

Correction to: Analysis of medications change in Parkinson's disease progression data

Anita Valmarska^{1,2} · Dragana Miljkovic¹ ·
Nada Lavrač^{1,2,3} · Marko Robnik-Šikonja⁴

Published online: 22 June 2018

© Springer Science+Business Media, LLC, part of Springer Nature 2018

Correction to: J Intell Inf Syst

<https://doi.org/10.1007/s10844-018-0502-y>

The original version of this article unfortunately contained a mistake. Figure 4 and Figure 5 in Section 5.4 have mistakenly been switched, while the captions of Figure 4 and Figure 5 are correct and correspond to the references in the text. The corrected figures are shown next page.

The online version of the original article can be found at <https://doi.org/10.1007/s10844-018-0502-y>.

✉ Anita Valmarska
anita.valmarska@ijs.si

Dragana Miljkovic
dragana.miljkovic@ijs.si

Nada Lavrač
nada.lavrac@ijs.si

Marko Robnik-Šikonja
marko.robnik@fri.uni-lj.si

¹ Jožef Stefan Institute, Jamova 39, 1000 Ljubljana, Slovenia

² Jožef Stefan International Postgraduate School, Jamova 39, 1000 Ljubljana, Slovenia

³ University of Nova Gorica, Vipavska 13, 5000 Nova Gorica, Slovenia

⁴ Faculty of Computer and Information Science, University of Ljubljana, Večna pot 113, 1000 Ljubljana, Slovenia

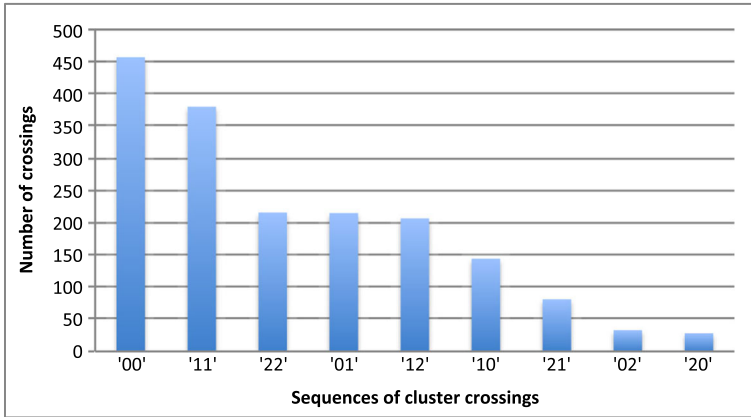


Fig. 4 Histogram resulting from 3-skip-2-gram analysis. The possible cluster crossings are listed on the X-axis (e.g., 01 indicates that a patient has moved from *Cluster 0* to *Cluster 1*), while the Y-axis represents the number of cluster crossings

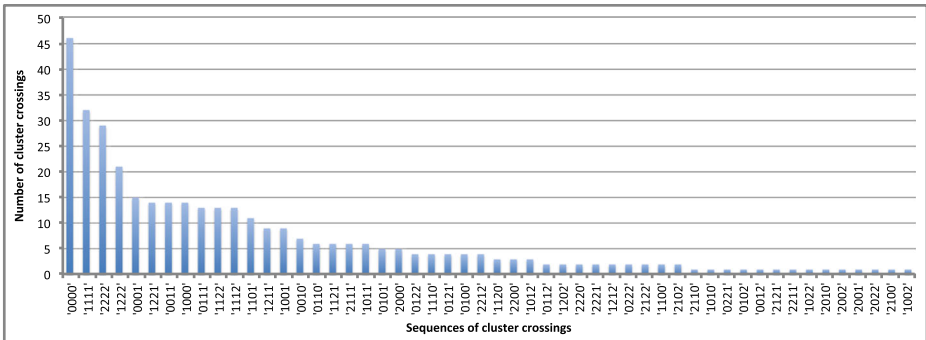


Fig. 5 Histogram resulting from 3-skip-4-gram analysis. The possible cluster crossings are listed on the X-axis and the Y-axis represents the number of cluster crossings