实现等。2016年11月，该论文还被《IEEE计算智能期刊》（IEEE Computational Intelligence Magazine）作为当期首个出版亮点（publication spotlight）推介。

许进课题组长期从事生物计算与新型计算机研究。2006年，他主导创建了

生物计算——理论与应用国际会议（International Conference on Bio-inspired Computing: Theory and Applications），迄今已在中国、英国、澳大利亚、印度、马来西亚等国家和地区召开11届，极大推动了国内外生物计算方向的交流与发展，成为新兴智能计算领域具有重要影响力的国际会议。由他作为第一完成人的项目“生物计算中数据编码与模型构建理论方法研究”获2013年度国家自然科学二等奖。



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软件研究所许进教授所撰写论文入选美国电气电子工程师学会计算智能分会

发布时间：2017-02-16

信息来源：本站

近日，北京大学信息科学技术学院软件研究所、高可信软件技术教育部重点实验室许进教授所撰写电子工程师学会（the Institute of Electrical and Electronics Engineers, IEEE）计算智能分会（Computational Intelligence）特刊（feature paper；见<http://cis.ieee.org/>）。

IEEE计算智能分会专注于生物和语言驱动计算模式中的理论、设计、应用与开发，特别是神经网络智能系统及其相关领域。按照惯例，分会每年度从已出版的旗下期刊遴选特色论文，2016年度选出三篇系统汇刊》（IEEE Transactions on Neural Networks and Learning Systems, 27(7): 1405-1416; <http://ieeexplore.ieee.org/xpl/articleDetail.jsp?arnumber=7466831&newsearch=true&queryText=probe%20machine>）的上述论文。

许进对计算机做出形如“计算机=数学计算模型+实现该模型的材料研制的机器”的分解性定义，即“电子计算机的图灵机（Turing machine）模型——探针机（生物神经网络就是一种稀疏的固定通道型探针机）”。探针机可以处理计算机无法处理的NP完全问题，利用探针机，只需一次探针运算，即可求出问题的全部解；由于基于图灵机就意味着在探针机模型下不再有困惑人类的NP完全问题。文中还讨论了探针机的硬件实现等。2016年11月，该论文在《IEEE Computational Intelligence Magazine》作为当期首个出版亮点（publication spotlight）推介。

许进课题组长期从事生物计算与新型计算机研究。2006年，他主导创建了生物计算——理论与应用（Computing: Theory and Applications），迄今已在中国、英国、澳大利亚、印度、马来西亚等国家和地区发展，成为新兴智能计算领域具有重要影响力的国际会议。由他作为第一完成人的项目“生物计算中数据

科学二等奖。



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----- Original Message -----

On Saturday, September 11th, 2021 at 6:37 AM, Scott Aaronson <scott@scottaaronson.com> wrote:

Hi ,

The obvious problem with the “probe model” in this paper is that the amount of DNA that’s needed will grow exponentially with the size n of the problem to be solved — becoming more than the size of the known universe even for $n=1000$ or so. That’s why the model isn’t scalable in our actual universe, and why there’s no serious challenge here to the Extended (Polynomial-Time) Church-Turing Thesis. A word of advice: don’t take so seriously every obscure random paper you find that makes a shocking claim — in >99% of cases, the resolution is just that the author doesn’t understand the relevant issues and the paper is wrong! :-)

Hope that helps and best regards,
Scott

Dear Prof. Aaronson,

I am a computer science student in China. I have a quick question that puzzled me for a while and I appreciate you can help me with some answers. In one of our classes, Prof. Jin Xu introduced the notion of “Probe Machine” (PM), which he claims to have computational power stronger than that of Turing machine (TM). He also published a paper (attached): <https://ieeexplore.ieee.org/document/7466831>.

However, I am truly puzzled by such a claimed, I have checked several books, which include the Church-Turing thesis: nothing computationally stronger than a TM. Indeed, the paper was published later than the book, but if such claim is true, I would expect that it would be drastic for computer science community since it implies that PM may be able to solve NP problems?

The main reason I send this email to you is that, it is very hard for me to find exactly where this argument goes wrong because large parts of the paper are written in some abstruse way. Some conventional mathematical notions are used to describe something other than its conventional meaning. For example, a “matrix” where the length of whose columns varies by column. It also makes a few ambiguous claims like “In this linear data placement mode, only adjacently placed data can be processed simultaneously, which greatly limits the computation capabilities of calculation tools.”

As a student who is interested in doing TCS research, your help (even some brief comments) on how can I logically argue the problem with this paper is really appreciated. Personally, I don't think this claim is true but it is published in an IEEE journal.

Thank you.



Tutte polynomials and a stronger version of the Akiyama-Harary problem

Jernej Azarija
Institute of Mathematics, Physics and Mechanics
Jadranska 19, 1000 Ljubljana, Slovenia
jernej.azarija@imfm.si

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Abstract

Can a non self-complementary graph have the same chromatic polynomial as its complement? The answer to this question of Akiyama and Harary is positive and was given by J. Xu and Z. Liu. They conjectured that every such graph has the same degree sequence as its complement. In this paper we show that there are infinitely many graphs for which this conjecture does not hold. We then solve a more general variant of the Akiyama-Harary problem by showing that there exists infinitely many non self-complementary graphs having the same Tutte polynomial as their complements.

Keywords: graph complement, chromatic number, chromatic polynomial, Tutte polynomial

AMS Subj. Class. (2010): 05C31, 05C76

1 Introduction

Let $p_G(k)$ be the *chromatic polynomial* of a simple graph G that is $p_G(k)$ is the number of proper k -colorings of G . In 1980 Akiyama and Harary [3] raised the following question ‘Is there a graph G that is not self-complementary and has a chromatic polynomial that equals to the chromatic polynomial of \overline{G} ?’ Observe that since $p_G(k)$ encodes the number of edges of G a necessary condition for a graph to have the posed property is that it has precisely $\binom{|V(G)|}{2}/2$ edges.

The question received little attention until 1995 when J. Xu and Z. Liu [4] showed that such a graph indeed exists. They have shown that for any $n \geq 8$ congruent to 0 or 1 modulo 4 there exists a graph G of order n such that G is not self-complementary and $p_G(k) = p_{\overline{G}}(k)$. In their paper they constructed graphs with a specific degree sequence and then used the degree sequence to compute the chromatic polynomial of the corresponding graph. Given the nature of their construction they posed

Conjecture 1 (J. Xu, Z. Liu). *If a graph G has the property that $p_G(k) = p_{\overline{G}}(k)$ then G has the same degree sequence as \overline{G} .*

As it turns out, their conjecture is false. In this paper we present an infinite family of graphs not adhering to this condition.

Finally we turn our attention to a more general variant of the problem introduced by Akiyama and Harary. For a subset $F \subseteq E(G)$ we denote by $c(F)$ the number of connected components of the graph with edge set F and vertex set $V(G)$. With this in mind the *Tutte polynomial* of a graph G is defined as

$$T_G(x, y) = \sum_{F \subseteq E(G)} (x - 1)^{c(F) - c(E)} \cdot (y - 1)^{c(F) + |F| - |V(G)|}. \quad (1)$$

The Tutte polynomial $T_G(x, y)$ contains much more information about the structure of G than $p_G(k)$ does. Indeed, it is well known that

$$p_G(k) = (-1)^{|V(G)| - k(E)} k^{c(E)} T_G(1 - k, 0).$$

Among the many other interesting evaluations of the Tutte polynomial are $T_G(1, 1)$ - the number of spanning trees of G and $T_G(2, 0), T_G(0, 2)$ the number of cyclic and acyclic orientations of G respectively. For a survey of known results about the Tutte polynomial see [2].

A natural generalization of the Harary-Akiyama question following from these properties of the Tutte polynomial is, whether there exists non self-complementary graphs having the same Tutte polynomial as their complement. In this paper we shall prove

Theorem 1. *There exists infinitely many graphs that are not self-complementary and have the same Tutte polynomial as their complement.*

2 Chromatic polynomials and graph complements

In this section we present a family of graphs having equal chromatic polynomials as their complements but different degree sequence. We start with the graph depicted on Figure 1 together with its complement. Its *graph6* string [1] is HCpVdZY. First, we establish that G has the desired properties.

Lemma 2. *There exists a graph G of order 9 such that G and \overline{G} have different degree sequences but $p_G(k) = p_{\overline{G}}(k)$.*

Proof. We observe that the graph G from Figure 1 has degree sequence (5, 5, 5, 4, 4, 4, 4, 3, 2) while its complement has degree sequence (6, 5, 4, 4, 4, 4, 3, 3, 3). Using the well known *deletion-contraction* recurrence for computing the chromatic polynomial of a graph we can verify that

$$p_G(k) = p_{\overline{G}}(k) = (k - 2) \cdot (k - 1) \cdot k \cdot (k - 3)^2 \cdot (k^4 - 9k^3 + 35k^2 - 69k + 57).$$

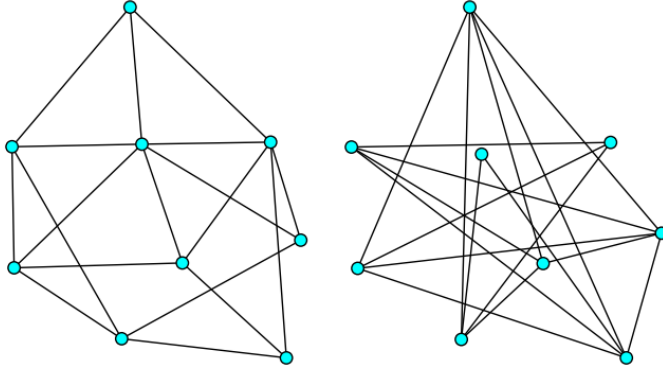


Figure 1: A graph and its complement.

Alternatively we can verify the stated claim using the Sage program presented in the Appendix. \square

Before showing the main claim of this section, we introduce a useful construction. Given a graph G we form the graph \widehat{G} by taking a vertex disjoint 4-path P and joining every vertex of G to both endpoints of P . Conveniently, we have $\overline{\widehat{G}} = \widehat{\overline{G}}$. Using this property it is not difficult to establish the following claim.

Theorem 3. *There exists infinitely many graphs G not having the same degree sequence as \overline{G} but having the same chromatic polynomial as their complements.*

Proof. We compute the chromatic polynomial of \widehat{G} . Suppose we wish to properly color \widehat{G} with k colors. Let x, y be the endpoints of the 4-path P introduced in \widehat{G} and let x', y' be the respective neighbors of x and y in P . There are essentially two different ways to color \widehat{G} . If we color x, y with equal colors then there are $(k-1)$ choices to color x' and $(k-2)$ colors to color y' and hence $k(k-1)(k-2)p_G(k-1)$ ways to properly k -color \widehat{G} . If x, y are colored with different colors then we again have two cases. If y' is colored with the same color as x then we have $k(k-1)^2 p_G(k-2)$ total ways to color \widehat{G} . If however y' is not colored with the same color as x we end up having $k(k-1)(k-2)^2 p_G(k-2)$ ways to properly color our graph using k colors. Summing up the obtained quantities we infer

$$\begin{aligned} p_{\widehat{G}}(k) &= k(k-1)(k-2)p_G(k-1) + k(k-1)^2 p_G(k-2) + k(k-1)(k-2)^2 p_G(k-2) \\ &= k(k-1)((k-2)p_G(k-1) + (k(k-3) + 3)p_G(k-2)). \end{aligned}$$

In particular we see from the above expression that \widehat{G} is in fact a function of $p_G(k)$. The main claim now follows quickly with an inductive argument. By Lemma 2 we have a graph G of order 9 having a different degree sequence than \overline{G} but the same

chromatic polynomial. But then the degree sequences of \widehat{G} and \overline{G} differ while for their chromatic polynomials the above identity implies

$$\begin{aligned} p_{\widehat{G}}(k) &= k(k-1)((k-2)p_G(k-1) + (k(k-3) + 3)p_G(k-2)) \\ &= k(k-1)((k-2)p_{\overline{G}}(k-1) + (k(k-3) + 3)p_{\overline{G}}(k-2)) \\ &= p_{\overline{G}}(k) = p_{\widehat{G}}(k). \end{aligned}$$

Hence by using this construction iteratively we obtain an infinite family of graphs with the stated property. \square

Making a computer search it can be seen that there are graphs on 12 vertices that have the property stated in Theorem 3. Hence it is easy to extend the proof of Theorem 3 to show that for any $n \geq 9$ congruent to 0 or 1 (mod 4) there exist a graph G not having the same degree sequence as \overline{G} but sharing the same chromatic polynomial.

3 The Tutte polynomial

A very useful property of the chromatic polynomial that we exploited in the proof of Theorem 3 is the fact that the chromatic polynomial of a graph operation is often a function of the chromatic polynomials of its operands. Unfortunately the same is not generally true for the Tutte polynomial. Indeed, consider two trees of order 4, the star graph $K_{1,3}$ and the path graph P_4 . Both have the same Tutte polynomial namely x^3 . Consider now their *cone graph*, that is the graph obtained by adding a new vertex and joining it to all other vertices. The cone of $K_{1,3}$ has 20 spanning trees while while the cone of P_4 has 21 spanning trees. Hence the Tutte polynomials of the cones of $K_{1,3}$ and P_4 are different.

In order to apply the construction introduced in the previous section, we need an additional structure of our graphs that will assure that if two graphs G and H have equal Tutte polynomials then so do \widehat{G} and \widehat{H} .

As it turns out, the following concept is quite useful for this purpose. Let H be a spanning subgraph of G having connected components of order $h_1 \geq h_2 \geq \dots \geq h_k$. We say that $(|E(H)|, h_1, h_2, \dots, h_k)$ is a *subgraph description* of H . Let now $s(G)$ be the lexicographically sorted tuple of subgraph descriptions for every subgraph of G . We call $s(G)$ the *subgraph sequence* of G . Observe that equation 1 implies that if two graphs have the same subgraph sequence then they also have the same Tutte polynomial. The converse is of course not true as witnessed by the above example with P_4 and $K_{1,3}$. Our next lemma asserts that the property of having the same subgraph sequence is preserved by the construction introduced in the previous section.

Lemma 4. *If G and H are graphs such that $s(G) = s(H)$ then $s(\widehat{G}) = s(\widehat{H})$.*

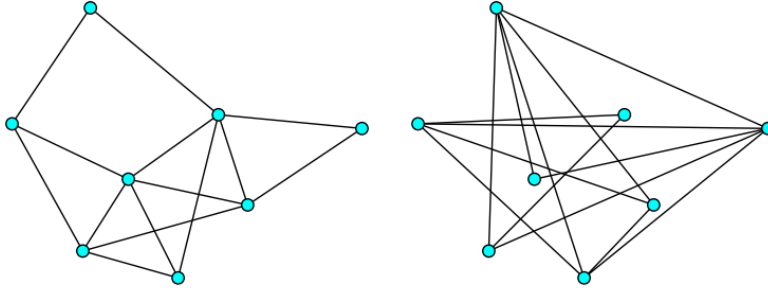


Figure 2: A graph with equal Tutte polynomial as its complement.

Proof. Let G' be a spanning subgraph of \widehat{G} . Observe that G' is obtained by taking a spanning subgraph of G with subgraph description $d = (|E(G')|, g_1, \dots, g_k)$ adding the remaining four vertices of \widehat{G} coming from the introduced 4-path P and finally adding some of the edges with at least one endpoint in P . That is we add some of the edges of P and then some of the edges from the endpoints of P to some vertices of the connected components of G .

By assumption G has the same subgraph sequence as H hence there is a bijective mapping between their subgraph sequences. Let H' be the subgraph of H with subgraph sequence d that is prescribed by such bijection. Since H' and G' have the same subgraph description there is bijective way to map every extension of G' to a subgraph of \widehat{G} to an extension of H' to a subgraph of \widehat{H} . Indeed, we may assume the vertices of G and H to be ordered and then for every edge that is added from one of the endpoints x of P to the the i 'th vertex of the j 'th component of G we add the edge between x and the i 'th vertex of the j 'th component of H . This is always well defined since H and G have the same subgraph description. \square

In order to apply Lemma 4 we need to find a non self-complementary graph G such that $s(G) = s(\overline{G})$. As already noted this immediately implies $T_G(x, y) = T_{\overline{G}}(x, y)$. One of the smallest graphs with such property has order 8 and is presented on Figure 2. Its graph6 string is `GCRdvK`.

Lemma 5. *There exist a non self-complementary graph of order 8 such that $s(G) = s(\overline{G})$.*

Proof. Consider the graph G from Figure 2. Observe that G and \overline{G} both have two vertices of degree 2. In G these two vertices share a common neighbor while the vertices of degree 2 in \overline{G} have no common neighbors. Hence G and \overline{G} are not isomorphic. To verify the second part of the claim, that is $s(G) = s(\overline{G})$, is a tedious process hence we invite the reader to inspect Appendix A presenting a Sage program verifying the claim. \square

We are now ready to prove the main claim of this section.

Theorem 6. *There exist infinitely many graphs G such that $G \not\cong \overline{G}$ but $T_G(x, y) = T_{\overline{G}}(x, y)$.*

Proof. By Lemma 5 there is a non self-complementary graph on 9 vertices such that $s(G) = s(\overline{G})$ which implies $T_G(x, y) = T_{\overline{G}}(x, y)$. But then, by Lemma 4 the graph \widehat{G} again has the same subgraph description as its complement and is not self-complementary. Hence applying this operation iteratively on G we end up with an infinite family of graphs possessing the stated property. \square

Again as with the chromatic polynomial we can find a graph of order 9 having the properties of Lemma 5. Hence it is possible to show in the same way as we did in the proof of Theorem 6 that for any $n \geq 8$ congruent to 0, 1 modulo 4 there exist a non self-complementary graph of order n having the same Tutte polynomial as its complement.

4 Final remarks

We were not able to find an example of a graph G with different degree sequence from \overline{G} but same Tutte polynomial. A computer search indicates that such a graph would have to have at least 16 vertices. Hence we leave the following problem.

Problem 1. *Find a graph G with different degree sequence than \overline{G} but same Tutte polynomial or show that such a graph does not exist.*

Interestingly the equivalent problem for chromatic polynomials motivated this paper.

5 Acknowledgements

We are thankful to thank Sandi Klavžar for constructive remarks to Gordon Royle and Georgi Guninski for help with some computational aspects of the problem and to Nejc Trdin for kindly sharing his computational resources.

A Sage programs used in the proofs

In this appendix we show how to prove the claims of Lemmas 4, 5 using the open source mathematical software Sage 5. All examples can be directly copy-pasted into Sage's shell.

In order to prove Lemma 2 we need to verify that the presented graph has a different degree sequence than its complement but equal chromatic polynomial.

```
sage: G = Graph('HCpVdZY')
sage: Gc = G.complement()
sage: G.degree_sequence() == Gc.degree_sequence()
False
sage: G.chromatic_polynomial() == Gc.chromatic_polynomial()
True
```

To check Lemma 4 we need to first define a function computing the subgraph description of a graph.

```
def s(Gr):
    ds = []

    for A in subsets(Gr.edges()):
        G = Graph()
        G.add_vertices(Gr.vertices())
        G.add_edges(A)
        cs = [H.order() for H in G.connected_components_subgraphs()]
        ds.append([len(A)] + sorted(cs))

    return sorted(ds)
```

It is now a matter of a few lines to verify Lemma 4.

```
sage: G = Graph('GCRdvK')
sage: Gc = G.complement()
sage: G.is_isomorphic(Gc)
False
sage: s(G) == s(Gc)
True
```

References

- [1] B.D. McKay, *graph6 and sparse6 graph formats*, <http://cs.anu.edu.au/~bdm/data/formats.html>
- [2] J. Ellis-Monaghan, C. Merino, *Graph polynomials and their applications. I. The Tutte polynomial*, [arXiv:0803.3079](https://arxiv.org/abs/0803.3079)
- [3] J. Akiyama, F. Harary, *A graph and its complement with specified properties. VII. A survey*, The theory and applications of graphs, 1–12, Wiley, New York, 1981.

- [4] J. Xu, Z. Liu, *The chromatic polynomial between graph and its complement-about Akiyama and Hararys open problem*, *Graphs and Combinatorics*, 1995, 11 4, 337–345
- [5] W. A. Stein et al., *Sage Mathematics Software (Version 5.10)*, The Sage Development Team, 2013, <http://www.sagemath.org>