UNDERSTANDING ROLE OF MECHANICAL FORCES IN HUMAN NEURAL TUBE DEVELOPMENT AND NEURAL TUBE DEFECTS

A Data Management Plan created using DMPonline.be

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Funder: Fonds voor Wetenschappelijk Onderzoek - Research Foundation Flanders (FWO)

Template: FWO DMP (Flemish Standard DMP)

Grant number / URL: G0ACA24N

ID: 209106

Start date: 01-01-2024

End date: 31-12-2027

Project abstract:

The formation of the neural tube is the earliest event in the establishment of the central nervous system. Cell acquire their identity at the same time as the tissue undergoes large-scale tissue deformations, driven by cellular contractility and mechanical forces. However, the relationship between these tissue deformations, the developed mechanical forces and the establishment of cellular identities remains largely unexplored. In addition, it is unclear how mechanical dysregulation during neural tube development leads to neural tube defects. Here we propose to use a novel human pluripotent stem cell derived model of neural tube closure to understand how mechanical forces coordinate the specification of cellular identities across the dorso-ventral and anterior-posterior axis. We will use bioengineering technologies, including mechanical actuation devices and microfluidics to manipulate this model in order to determine the response of cells to mechanical stimuli involved in neural tube development. We will also use cells derived from neural tube defect patients to understand whether failures in the various steps of neural tube development, including bending, folding and closure, result from perturbations in the mechanical microenvironment.

Last modified: 18-07-2024

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FWO DMP (Flemish Standard DMP)

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1. 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.

				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
Microscopy images	Images acquired from various microscopes, mainly immunohistochemistry, also time-lapse imaging	*New data*	Digital	*Experimental*	*.tiff, .lif*	*<5TB* • <100MB • <1GB • <100GB • <1TB • <5TB • <10TB • <50TB • >50TB • NA	
Single cell transcriptome data	Processed data from scRNAseq runs	New data	Digital	Experimental	.csv	<1TB	
R and Matlab code	Code to run data analysis	New data	Digital	Code	.r and .mat	<100MB	
Powepoint, Illustrator and Word documents	Documents containing processed data, figure files, paper drafts	New data	Digital	End point data	.ppt, .doc, .ai	<100GB	
Experimental samples	Fixed organoid samples	New data	Physical				Fridge

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:

We will reuse data from:
Human neural tube morphogenesis in vitro by geometric constraints
https://doi.org/10.1038/s41586-021-04026-9

Are there any ethical issues concerning the creation and/or use of the data (e.g. experiments on humans or animals, dual use)? Describe these issues in the comment section. Please refer to specific datasets or data types when appropriate.

- No

no dual use

Will you process personal data? If so, briefly describe the kind of personal data you will use in the comment section. Please refer to specific datasets or data types when appropriate.

- No

no personal data

Does your work have potential for commercial valorization (e.g. tech transfer, for example spin-offs, commercial exploitation, …)? If so, please comment per dataset or data type where appropriate.

- No

Do existing 3rd party agreements restrict exploitation or dissemination of the data you (re)use (e.g. Material/Data transfer agreements/ research collaboration agreements)? If so, please explain in the comment section to what data they relate and what restrictions are in place.

- Yes

We use cell lines provided by collaborators or commercial sources in this project.
Additionally we use plasmids from addgene in this project.
These materials are covered by MTAs. This relates to all forms of data above but do not have any specific restrictions in place regarding data management.

Are there any other legal issues, such as intellectual property rights and ownership, to be managed related to the data you (re)use? If so, please explain in the comment section to what data they relate and which restrictions will be asserted.

- No

no foreseeen legal issues with data (re)use

2. Documentation and Metadata

Clearly describe what approach will be followed to capture the accompanying information necessary to keep data understandable and usable, 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).

All information related to experimental data is stored in an electronic lab book.
All data is stored on KU Leuven OneDrive cloud-based drive.
Additionally we all results (i.e. post-processed) and documentation are stored on a dedicated lab google drive account.
All data is preserved for at least 5 years after the end of the research.

Will a metadata standard be used to make it easier to find and reuse the data? If so, please specify (where appropriate per dataset or data type) which metadata standard will be used. If not, please specify (where appropriate per dataset or data type) which metadata will be created to make the data easier to find and reuse.

- Yes

Documents including .doc and .xls data pertaining to each set of experiments are stored together with the experimental data in the same folder. These documents contain key information related to the experiments (types of samples, experimental conditions, analysis procedure) to ensure

reusability of the data and to ensure the data is easy to find and reuse.

3. Data storage & back-up during the research project

Where will the data be stored?

All data is stored on KU Leuven One Drive.
Additionally, selected data is stored on Google Drive (eg. presentations, key documents, protocols, inventory).

How will the data be backed up?

KU Leuven ICTS ensures that that all data is backed up regularly according to KU Leuven data storage policies.
We also keep key data on the google drive as an additional mitigating procedure.

Is there currently sufficient storage & 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.

- Yes

The current capacity of the KU Leuven OneDrive is expected to enough for storing data for the entire duration of the project. In case of need, Large Volume Storage with KU Leuven ICTS will be used.

How will you ensure that the data are securely stored and not accessed or modified by unauthorized persons?

Data stored in the KU Leuven One Drive is only accessible to the researcher which is accessed via two-step authentication system.

What are the expected costs for data storage and backup during the research project? How will these costs be covered?

KU Leuven One Drive does not incur any additional charges. if Large Volume Storage is required, costs will be covered by Prof.Ranga.

4. Data preservation after the end of the research project

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...).

All digital data including microscopy images, scRNAseq datasets, code, and post-processed data documents will be stored for at least 5 years.
Physical samples will usually be preserved for a maximum of one month in the fridge after imaging, in case re-imaging is needed. Sample quality generally degrades within a week, so we do not foresee keeping physical samples for longer than one month.

Where will these data be archived (stored and curated for the long-term)?

Data will be stored on KU Leuven OneDrive, and, if additional storage space is needed, will be moved to Large Volume Storage.

What are the expected costs for data preservation during the expected retention period? How will these costs be covered?

No additional costs are currently foreseen for data storage. In case Large Volume Storage is required, Prof.Ranga will cover such costs.

5. Data sharing and reuse

Will the data (or part of the data) be made available for reuse after/during the project? In the comment section please explain per dataset or data type which data will be made available.

- Yes, in an Open Access repository

scRNAseq datasets will be deposited in the GEO (Gene Expression Omnibus - NCBI) repository, which is open access and available for reuse.
Code will be uploaded to GitHub.
Datasets and code will be deposited at the time of upload of associated manuscripts to bioRxiv preprint repository.

If access is restricted, please specify who will be able to access the data and under what conditions.

All data other than above-mentioned publicly available scRNAseq and code will be available to all members of the Ranga lab.
Should external requests for other data be made, these will be processed by Prof.Ranga and lab manager Julian Diender.

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 in the comment section per dataset or data type where appropriate.

- No

Where will the data be made available? If already known, please provide a repository per dataset or data type.

scRNAseq data will be available on GEO and code will be available on Github.

When will the data be made available?

scRNAseq data and code will be made available simultaneously with upload of associated manuscripts on bioRxiv. Standard policy in the lab is that all manuscripts are uploaded to bioRxiv at the same time as submission to journals. This process ensures that data is available to the scientific community at the same time as the manuscript, and before the often lengthy journal review process.

Which data usage licenses are you going to provide? If none, please explain why.

No license is associated to the use of scRNAseq datasets.
Code wil be licensed under MIT license.

Do you intend to add a PID/DOI/accession number to your dataset(s)? If already available, you have the option to provide it in the comment section.

- Yes

DOI/accession numbers will be available at the time manuscripts are publicly seen on bioRxiv.

What are the expected costs for data sharing? How will these costs be covered?

GEO and Github do not have any associated costs.

6. Responsibilities

Who will manage data documentation and metadata during the research project?

Julian Diender, lab manager

Who will manage data storage and backup during the research project?

Julian Diender, lab manager

Who will manage data preservation and sharing?

Julian Diender, lab manager

Who will update and implement this DMP?

Prof. Adrian Ranga