

## FWO DMP Template - Flemish Standard Data Management Plan

### Version KU Leuven

Project supervisors (from application round 2018 onwards) and fellows (from application round 2020 onwards) will, upon being awarded their project or fellowship, be invited to develop their answers to the data management related questions into a DMP. The FWO expects a **completed DMP no later than 6 months after the official start date** of the project or fellowship. The DMP should not be submitted to FWO but to the research co-ordination office of the host institute; FWO may request the DMP in a random check.

At the end of the project, the **final version of the DMP** has to be added to the final report of the project; this should be submitted to FWO by the supervisor-spokesperson through FWO's e-portal. This DMP may of course have been updated since its first version. The DMP is an element in the final evaluation of the project by the relevant expert panel. Both the DMP submitted within the first 6 months after the start date and the final DMP may use this template.

The DMP template used by the Research Foundation Flanders (FWO) corresponds with the Flemish Standard Data Management Plan. This Flemish Standard DMP was developed by the Flemish Research Data Network (FRDN) Task Force DMP which comprises representatives of all Flemish funders and research institutions. This is a standardized DMP template based on the previous FWO template that contains the core requirements for data management planning. To increase understanding and facilitate completion of the DMP, a standardized **glossary** of definitions and abbreviations is available via the following [link](#).

| 1. General Project Information        |  |
|---------------------------------------|--|
| Name Grant Holder & ORCID             | Name Grant Holder: Joon Klaps<br>ORCID: 0000-0002-2507-0430  |
| Contributor name(s) (+ ORCID) & roles | Contributor name: Philippe Lemey<br>ORCID: 0000-0003-2826-5353<br>Contributor name: Liana Kafetzopoulou<br>ORCID: 0000-0003-4531-1374  |
| Project number <sup>1</sup> & title   | Project number: 1SH2V24N<br>Project Title: The evolutionary genomics of Lassa Virus virulence and persistence  |
| Funder(s) GrantID <sup>2</sup>        | FWO GrantID: 1SH2V24N  |
| Affiliation(s)                        | <input checked="" type="checkbox"/> KU Leuven<br><input type="checkbox"/> Universiteit Antwerpen<br><input type="checkbox"/> Universiteit Gent<br><input type="checkbox"/> Universiteit Hasselt<br><input type="checkbox"/> Vrije Universiteit Brussel<br><input type="checkbox"/> Other:<br>ROR identifier KU Leuven: 05f950310 |

---

<sup>1</sup> "Project number" refers to the institutional project number. This question is optional. Applicants can only provide one project number.

<sup>2</sup> Funder(s) GrantID refers to the number of the DMP at the funder(s), here one can specify multiple GrantIDs if multiple funding sources were used.

|  |   |
|--|---|
| Please provide a short project description | <p>Lassa virus (LASV) infects hundreds of thousands of individuals each year and is endemic in West Africa. People mainly become infected through spill-over from rodents. While most infected individuals remain asymptomatic, acute viral hemorrhagic illness develops in 1 in 5 cases. With no effective treatments or vaccines and little knowledge of the determinants of disease development, LASV is a WHO priority disease. Lassa fever survivors have been identified to continue to carry the virus up to 12 months post-infection, however, the impact of viral persistence on viral evolution has yet to be determined. This project aims to disentangle the role of viral genotypes as well as intrahost evolution in disease outcome and persistence. In collaboration with the Bernhard-Nocht Institute for Tropical Medicine, we will leverage the comprehensive sampling from ongoing longitudinal studies in Nigeria. Whole-genome deep sequencing data will be analyzed from multiple time points from patients that succumb to infection and patients that survive with varying degrees of persistence. Using this data, we will unravel intrahost evolutionary dynamics including the role of immune escape in LASV infections, and perform an extensive phylogenomics study to determine to what extent the viral genotype determines virulence and to elucidate its molecular determinants. Finally, LASV virulence will be mapped spatially through phylogeographic inference in order to inform intervention strategies.</p> |
|--|---|

## 2. Research Data Summary

List and describe all datasets or research materials that you plan to generate/collect or reuse during your research project. For each dataset or data type (observational, experimental etc.), provide a short name & description (sufficient for yourself to know what data it is about), indicate whether the data are newly generated/collected or reused, digital or physical, also indicate the type of the data (the kind of content), its technical format (file extension), and an estimate of the upper limit of the volume of the data <sup>3</sup>.

---

<sup>3</sup> Add rows for each dataset you want to describe.

|                               |   |   |   | ONLY FOR DIGITAL DATA   | ONLY FOR DIGITAL DATA          | ONLY FOR DIGITAL DATA   | ONLY FOR PHYSICAL DATA |
|-------------------------------|---|---|---|---|--------------------------------|---|------------------------|
| Dataset Name                  | Description   | New or Reused   | Digital or Physical   | Digital Data Type   | Digital Data Format            | Digital Data Volume (MB, GB, TB)  | Physical Volume        |
| Sample metadata               | Pseudo-anonymised metadata relating to samples collected from patients including: age, sex, results diagnostic test Lassa, country, state, city, diagnostic test location, date seen at health facility, date of onset of disease, date of specimen collection, symptoms, disease outcome | <input type="checkbox"/> Generate new data<br><input checked="" type="checkbox"/> Reuse existing data | <input checked="" type="checkbox"/> Digital<br><input type="checkbox"/> Physical            | <input type="checkbox"/> Audiovisual<br><input type="checkbox"/> Images<br><input type="checkbox"/> Sound<br><input checked="" type="checkbox"/> Numerical<br><input checked="" type="checkbox"/> Textual<br><input type="checkbox"/> Model<br><input type="checkbox"/> Software<br><input type="checkbox"/> Other: | Excel files and MySQL database | <input type="checkbox"/> < 1 GB<br><input checked="" type="checkbox"/> < 100 GB<br><input type="checkbox"/> < 1 TB<br><input type="checkbox"/> < 5 TB<br><input type="checkbox"/> > 5 TB<br><input type="checkbox"/> NA | NA                     |
| Laboratory procedure metadata | Data relating to samples processed in the laboratory, all necessary information relating to the laboratory procedures performed   | <input checked="" type="checkbox"/> Generate new data<br><input type="checkbox"/> Reuse existing data | <input checked="" type="checkbox"/> Digital<br><input type="checkbox"/> Physical            | <input type="checkbox"/> Audiovisual<br><input type="checkbox"/> Images<br><input type="checkbox"/> Sound<br><input checked="" type="checkbox"/> Numerical<br><input checked="" type="checkbox"/> Textual<br><input type="checkbox"/> Model<br><input type="checkbox"/> Software<br><input type="checkbox"/> Other: | Excel files and MySQL database | <input type="checkbox"/> < 1 GB<br><input checked="" type="checkbox"/> < 100 GB<br><input type="checkbox"/> < 1 TB<br><input type="checkbox"/> < 5 TB<br><input type="checkbox"/> > 5 TB<br><input type="checkbox"/> NA | NA                     |
| Sequencing reads              | Sequencing reads output from Illumina deep sequencing   | <input checked="" type="checkbox"/> Generate new data<br><input type="checkbox"/> Reuse existing data | <input checked="" type="checkbox"/> Digital<br><input checked="" type="checkbox"/> Physical | <input type="checkbox"/> Audiovisual<br><input type="checkbox"/> Images<br><input type="checkbox"/> Sound<br><input type="checkbox"/> Numerical<br><input checked="" type="checkbox"/> Textual<br><input type="checkbox"/> Model<br><input type="checkbox"/> Software   | Fastq files                    | <input type="checkbox"/> < 1 GB<br><input type="checkbox"/> < 100 GB<br><input type="checkbox"/> < 1 TB<br><input checked="" type="checkbox"/> < 5 TB<br><input type="checkbox"/> > 5 TB<br><input type="checkbox"/> NA | NA                     |

|                                      |   |   |  |   |  |   |    |
|--------------------------------------|---|---|--|---|--|---|----|
|                                      |   |   |  | <input type="checkbox"/> Other:   |  |   |    |
| Sequencing data analysis and results | Sequencing data analysis and result output files including: fasta, fastq, csv, vcf  | <input checked="" type="checkbox"/> Generate new data<br><input type="checkbox"/> Reuse existing data | <input checked="" type="checkbox"/> Digital<br><input type="checkbox"/> Physical | <input type="checkbox"/> Audiovisual<br><input type="checkbox"/> Images<br><input type="checkbox"/> Sound<br><input checked="" type="checkbox"/> Numerical<br><input checked="" type="checkbox"/> Textual<br><input type="checkbox"/> Model<br><input type="checkbox"/> Software<br><input type="checkbox"/> Other: | Text files (including following formats: fasta, fastq, csv, vcf) | <input type="checkbox"/> < 1 GB<br><input type="checkbox"/> < 100 GB<br><input type="checkbox"/> < 1 TB<br><input type="checkbox"/> < 5 TB<br><input checked="" type="checkbox"/> > 5 TB<br><input type="checkbox"/> NA | NA |
| Custom made algorithms               | Portfolio of custom-made scripts for the processing and analysis of the metadata and results generated as part of the project | <input checked="" type="checkbox"/> Generate new data<br><input type="checkbox"/> Reuse existing data | <input checked="" type="checkbox"/> Digital<br><input type="checkbox"/> Physical | <input type="checkbox"/> Audiovisual<br><input type="checkbox"/> Images<br><input type="checkbox"/> Sound<br><input type="checkbox"/> Numerical<br><input checked="" type="checkbox"/> Textual<br><input type="checkbox"/> Model<br><input checked="" type="checkbox"/> Software<br><input type="checkbox"/> Other: | Text files   | <input checked="" type="checkbox"/> < 1 GB<br><input type="checkbox"/> < 100 GB<br><input type="checkbox"/> < 1 TB<br><input type="checkbox"/> < 5 TB<br><input type="checkbox"/> > 5 TB<br><input type="checkbox"/> NA | NA |
| Data on phylogenetic inference       | Phylogenetic inference of the sequences obtained and result output files  | <input checked="" type="checkbox"/> Generate new data<br><input type="checkbox"/> Reuse existing data | <input checked="" type="checkbox"/> Digital<br><input type="checkbox"/> Physical | <input type="checkbox"/> Audiovisual<br><input type="checkbox"/> Images<br><input type="checkbox"/> Sound<br><input checked="" type="checkbox"/> Numerical<br><input checked="" type="checkbox"/> Textual<br><input type="checkbox"/> Model<br><input type="checkbox"/> Software<br><input type="checkbox"/> Other: | Text files and nexus/newick/xml tree files                       | <input type="checkbox"/> < 1 GB<br><input checked="" type="checkbox"/> < 100 GB<br><input type="checkbox"/> < 1 TB<br><input type="checkbox"/> < 5 TB<br><input type="checkbox"/> > 5 TB<br><input type="checkbox"/> NA | NA |

|  |   |
|--|---|
| <p><b>GUIDANCE:</b></p> <p><i>The data description forms the basis of your entire DMP, so make sure it is detailed and complete. It includes digital and physical data and encompasses the whole spectrum ranging from raw data to processed and analysed data including analysis scripts and code. Physical data are all materials that need proper management because they are valuable, difficult to replace and/or ethical issues are associated. Materials that are not considered data in an RDM context include your own manuscripts, theses and presentations; documentation is an integral part of your datasets and should be described under documentation/metadata.</i></p> <p><u><a href="#">RDM Guidance on data</a></u></p> |   |
| <p>If you reuse existing data, please specify the source, preferably by using a persistent identifier (e.g. DOI, Handle, URL etc.) per dataset or data type.</p>   | <p>The project re-uses existing data which are partly published and partly unpublished or available online. Sample metadata will be used from three pre-existing studies: (1) “Leftover samples” protocol (access to the initial diagnostic sample) (2) the “Pathogenesis study” and (3) the “Follow-up study”. Published data exists under the following DOI:</p> <ol style="list-style-type: none"> <li>1. Metagenomic sequencing at the epicenter of the Nigeria 2018 Lassa fever outbreak:<br/>10.1126/science.aau9343</li> <li>2. Virus persistence after recovery from acute Lassa fever in Nigeria: a 2-year interim analysis of a prospective longitudinal cohort study:<br/>10.1016/S2666-5247(21)00178-6</li> </ol> |
| <p>Are there any ethical issues concerning the creation and/or use of the data (e.g. experiments on humans or animals, dual use)? If so, refer to specific datasets or data types when appropriate and provide the relevant ethical approval number.</p>   | <p><input checked="" type="checkbox"/> Yes, human subject data; provide SMEC or EC approval number: S67612</p> <p><input type="checkbox"/> Yes, animal data; provide ECD reference number:</p> <p><input type="checkbox"/> Yes, dual use; provide approval number:</p> <p><input type="checkbox"/> No</p> <p>Additional information:<br/>S67612</p>   |
| <p>Will you process personal data<sup>4</sup>? If so, please refer to specific datasets or data types when appropriate and provide the KU Leuven or UZ Leuven privacy register number (G or S number).</p>   | <p><input checked="" type="checkbox"/> Yes (provide PRET G-number or EC S-number below)</p> <p><input type="checkbox"/> No</p> <p>Additional information:<br/>S67612</p>  |

<sup>4</sup> See Glossary Flemish Standard Data Management Plan

|   |  |
|---|--|
| <p>Does your work have potential for commercial valorization (e.g. tech transfer, for example spin-offs, commercial exploitation, ...)?</p> <p>If so, please comment per dataset or data type where appropriate.</p>  | <p><input checked="" type="checkbox"/> Yes<br/> <input type="checkbox"/> No</p> <p>If yes, please comment:</p> <p>Sequencing data analysis and results - Custom made algorithms - Data phylogenetic inference will LASV sequencing data, immune escape of LASV in patients, and database infrastructures for diagnostic investigations can elicit interest from companies that develop diagnostic tools, vaccines, and treatments for Lassa fever. If our 'custom made algorithms' has high efficacy to pinpoint molecular determinants of Lassa fever this can be extend towards other viral infectious diseases and facilitate treatment development towards those diseases as well.</p> |
| <p>Do existing 3rd party agreements restrict exploitation or dissemination of the data you (re)use (e.g. Material/Data transfer agreements, research collaboration agreements)?</p> <p>If so, please explain to what data they relate and what restrictions are in place.</p> | <p><input type="checkbox"/> Yes<br/> <input checked="" type="checkbox"/> No</p> <p>If yes, please explain:</p>   |
| <p>Are there any other legal issues, such as intellectual property rights and ownership, to be managed related to the data you (re)use?</p> <p>If so, please explain to what data they relate and which restrictions will be asserted.</p>                                    | <p><input type="checkbox"/> Yes<br/> <input checked="" type="checkbox"/> No</p> <p>If yes, please explain:</p>   |

### 3. Documentation and Metadata



|   |   |
|---|---|
| <p>Clearly describe what approach will be followed to capture the accompanying information necessary to keep <b>data understandable and usable</b>, for yourself and others, now and in the future (e.g. in terms of documentation levels and types required, procedures used, Electronic Lab Notebooks, README.txt files, Codebook.tsv etc. where this information is recorded).</p> <p><u><a href="#">RDM guidance on documentation and metadata.</a></u></p> | <p>Sample metadata will be combined in a relational database allowing for fast and efficient information interrogation.</p> <p>All laboratory procedures, all bioinformatics analysis and testing and any relating data is heavily documented; an electronic lab book system has been created and implemented for tracking all processes conducted.</p> <p>All scripts generated will be commented/documentated and will include README files. Log files will be generated during data analysis with detailed information on the analysis process performed on each run and sample analysed. All public databases used within our analysis (eg. Genome reference database) will contain download dates and/or version control Version control is used across all scripts. Software is also packaged within container environments like Docker and Singularity to guarantee reproducibility.</p> |
| <p>Will a metadata standard be used to make it easier to <b>find and reuse the data</b>?</p> <p>If so, please specify which metadata standard will be used. If not, please specify which metadata will be created to make the data easier to find and reuse.</p> <p><i>REPOSITORIES COULD ASK TO DELIVER METADATA IN A CERTAIN FORMAT, WITH SPECIFIED ONTOLOGIES AND VOCABULARIES, I.E. STANDARD LISTS WITH UNIQUE IDENTIFIERS.</i></p>                         | <p><input checked="" type="checkbox"/> Yes<br/> <input type="checkbox"/> No</p> <p>If yes, please specify (where appropriate per dataset or data type) which metadata standard will be used:</p> <p>A data schema was internally designed to ensure Findable, Accessible, Interoperable and Reusable (FAIR) metadata. All sample metadata is stored within a relational (MySQL) database. Within the database, data is structured with unique identifiers containing specific attributes with data type declaration and is therefore machine-readable.</p> <p>If no, please specify (where appropriate per dataset or data type) which metadata will be created:</p>  |

#### 4. Data Storage & Back-up during the Research Project

|  |   |
|--|---|
| <p>Where will the data be stored?</p> <p><i>Consult the <a href="#">interactive KU Leuven storage guide</a> to find the most suitable storage solution for your data.</i></p>  | <p> <input type="checkbox"/> Shared network drive (J-drive)<br/> <input type="checkbox"/> Personal network drive (I-drive)<br/> <input type="checkbox"/> OneDrive (KU Leuven)<br/> <input type="checkbox"/> Sharepoint online<br/> <input type="checkbox"/> Sharepoint on-premis<br/> <input checked="" type="checkbox"/> Large Volume Storage<br/> <input type="checkbox"/> Digital Vault<br/> <input checked="" type="checkbox"/> Other: <ul style="list-style-type: none"> <li>- KUL hosted MySQL Server</li> <li>- HPC Tier-2 data -staging</li> <li>- HPC Tier-1 data</li> <li>- Large volume storage -archive (K-drive)</li> </ul> </p> |
| <p>How will the data be backed up?</p> <p><i>WHAT STORAGE AND BACKUP PROCEDURES WILL BE IN PLACE TO PREVENT DATA LOSS?</i></p>   | <p> <input checked="" type="checkbox"/> Standard back-up provided by KU Leuven ICTS for my storage solution.<br/> <input type="checkbox"/> Personal back-ups I make (specify)<br/> <input type="checkbox"/> Other (specify) </p>  |
| <p>Is there currently sufficient storage &amp; backup capacity during the project? If yes, specify concisely. If no or insufficient storage or backup capacities are available, then explain how this will be taken care of.</p> | <p> <input checked="" type="checkbox"/> Yes<br/> <input type="checkbox"/> No </p> <p>If no, please specify:</p>   |

|   |  |
|---|--|
| <p>How will you ensure that the data are securely stored and not accessed or modified by unauthorized persons?</p> <p><i>CLEARLY DESCRIBE THE MEASURES (IN TERMS OF PHYSICAL SECURITY, NETWORK SECURITY, AND SECURITY OF COMPUTER SYSTEMS AND FILES) THAT WILL BE TAKEN TO ENSURE THAT STORED AND TRANSFERRED DATA ARE SAFE.</i></p> <p><u><a href="#">Guidance on security for research data</a></u></p> | <p>All data is stored on locations where only authorized persons can access. No unauthorized persons can access the data. All data and files generated as part of this project will be stored on KU Leuven servers using the network drives or SharePoint. Additionally, all researchers actively working on the project follow a clean desk policy. Secure solutions (Belnet Filesender) for sharing data with persons outside KU Leuven will be used when data and files need to be shared between the project partners.</p> |
| <p>What are the expected costs for data storage and backup during the research project? How will these costs be covered?</p>  | <p>L drive: €569,2/year<br/> KUL hosted MySQL Server : € 91,46/year<br/> HPC tier-1 data: € 0/year (grant application)<br/> HPC tier-2 data staging: €160/year<br/> K drive: €569,2/year</p> <p><b>Total: € 1389,86/year</b><br/> These costs have been anticipated and will be covered from project funding that is already available.</p>  |

## 5. Data Preservation after the end of the Research Project

|  |   |
|--|---|
| <p>Which data will be retained for at least five years (or longer, in agreement with other retention policies that are applicable) after the end of the project? In case some data cannot be preserved, clearly state the reasons for this (e.g. legal or contractual restrictions, storage/budget issues, institutional policies...).</p> <p><a href="#"><u>Guidance on data preservation</u></a></p> | <p><input checked="" type="checkbox"/> All data will be preserved for 10 years according to KU Leuven RDM policy</p> <p><input type="checkbox"/> All data will be preserved for 25 years according to CTC recommendations for clinical trials with medicinal products for human use and for clinical experiments on humans</p> <p><input type="checkbox"/> Certain data cannot be kept for 10 years (explain)</p> |
| <p>Where will these data be archived (stored and curated for the long-term)?</p> <p><i><a href="#"><u>Dedicated data repositories</u></a> are often the best place to preserve your data. Data not suitable for preservation in a repository can be stored using a KU Leuven storage solution, consult the <a href="#"><u>interactive KU Leuven storage guide</u></a>.</i></p>                         | <p><input type="checkbox"/> KU Leuven RDR</p> <p><input checked="" type="checkbox"/> Large Volume Storage (longterm for large volumes)</p> <p><input type="checkbox"/> Shared network drive (J-drive)</p> <p><input type="checkbox"/> Other (specify):</p> <ul style="list-style-type: none"> <li>- Large volume storage -archive (K-drive)</li> </ul>  |
| <p>What are the expected costs for data preservation during the expected retention period</p> <p>? How will these costs be covered?</p>  | <p>These involve the same costs as during the project duration</p> <p>L drive: €569,2/year</p> <p>KUL hosted MySQL Server: € 91,46/year</p> <p>K drive: €569,2/year</p> <p><b>Total: € 1229.86/year</b></p> <p>These costs have been anticipated and will be covered from funds that are available to the PI.</p>   |

## 6. Data Sharing and Reuse

|  |  |
|--|--|
| <p>Will the data (or part of the data) be made available for reuse after/during the project?<br/>Please explain per dataset or data type which data will be made available.</p> <p><i>NOTE THAT 'AVAILABLE' DOES NOT NECESSARILY MEAN THAT THE DATA SET BECOMES OPENLY AVAILABLE, CONDITIONS FOR ACCESS AND USE MAY APPLY. AVAILABILITY IN THIS QUESTION THUS ENTAILS BOTH OPEN &amp; RESTRICTED ACCESS. FOR MORE INFORMATION:</i><br/><a href="https://wiki.surfnet.nl/display/STANDARDS/INFO-EU-REPO/#INFOEUREPO-ACCESSRIGHTS">https://wiki.surfnet.nl/display/STANDARDS/INFO-EU-REPO/#INFOEUREPO-ACCESSRIGHTS</a></p> | <p> <input checked="" type="checkbox"/> Yes, as open data<br/> <input type="checkbox"/> Yes, as embargoed data (temporary restriction)<br/> <input checked="" type="checkbox"/> Yes, as restricted data (upon approval, or institutional access only)<br/> <input checked="" type="checkbox"/> No (closed access)<br/> <input type="checkbox"/> Other, please specify:         </p> <p>Sample metadata: closed access</p> <p>Laboratory procedure metadata: restricted access</p> <p>Sequencing reads: restricted access</p> <p>Sequencing data analysis and results: open data</p> <p>Custom made scripts: open data</p> <p>Data on phylogenetic inference: open data</p> |
| <p>If access is restricted, please specify who will be able to access the data and under what conditions.</p>  | <p>Laboratory procedure metadata: institutional access</p> <p>Sequencing reads: as read data could contain human reads this is restricted. However, upon request we can map and share viral reads only.</p>  |

|  |   |
|--|---|
| <p>Are there any factors that restrict or prevent the sharing of (some of) the data (e.g. as defined in an agreement with a 3rd party, legal restrictions)? Please explain per dataset or data type where appropriate.</p> | <div data-bbox="728 156 1178 399"> <input type="checkbox"/> Yes, privacy aspects<br/> <input type="checkbox"/> Yes, intellectual property rights<br/> <input type="checkbox"/> Yes, ethical aspects<br/> <input type="checkbox"/> Yes, aspects of dual use<br/> <input type="checkbox"/> Yes, other<br/> <input checked="" type="checkbox"/> No </div> <p data-bbox="728 443 1005 480">If yes, please specify:</p>  |
| <p>Where will the data be made available?<br/>If already known, please provide a repository per dataset or data type.</p>  | <div data-bbox="728 566 1249 683"> <input type="checkbox"/> KU Leuven RDR<br/> <input checked="" type="checkbox"/> Other data repository (specify): NCBI<br/> <input checked="" type="checkbox"/> Other (specify) </div> <p data-bbox="728 727 1283 764">Sequencing data analysis and results: NCBI</p> <p data-bbox="728 809 1106 845">Custom made scripts: Github</p> <p data-bbox="728 890 1827 927">Data on phylogenetic inference: Github or as manuscript supplementary information</p> |
| <p>When will the data be made available?</p>   | <div data-bbox="728 968 1243 1085"> <input checked="" type="checkbox"/> Upon publication of research results<br/> <input type="checkbox"/> Specific date (specify)<br/> <input type="checkbox"/> Other (specify) </div>   |

|   |  |
|---|--|
| <p>Which data usage licenses are you going to provide? If none, please explain why.</p> <p><i>A DATA USAGE LICENSE INDICATES WHETHER THE DATA CAN BE REUSED OR NOT AND UNDER WHAT CONDITIONS. IF NO LICENCE IS GRANTED, THE DATA ARE IN A GREY ZONE AND CANNOT BE LEGALLY REUSED. DO NOTE THAT YOU MAY ONLY RELEASE DATA UNDER A LICENCE CHOSEN BY YOURSELF IF IT DOES NOT ALREADY FALL UNDER ANOTHER LICENCE THAT MIGHT PROHIBIT THAT.</i></p> <p>Check the <a href="#">RDR guidance on licences</a> for data and software sources code or consult the <a href="#">License selector tool</a> to help you choose.</p> | <input type="checkbox"/> CC-BY 4.0 (data)<br><input type="checkbox"/> Data Transfer Agreement (restricted data)<br><input checked="" type="checkbox"/> MIT licence (code)<br><input type="checkbox"/> GNU GPL-3.0 (code)<br><input type="checkbox"/> Other (specify) |
| <p>Do you intend to add a PID/DOI/accession number to your dataset(s)? If already available, please provide it here.</p> <p><i>INDICATE WHETHER YOU INTEND TO ADD A PERSISTENT AND UNIQUE IDENTIFIER IN ORDER TO IDENTIFY AND RETRIEVE THE DATA.</i></p>  | <input checked="" type="checkbox"/> Yes, a PID will be added upon deposit in a data repository<br><input type="checkbox"/> My dataset already has a PID<br><input type="checkbox"/> No   |
| <p>What are the expected costs for data sharing?<br/>How will these costs be covered?</p>   | <p>No costs are expected for data sharing on locations where the data and scripts will be made publicly available (NCBI, Github). Any publications costs associated will be covered by project funding already available.</p>  |

| 7. Responsibilities  |   |
|--|---|
| Who will manage data documentation and metadata during the research project? | Ine Boonen, Liana Kafetzopoulou, Joon Klaps     |
| Who will manage data storage and backup during the research project?         | Ine Boonen, Liana Kafetzopoulou, Joon Klaps     |
| Who will manage data preservation and sharing?                               | Ine Boonen, Liana Kafetzopoulou, Joon Klaps     |
| Who will update and implement this DMP?                                      | Joon Klaps, Liana Kafetzopoulou, Philippe Lemey |

