UK COVID-19 Inquiry: Module 2 - Rule 9 Request to Dr Andrew Page - Reference: M2/SAGE/01/AXP

1. A brief overview of your qualifications, career history, professional expertise and major publications.

1.1 Education and Qualifications;

2003-2008: PhD Computer Science, Adaptive scheduling in heterogenous distributed systems using machine learning, National University of Ireland Maynooth. Thesis included method development for pathogen genomics.

1999-2003: BSc (hons) Computer Science and Software Engineering: 1.1, National University of Ireland Maynooth. Thesis included work on analysing bacterial pathogens using genomics.

1.2 Employment history;

2018-Present: Head of Informatics, Quadram Institute Bioscience.
Lead the core bioinformatics, cloud computing, and sequencing teams in a publicly funded (BBSRC/UKRI) food science research institute. This encompasses bioinformatics infrastructure, novel method development, genome sequencing and data analysis support for high throughput sequence analysis, including pathogens. Lead a SARS-CoV-2 sequencing centre COG-UK and as a resilience lab for UKHSA, genome sequencing 87,000 SARS-CoV-2 samples and undertaking bioinformatics and genomic epidemiological analysis.

2011-2018: Principal Computer Biologist in Pathogen Informatics, Wellcome Sanger Institute.
Lead developer and deputy head of the Pathogen Informatics team. Development of microbial bioinformatics methods and genomic analysis in the field of human infectious diseases (viral, bacterial, parasites).

2009-2011: Senior Software Developer in Sequencing Informatics, Wellcome Sanger Institute. Development of software for genome sequencing labs.

2008-2009: PostDoc in machine learning, National College of Ireland.

1.3 Selected Publications; Author of more than 130 publications since 2003, notably:

1.3.1 Twin peaks: The Omicron SARS-CoV-2 BA.1 and BA.2 epidemics in England. Science (2022).

1.3.2 Rapid increase in Omicron infections in England during December 2021: REACT-1 study. Science (2022).

1.3.3 SARS-CoV-2 infection and vaccine effectiveness in England (REACT-1): a series of cross-sectional random community surveys. Lancet Resp Med (2022).

1.3.4 Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. Nature Communications (2022).

1.3.5 CoronaHiT: large scale multiplexing of SARS-CoV-2 genomes using Nanopore sequencing. Genome Medicine (2021).

1.3.6 Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. Science (2021).

1.3.7 The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities. Lancet Microbe (2021).

1.3.8 Large-scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management. Microbial Genomics (2021).

1.3.9 AlbaTraDIS: comparative analysis of large datasets from parallel transposon mutagenesis experiments. PLoS Computational Biology (2020).

1.3.10 Socru: Typing of genome level order and orientation in bacteria. Microbial Genomics (2020).

1.3.11 Taxonomic resolution of the ribosomal RNA operon in bacteria: implications for its use with long-read sequencing. NAR Genomics and Bioinformatics (2020).

1.3.12 Emergence of an Extensively Drug-Resistant S. Typhi Clone Harboring a Promiscuous Plasmid Encoding Resistance to Fluoroquinolones and Third-Generation Cephalosporins. MBio (2018).

1.3.13 Rapid multi-locus sequence typing direct from uncorrected long reads using Krocus. PeerJ (2018).

1.3.14 Roary: rapid large-scale prokaryote pan genome analysis. Bioinformatics (2015).

1.3.15 Rapid phylogenetic analysis of large samples of recombinant bacterial whole genome sequences using Gubbins. Nucleic acids research (2014).

2. A list of the groups (i.e. SAGE and/or any of its sub-groups) in which you have been a participant, and the relevant time periods.

I served on the Social Care Working Group (SCWG) as a core scientific attendee from 2 October 2020 to 1 April 2022.

3. An overview of your involvement with those groups between January 2020 and February 2022, including:

3.1 **a. When and how you came to be a participant;**

3.1.1 I was a Principal Investigator (PI) for the Quadram Institute sequencing centre for the COVID-19 Genomics Consortium (COG-UK). The head of the consortium, Prof Sharon Peacock, asked for a volunteer on 22 Sept 2020 to represent COG-UK on the Social Care Working Group to provide genomics expertise to the group and to act as a conduit for information & requests between COG-UK and the SCWG.I volunteered as I had already undertaken genomic analysis of linked care home outbreaks (published in Microbial Genomics: https://doi.org/10.1099/mgen.0.000589).

3.2 **b. The number of meetings you attended, and your contributions to those meetings;**

3.2.1 I attended the vast majority of SCWG meeting between 2 October 2020 and 1 April 2022. Where meeting attendance was recorded (incomplete) by the secretariat I attended 17 out of 21 meetings. I was primarily a

passive participant. I provided expertise on genomics and advised on the impact of its use and the impact of testing strategies on genomic surveillance.

3.3 **c. Your role in providing research, information and advice.**

3.3.1 I led a review on the use of genomics in understanding outbreaks in long term care facilities (published in Lancet Microbe: https://doi.org/10.1016/S2666-5247(21)00208-1).Through COG-UK I contributed through groups other than SCWG to inform the pandemic response. I primarily provided expertise on genomics.

4. A summary of any documents to which you contributed for the purpose of advising SAGE and/or its related subgroups on the Covid-19 pandemic. Please include links to those documents where possible.

4.1 "COG-UK: Impact of travel restrictions on importations to England from May to September 2020, 16 March 2021", https://www.gov.uk/government/publications/cog-uk-impact-of-travel-restrictions-on-importations-to-england-from-may-to-september-2020-16-march-2021

4.2 "What are the appropriate mitigations to deploy in care homes in the context of the post vaccination risk landscape?", https://www.gov.uk/government/publications/scwg-what-are-the-appropriate-mitigations-to-deploy-in-care-homes-in-the-context-of-the-post-vaccination-risk-landscape-26-may-2021

4.3 "SCWG Consensus Statement on Family or friend Visitor Policy into Care Home Settings.", https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/1012407/S0875_Social_Care_Working_Group_Consensus_statement_on_visitor_policies.pdf

4.4 "The role of genomics in understanding COVID-19 outbreaks in long term care facilities", https://www.thelancet.com/journals/lanmic/article/PIIS2666-5247(21)00208-1/fulltext

4.5 "Consensus statement on the association between the discharge of patients from hospitals and COVID in care homes", https://www.gov.uk/government/publications/the-association-between-the-discharge-of-patients-from-hospitals-and-covid-in-care-homes/consensus-

statement-on-the-association-between-the-discharge-of-patients-from-hospitals-and-covid-in-care-homes

5. A summary of any articles you have written, interviews and/or evidence you have given regarding the work of the above-mentioned groups and/or the UK's response to the Covid-19 pandemic. Please include links to those documents where possible.

5.1 Reports to SAGE formalised as peer reviewed articles:

5.1.1 "The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities", published in Lancet Microbe: https://doi.org/10.1016/S2666-5247(21)00208-1

I led a review (senior author) on the use of genomics in understanding outbreaks in long term care facilities. I performed the review and wrote the first draft.

5.1.2 "Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission", published in Nature Communications https://doi.org/10.1038/s41467-022-28371-z

I contributed an analysis (2nd author) on the use of genomics related to importations. My role was primarily on bioinformatics analysis.

5.2 Media interviews providing expertise on COVID-19 to general public (a full record of interviews wasn't kept):

3/2/22 – TV interview, BBC Look East

2/2/22 – print interview, Eastern Daily Press

1/2/22 – TV interview, BBC Look East: Expert comment on Omicron BA.2

30/11/21 – TV interview, ITV Anglia News

29/11/21 – Radio interview: BBC Radio Norfolk

27/11/21 - print interview, Eastern Daily Press

13/11/21 - Clinical Omics

21/7/21 – TV interview, BBC Look East

24/5/21 – TV interview, BBC Look East

21/5/21 – Radio interview, BBC Radio Norfolk

14/5/21 – TV interview, BBC Look East

19/3/21 – print interview, Associated Press

19/3/21 – print article, Sky news

11/2/21 – print interview, Eastern Daily Press

15/12/20 – TV interview, BBC Look East

5.3 Podcasts I hosted on SARS-CoV-2:

5.3.1 "The people behind the benchmark datasets for SARS-CoV-2", https://soundcloud.com/microbinfie/behind-sars-cov-2-datasets

5.3.2 "Benchmark datasets for SARS-CoV-2", https://soundcloud.com/microbinfie/sars-cov-2-datasets-part-1

5.3.3 "SARS-CoV-2 And Sequencing Spike With Sanger Sequencing part 2", https://soundcloud.com/microbinfie/56-sars-cov-2-and-sequencing-spike-with-sanger-sequencing-welcome-to-1995

5.3.4 "SARS-CoV-2 And Sequencing Spike With Sanger Sequencing - Welcome To 1995", https://soundcloud.com/microbinfie/55-sars-cov-2-and-sequencing-spike-with-sanger-sequencing-welcome-to-1996

5.3.5 "SARS-CoV-2 In Canada and addressing data sharing and privacy", https://soundcloud.com/microbinfie/54-harmonising-sars-cov-2-surveillance-in-canada-with-cancogen

5.3.6 "SARS-CoV-2 surveillance in Canada with CANCOGEN", https://soundcloud.com/microbinfie/sars-cov-2-surveillance-in-canada-with-cancogen

5.3.7 "SARS-CoV-2 sequencing in Denmark with Mads Albertsen", https://soundcloud.com/microbinfie/sars-cov-2-sequencing-in-denmark-with-mads-albertsen

5.3.8 "SARSCOV2 Round-up 3 and updates from Denmark", https://soundcloud.com/microbinfie/51-sarscov2-round-up-3-and-updates-from-denmark

5.3.9 "SARS-CoV-2 Tools and resources update", https://soundcloud.com/microbinfie/49-sars-cov-2-tools-and-resources-update

5.3.10 "SARS-CoV-2 More Variants of Concern and updates from Africa", https://soundcloud.com/microbinfie/48-sars-cov-2-more-variants-of-concern-and-updates-from-africa

5.3.11 "SARS-CoV-2 Rapid roundup and questions answered", https://soundcloud.com/microbinfie/47-sars-cov-2-rapid-roundup-and-questions-answered

5.3.12 "SARS-CoV-2 genomics resources", https://soundcloud.com/microbinfie/46-sars-cov-2-genomics-resources

5.3.13 "How to sequence SARS-CoV-2 using the ARTIC protocol with Joshua Quick", https://soundcloud.com/microbinfie/44-how-to-sequence-sars-cov-2-using-the-artic-protocol

5.3.14 "Why use genomics in an epidemic? with Sam Sheppard", https://soundcloud.com/microbinfie/43-why-use-genomics-in-an-epidemic

5.3.15 "Overcoming barriers to SARS-CoV-2 data analysis", https://soundcloud.com/microbinfie/42-overcoming-barriers-to-sars-cov-2-data-analysis

5.3.16 "SARS-CoV-2 Phylogenomics questions answered", https://soundcloud.com/microbinfie/41-sars-cov-2-phylogenomics-questions-answered

5.3.17 "A crash course in SARS-CoV-2 bioinformatics", https://soundcloud.com/microbinfie/40-a-crash-course-in-sars-cov-2-bioinformatics

5.3.18 "Explaining the naming of SARS-CoV-2 new variants", https://soundcloud.com/microbinfie/explaining-the-naming-of-sars-cov-2-new-variants

5.3.19 "Looking behind Majora's Mask and nation wide tracking of SARS-CoV-2 genomics", https://soundcloud.com/microbinfie/majora

5.3.20 "Large scale sequencing of SARS-CoV-2 genomes from one region", https://soundcloud.com/microbinfie/31-large-scale-sequencing-of-sars-cov-2-genomes-from-one-region

5.3.21 "SARS-CoV-2 contextual data specification for open genomic epidemiology", https://soundcloud.com/microbinfie/26-sars-cov-2-metadata

5.3.22 "CoronaHiT: large scale multiplexing of SARS-CoV-2 genomes on Nanopore", https://soundcloud.com/microbinfie/23-coronahit-nanopore

5.3.23 "Setting up coronavirus sequencing for real-time public health surveillance", https://soundcloud.com/microbinfie/coronavirus-sequencing-qib

5.4 Academic articles/reports I contributed to informing the UK's pandemic response:

5.4.1 "An integrated national scale SARS-CoV-2 genomic surveillance network", https://www.thelancet.com/journals/lanmic/article/PIIS2666-5247(20)30054-9/fulltext

5.4.2 "Application of respiratory metagenomics for COVID-19 patients on the intensive care unit to inform appropriate initial antimicrobial treatment and rapid detection of nosocomial transmission", https://www.medrxiv.org/content/10.1101/2020.11.26.20229989v1

5.4.3 "Characterising the persistence of RT-PCR positivity and incidence in a community survey of SARS-CoV-2", https://www.medrxiv.org/content/10.1101/2021.08.12.21261987v1

5.4.4 "CoronaHiT: high-throughput sequencing of SARS-CoV-2 genomes", https://genomemedicine.biomedcentral.com/articles/10.1186/s13073-021-00839-5

5.4.5 "Defining the analytical and clinical sensitivity of the ARTIC method for the detection of SARS-CoV-2", https://www.medrxiv.org/content/10.1101/2021.10.09.21264695v1

5.4.6 "Evaluating the potential for respiratory metagenomics to improve treatment of secondary infection and detection of nosocomial

transmission on expanded COVID-19 intensive care units", https://genomemedicine.biomedcentral.com/articles/10.1186/s13073-021-00991-y

5.4.7 "Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant", https://www.science.org/doi/10.1126/science.abl9551

5.4.8 "Large-scale sequencing of SARS-CoV-2 genomes from one region allows detailed epidemiology and enables local outbreak management", https://www.microbiologyresearch.org/content/journal/mgen/10.1099/mgen.0.000589

5.4.9 "REACT-1 round 11 report: low prevalence of SARS-CoV-2 infection in the community prior to the third step of the English roadmap out of lockdown", https://www.medrxiv.org/content/10.1101/2021.05.13.21257144v1

5.4.10 "REACT-1 round 12 report: resurgence of SARS-CoV-2 infections in England associated with increased frequency of the Delta variant", https://www.medrxiv.org/content/10.1101/2021.06.17.21259103v1

5.4.11 "REACT-1 round 13 final report: exponential growth, high prevalence of SARS-CoV-2 and vaccine effectiveness associated with delta variant in England during May to July 2021", https://www.medrxiv.org/content/10.1101/2021.09.02.21262979v1

5.4.12 "REACT-1 round 15 final report: Increased breakthrough SARS-CoV-2 infections among adults who had received two doses of vaccine, but booster doses and first doses in children are providing important protection", https://www.medrxiv.org/content/10.1101/2021.12.14.21267806v1

5.4.13 "REACT-1 round 15 interim report: High and rising prevalence of SARS-CoV-2 infection in England from end of September 2021 followed by a fall in late October 2021", https://www.medrxiv.org/content/10.1101/2021.11.03.21265877v1

5.4.14 "REACT-1 study round 14: High and increasing prevalence of SARS-CoV-2 infection among school-aged children during September 2021 and vaccine effectiveness against infection in England", https://www.medrxiv.org/content/10.1101/2021.10.14.21264965v1

5.4.15 "SARS-CoV-2 lineage dynamics in England from January to March 2021 inferred from representative community samples", https://www.medrxiv.org/content/10.1101/2021.05.08.21256867v1

5.4.16 "The role of viral genomics in understanding COVID-19 outbreaks in long-term care facilities", https://www.thelancet.com/journals/lanmic/article/PIIS2666-5247(21)00208-1/fulltext

5.4.17 "Breakthrough SARS-CoV-2 infections in double and triple vaccinated adults and single dose vaccine effectiveness among children in Autumn 2021 in England: REACT-1 study", https://www.thelancet.com/journals/eclinm/article/PIIS2589-5370(22)00149-3/fulltext

5.4.18 "Cross-sectional community surveys to monitor the Omicron SARS-CoV-2 epidemic in England during February 2022", https://www.thelancet.com/journals/lanepe/article/PIIS2666-7762(22)00158-2/fulltext

5.4.19 "Dynamics of a national Omicron SARS-CoV-2 epidemic during January 2022 in England", https://www.nature.com/articles/s41467-022-32121-6

5.4.20 "Dynamics of competing SARS-CoV-2 variants during the Omicron epidemic in England", https://www.nature.com/articles/s41467-022-32096-4

5.4.21 "Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package", https://academic.oup.com/gigascience/article/doi/10.1093/gigascience/giac003/6529104

5.4.22 "Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission", https://www.nature.com/articles/s41467-022-28371-z

5.4.23 "Genomic epidemiology of SARS-CoV-2 in a UK university identifies dynamics of transmission", https://www.nature.com/articles/s41467-021-27942-w

5.4.24 "Omicron SARS-CoV-2 epidemic in England during February 2022: A series of cross-sectional community surveys",

https://www.thelancet.com/journals/lanepe/article/PIIS2666-7762(22)00158-2/fulltext

5.4.25 "Post-peak dynamics of a national Omicron SARS-CoV-2 epidemic during January 2022", https://www.medrxiv.org/content/10.1101/2022.02.03.22270365v1

5.4.26 "Rapid increase in Omicron infections in England during December 2021: REACT-1 study", https://www.science.org/doi/full/10.1126/science.abn8347

5.4.27 "SARS-CoV-2 infection and vaccine effectiveness in England (REACT-1): a series of cross-sectional random community surveys", https://www.thelancet.com/journals/lanres/article/PIIS2213-2600(21)00542-7/fulltext

5.4.28 "SARS-CoV-2 lineage dynamics in England from September to November 2021: high diversity of Delta sub-lineages and increased transmissibility of AY. 4.2", https://bmcinfectdis.biomedcentral.com/articles/10.1186/s12879-022-07628-4

5.4.29 "The new normal? Dynamics and scale of the SARS-CoV-2 variant Omicron epidemic in England", https://www.medrxiv.org/content/10.1101/2022.03.29.22273042v1

5.4.30 "The Omicron SARS-CoV-2 epidemic in England during February 2022", https://www.medrxiv.org/content/10.1101/2022.03.10.22272177v1

5.4.31 "Twin peaks: the omicron SARS-CoV-2 BA. 1 and BA. 2 epidemics in England", https://www.science.org/doi/10.1126/science.abq4411

6. **Your views as to whether the work of the above-mentioned groups in responding to the Covid-19 pandemic (or the UK's response more generally) succeeded in its aims. This may include, but is not limited to, your views on:**

6.1 **a. The composition of the groups and/or their diversity of expertise;**

The Social Care Working Group (SCWG) had a diverse set of expertise from a broad spectrum. This was very useful as there were different insights available. Social care is a large complex area, with a vulnerable population, so having a wide set of

expertise to draw on helped greatly in putting papers together. For example individuals had expertise in molecular biology, mathematical modelling, epidemiology, community care, public health, genomics, geriatrics, infection control, care sector operations and palliative care amongst many others.

6.2 **b. The way in which the groups were commissioned to work on the relevant issues;**

Commissions would come from SAGE or from the Department of Health and Social Care (DHSC) periodically with specific questions to answer. These were appropriate. When there were no live commissions, the group still met to ensure there was continuity of assistance.

6.3 **c. The resources and support that were available;**

Administrative support to the SCWG was provided by one individual from UKHSA for an extended period. This was subsequently enhanced with further staff. DHSC eXchange was made available for document sharing and archiving. Summary/trend data was made available to the working group from DHSC/UKHSA.

6.4 **d. The advice given and/or recommendations that were made;**

Advice and recommendations were made by consensus with independent attendees (scientists, clinicians, representatives of care sector) and public service attendees. Everyone attending the meeting had the opportunity to share knowledge or opinions when forming a consensus regardless of hierarchy. The consensus building could often take a lot of time and discussion, however it did lead to well thought out and measured documents. There was only one occasion where a consensus was not found and a majority view was reached instead. The advice I gave was always my considered view having regard to the information available at the time.

6.5 **e. The extent to which the groups worked effectively together;**

The SCWG worked effectively and quickly, often under very short turnaround times when given a commission. Subgroups would occasionally be formed to pull together the basis content of a response which was then circulated more widely to all for further development. The work was carried out on DHSC eXchange so all had access to the documents in real time, with tracked versions. It was highly collaborative in nature, predominantly lead by extremely experienced individuals who could analyse complex datasets and marshal domain expertise effectively. Work was carried out at weekends, public holidays and evenings if necessary to get the job done, often by independent volunteers who also had other fulltime jobs.

6.6 **f. The extent to which applicable structures and policies were utilised and/or complied with and their effectiveness.**

This was a well-run working group, with clear terms of reference when I joined. There were two chairs, providing consistency and continuity, with a secretariat (initially under resourced, but later expanded). The core attendees were in very regular attendance. The note taking, recording, attendance and minutes improved over time as the secretariat increased in capacity. Questions/commissions came from SAGE and sometimes directly from DHSC. Procedurally they should have come only from SAGE, however usually given the urgency and importance, the SCWG did do its best to assist DHSC.

7. Your views as to any lessons that can be learned from the UK's response to the Covid-19 pandemic, in particular relating to the work of the above-mentioned groups. Please describe any changes that have already been made, and set out any recommendations for further changes that you think the Inquiry should consider making.

There should be a permanent social care working group which can be stood up at short notice. Social care contains a highly vulnerable population which can be severely impacted by infectious diseases. The administrative support was stretched at the beginning (one person) and was later expanded. It would have been better to have had greater administrative support from the outset.

There was also a large time commitment placed on independent members for nearly two years, the cost of which was covered by their employers. Whilst I and others are happy to assist in a short term emergency, after a certain point the cost of the time commitment needs to be considered.

8. A brief description of documentation relating to these matters that you hold (including soft copy material held electronically). Please retain all such material. I am not asking for you to provide us with this material at this stage, but I may request that you do so in due course.

Emails: to/from the SCWG chairs and administrative staff, to/from individual attendees.

Internal memos, research papers, briefing papers, summary papers, including draft versions with comments.