

A readme file provides information about a dataset and is intended to help ensure that the data can be correctly interpreted, by yourself at a later date or by others when sharing or publishing data.

A readme file must be submitted along with the dataset file(s).

The outline below should be completed with information relevant to the submitted dataset.

Best practices

- **Create one readme file for each dataset**
- **Name the file README;** not readme, read_me, ABOUT, etc.
- **Write your readme document as a plain text file;** save as README.txt or README.md when writing in Markdown. Or use README.pdf when text formatting is important for your file.

Recommended content

Recommended minimum content is in bold.

1. *Introductory information*

- **Title of the dataset**
- **For each file or group of similar files, a short description of what data it contains**
- Explain the file naming convention, if applicable
- Format of the file if not obvious from the file name
- If the data set includes multiple files that relate to each other, the relationship between the files or a description of the file structure that holds them
- Contact information; in case users have questions regarding the data files

2. *Methodological information*

- **Method description for collecting or generating the data, as well as the methods for processing data, if data other than raw data are being contributed**
- Any instrument-specific information needed to understand or interpret the data
- Software (including version number) used to produce, prepare, render, compress, analyze and/or needed to read the dataset, if applicable
- Standards and calibration information, if appropriate

- Describe any quality-assurance procedures performed on the data
- Definitions of codes or symbols used to note or characterize low quality/questionable/outliers that people should be aware

3. *Data specific information*

- **Full names and definitions (spell out abbreviated words) of column headings for tabular data**
- **Units of measurement**
- **Definitions for codes or symbols used to record missing data**
- **Specialized formats or abbreviations used**

4. *Sharing and Access information*

- Licenses or restrictions placed on the data;
Licenses allow you to specify the 'terms-of-use' for your data. The archive provides a license that is explained in its [terms of use](#) and applies this license as default selection. You can use this licensing [wizard](#) to help you to pick a more appropriate license for the use of your data. This license will then be displayed in the metadata.

Example of a good README which was submitted to the data archive:

*** Mode I fatigue delamination growth in composite laminates with fibre bridging ***

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General Introduction

This dataset contains data collected during crack growth experiments at Delft University of Technology, as part of Liaojun Yao's PhD Thesis project (December 2015):

doi:10.4233/uuid:66e210e1-c884-45d6-b9d4-711907680452

It is being made public both to act as supplementary data for publications and the PhD thesis of Liaojun Yao and in order for other researchers to use this data in their own work.

The data in this data set was collected in the Structures and Materials Laboratory of the Delft University of Technology - Faculty of Aerospace Engineering, between October 2012 and December 2015.

This research project was made possible by a grant from the China Scholarship Council (CSC).

Purpose of the test campaign

The purpose of these experiments was to investigate delamination growth in CFRP composites. The Double Cantilever Beam (DCB) specimens were subjected to a variety of load cases, as detailed in "Text matrix.doc"

Test equipment

All tests were performed on a 10 kN MTS fatigue test machine. The crack length was measured by means of a camera system.

The applied force and displacement were measured by the fatigue test machine, and also sent as inputs to the camera, in order to facilitate synchronisation of the data.

Description of the data in this data set

The data included in this data set has been organised per specimen. The files follow the nomenclature system: Sp_X_Data_analysis_Y with

X = the specimen number 1 to 56

Y = indicating the number of runs with the same specimen.