

对 SARS-CoV-2 大流行进行实时测序：可以实现的目标？

Thomas Christie Williams 在 SARS-CoV-2 / COVID-19 研讨会上的演讲总结。

SARS-CoV-2 的实时测序可以通过多种方式发挥作用。它不但可以帮助区分输入性病例和社区“人传人”病例，还可以帮助描绘病毒在社区中群体聚集性的传播范围和在整个英国范围内的传播轨迹。

在医院内部，通过实时测序可以追踪病毒的传播链并最大限度的保证可用病房的数量。在更大的范围内，我们可以通过实时测序来跟踪干预措施对病毒传播的影响，也可以结合病毒传播动力学来估算未被报到的感染人数。

Thomas 和一支在爱丁堡皇家医院（NHS Lothian）的研究团队一起制定出了一个基于纳米孔测序技术的实时测序方案。这个方案中使用的测序方案和相关数据分析方法已经由 ARTIC Network（<https://artic.network/ncov-2019>）开发完成，其中包括了由爱丁堡大学 Andrew Rambaut 教授和他的博士研究生 Áine O'Toole 开发的数据处理软件 RAMPART。

这支位于爱丁堡皇家医院的研究团队隶属于 COG-UK，一个全英范围的协会，在苏格兰范围内还包括 NHS 格拉斯哥大区团队和 MRC 病毒研究中心。COG-UK 致力于绘制整个病毒流行过程中具有区域代表性的 SARS-CoV-2 基因组序列图谱，而苏格兰地区的研究团队主要负责每周完成 200-400 个 SARS-CoV-2 样品基因组的测序。

随着我们对病毒的深入了解，实时测序可能可以被直接用于指导对患者的护理。但在此之前，还需要投入更多的时间、精力和研究去论证可行性。

图例：英国各地的 COG-UK 研究团队正在使用不需要任何大型或昂贵实验室设备的纳米孔测序技术进行 SAR-CoV-2 基因组快速测序。

Real-time sequencing of the SARS-CoV-2 pandemic: An achievable goal?

A summary of Thomas Christie Williams' presentation at the SARS-CoV-2/COVID-19 workshop.

Real-time sequencing of SARS-CoV-2 could contribute in a number of ways. It can help to distinguish between cases which have been imported, and those which have been transmitted within the community, and help to characterise community-based clusters and spread throughout the UK.

Within hospitals, it could help to identify chains of transmission and thus help to keep as many wards open as possible. On a wider scale, we could use it to track the impact of intervention measures and to estimate how many cases are going unreported, based on phylogeographic dynamics.

Thomas and a team at NHS Lothian's Royal Infirmary of Edinburgh have put into place a real-time sequencing protocol which uses Nanopore sequencing technology. The sequencing protocol, and associated data analysis methods, have been developed by the ARTIC Network (<https://artic.network/ncov-2019>). This includes the RAMPART data software developed by the University of Edinburgh's Professor Andrew Rambaut and PhD student Áine O'Toole.

The team is part of a UK-wide consortium, COG-UK, which will generate a geographically representative selection of SARS-CoV-2 genome sequences throughout the epidemic. Together with other Scottish teams, such as NHS Greater Glasgow and the MRC Centre for Virus Research, the NHS Lothian team aim to be able to sequence 200-400 SARS-CoV-2 samples per week.

It is possible that, as we gain greater understanding of the virus, real-time sequencing could also be used to directly inform patient care. However, this will require careful thought and substantial investment of time, effort, and research expertise.

Figure Legend: Nanopore sequencing, which does not require any large or expensive lab equipment, is being used by the COG-UK consortium around the UK to rapidly sequence SAR-CoV-2 genomes.