Dear Dr. Michael Kane,

Attached please find a revised version of our paper (2019-81) and our response to the comments of the reviewers. We would like to thank them for the suggestions which lead to an improved update of the paper. The revisions we have made accordingly and the detailed responses are given in the attached document.

Yours sincerely,

Ana López-Cheda

1 Response to the reviewers

We would like to thank the reviewers for their detailed comments on our manuscript. We incorporated them in the new version of the document. We have used red color for highlighting the changes introduced into the paper. Thus they are easy to detect at a first glance. Some typos have been corrected as well.

1. *If not mistaken, the package only handles right-censored survival times, other complications such as left censoring, truncation (left or right) are not considered in the current development. This should be clearly stated in the abstract, introduction and conclusions.*

   Answer: The reviewer is right. In our approach we have considered only right-censored times, since this is the most common type of censoring. We have included this information in the abstract, introduction (last paragraph) and conclusions (second paragraph). The possibility of extending this work to left-censored, truncated or even interval-censored data remains as an open problem to be dealt with in the future.

2. *Though it is true that the package is based on previously published papers, some of the details may be included to make the manuscript self-content and clear. For example, please specify what the $K(\cdot/h)$ function is in Nadaraya-Watson weight on page 3. In Step 2 of the bootstrap resampling procedure on page 4, what is d in $I(T_i \leq t, \delta_i \leq d)$? Is d the uncensoring indicator defined on page 7?*

   Answer: We have added some more information related to the Nadaraya-Watson weights, $B_{h[i]}(x)$. Specifically, we have rewritten the paragraph and defined K as the Epanechnikov kernel after Equation (2). Note that the choice of the kernel, K, is of secondary importance, since the estimator is not very sensitive to its choice, and different kernels produce good estimates. Due to this reason, in the `npcure` package other kernels are not considered. Moreover, in Step 2 of the bootstrap resampling procedure, d was one of the parameters of the function $\hat{F}_h(t, d|x)$. For the sake of clarity, we have replaced d by δ.

3. *Do the bandwidth selectors of h_x and b_x share the same local pilot bandwidth, g_x? Are the grids of bandwidths $h_l \in \{h_1, \ldots, h_L\}$ and $b_m \in \{b_1, \ldots, b_M\}$ the same if the interesting covariates are different in the latency and in the cure probability?*

   Answer: The pilot bandwidths for the cure probability and the latency estimators are the ones considered in López-Cheda et al. (2017a,b), respectively.

   López-Cheda, A., Cao, R., Jácome, M. A., & Van Keilegom, I. (2017a). Nonparametric incidence estimation and bootstrap bandwidth selection in mixture cure models. *Comput. Stat. Data Anal.*, **105**, 144-165.

   López-Cheda, A., Jácome, M. A., & Cao, R. (2017b). Nonparametric latency estimation for mixture cure models. *Test*, **26**, 353-376.

   These pilot bandwidths, as well as the corresponding grids of bandwidths, depend on the distribution of the covariate X. Therefore, if the covariate for the cure probability and for the

latency are not the same and they follow different distributions, then the pilot bandwidths and the corresponding grids will be different too.

4. *In subsection 4.2 in the code "lopezcheda.R", the output using the local bootstrap bandwidths to estimate the latency function with $x_0 = 0$ shows the negative survival probability $(-4.552e-18)$ for $t > 1.187$. The similar case was also observed in the real data analysis for estimating the latency $(-3.462e-17)$ conditional on age 40 for $t \geq 625$. Could the authors double check this?*

   Answer: A new version of the `npcure` package that solves this numerical problem has been uploaded to CRAN. Nevertheless, it must be remarked that the problem pointed out by the reviewer is not reproducible in any of the Windows and Linux platforms the authors have used.

5. *The authors used different number of bootstrap resamples in the package, e.g., $B = 2000$ in the function probcure(), $B = 500$ in the function latency(), $B = 2500$ in the function testcov(). Any guides for choosing the number of bootstrap resamples when using the package?*

   Answer: On the one hand, a large number of bootstrap resamples is usually required. On the other hand, these methods (probcure, latency and testcov) are computationally expensive, since they are based on Monte Carlo. Therefore, the reason why we used different number of bootstrap resamples in each function, is that we tried to strike a balance between a reasonable number of resamples and a not very slow procedure. Note that these numbers of bootstrap resamples, used to level speed and efficiency, can be changed by the user with the `controlpars()` function.

   Some minor suggestions/comments:

6. *Please specify the section number in the manuscript.*

   Answer: The latex template provided by `https://journal.r-project.org/submissions.html` does not include the section numbers, nor the recently publised papers in the journal. That is the reason why we have not included them in the paper.

7. *Labels should not be reused for clarity. A potential option is to label the procedure of generating bootstrap resamples (I) through (III) on page 4. On page 6, the steps of covariate significance test using the CM and KS test statistics will perhaps necessitate new labels.*

   Answer: We have updated the paper. In particular, we have used labels with roman numbers in the procedure of generating bootstrap resamples on page 4, and we considered labels with alphabetic characters for the steps of the significance test on page 6.

8. *In the second paragraph on page 2, "probbility" should be "probability".*

   Answer: We have corrected the typo.