

A database of the healthy human spinal cord morphometry in the PAM50 template space

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Reproducible Preprint

- Jupyter Book

Code

- Technical Screening
- Submitted Repository

Reproducibility Assets

- Repository
- Dataset
- Jupyter Book
- Container

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Summary

Spinal cord morphometry measures derived from magnetic resonance imaging (MRI) scans serve as valuable prognostic biomarkers for various spinal cord pathologies. Despite their significance, interpreting these biomarkers is challenging due to substantial variability between subjects. The lack of a standardized normalization method to mitigate this variability and the need for a better understanding of morphometric distribution contribute to the current knowledge gap.

In this work, we present a database of healthy normative values for six commonly used measures of spinal cord morphometry built using a new fully-automatic normalization approach. Morphometric measures were computed from a large open-access dataset of healthy adult volunteers ($N = 203$) and brought to the common space of the PAM50 spinal cord template using a newly proposed normalization method based on linear interpolation **Figure 1**.

The database is interactive, available online (TODO: add a link to interactive preprint) and allows filtering for sex, age, and MRI vendors. The proposed method is open-source and easily accessible through the Spinal Cord Toolbox (SCT) v6.0 and higher.

This new morphometric database allows researchers to normalize morphometrics based on sex and age, thereby minimizing inter-subject variability associated with demographic and biological factors.

Figures

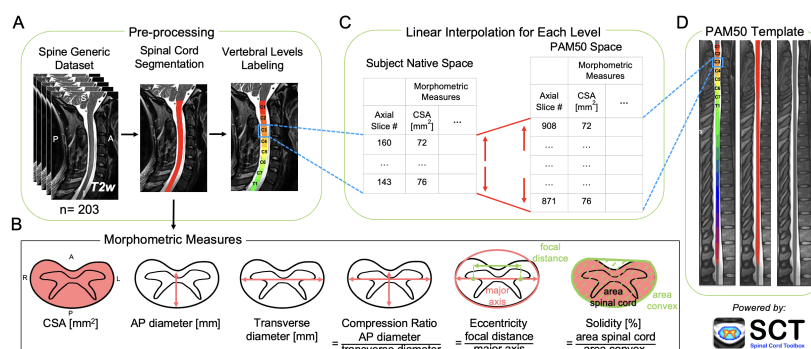


Figure 1: Schematic representation of the normalization approach. (A) T2-weighted images of 203 participants from the spine-generic dataset (multi-subject) were used. The spinal cord was segmented, and vertebral levels were identified automatically using the Spinal Cord Toolbox (SCT). (B) Six morphometric measures were computed for each axial slice from the single-subject segmentation masks. (C) For each level, the number of slices in the subject native space and the corresponding level in the PAM50 template (D) were identified. Then, the morphometric measures were linearly interpolated to the PAM50 space using the number of slices in the PAM50 template and the subject native space for each vertebral level.

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