**Table1.** Datasets summary

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Datasets summary** | | | | | |
| **Dataset (name used in this paper)** | **Number of observations** | **No. of variables** | **Type of data** | **Censoring rate (rounded to 4 decimal places)** | **Reference** |
| Melanoma\_itraq | 41 | 643 | Omics | 0.4146 | Wang,K.Y.X. et al. Cross-Platform Omics Prediction procedure: a game changer for implementing precision medicine in patients with stage-III melanoma.bioRxiv 2020.12.09.415927; doi: <https://doi.org/10.1101/2020.12.09.415927> |
| Melanoma\_nano | 45 | 207 | Omics | 0.4222 | Wang,K.Y.X. et al. Cross-Platform Omics Prediction procedure: a game changer for implementing precision medicine in patients with stage-III melanoma.bioRxiv 2020.12.09.415927; doi: <https://doi.org/10.1101/2020.12.09.415927> |
| Ovarian\_2 | 58 | 19818 | Omics | 0.3793 | Ganzfried,B.F. et al. (2013) curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. Database, 2013. |
| GE\_5 | 78 | 4753 | Omics | 0.5641 | van ’t Veer,L.J. et al. (2002) Gene expression profiling predicts clinical outcome of breast cancer. Nature, 415, 530–536. |
| GE\_3 | 86 | 6288 | Omics | 0.7209 | Bullinger,L. et al. (2004) Use of Gene-Expression Profiling to Identify Prognostic Subclasses in Adult Acute Myeloid Leukemia. New England Journal of Medicine, 350, 1605–1616. |
| Melanoma\_clinical | 77 | 16 | Clinical | 0.3939 | Wang,K.Y.X. et al. Cross-Platform Omics Prediction procedure: a game changer for implementing precision medicine in patients with stage-III melanoma.bioRxiv 2020.12.09.415927; doi: [https://doi.org/10.1101/2020.12.09.415927.](https://doi.org/10.1101/2020.12.09.415927) |
| GE\_1 | 115 | 551 | Omics | 0.6670 | Sorlie,T. et al. (2003) Repeated observation of breast tumor subtypes in independent gene expression data sets. Proc. Natl. Acad. Sci. U. S. A., 100, 8418–8423. |
| GE-\_4 | 116 | 6285 | Omics | 0.5641 | van de Vijver,M.J. et al. (2002) A gene-expression signature as a predictor of survival in breast cancer. N. Engl. J. Med., 347, 1999– 2009. |
| Veteran | 137 | 8 | Clinical | 0.0657 | Kalbfleisch,J.D. and Prentice,R.L. (2002) The Statistical Analysis of Failure Time Data. Wiley Series in Probability and Statistics. |
| Ovarian\_1 | 194 | 16050 | Omics | 0.7062 | Ganzfried,B.F. et al. (2013) curatedOvarianData: clinically annotated data for the ovarian cancer transcriptome. Database, 2013. |
| Lung | 228 | 9 | Clinical | 0.2763 | Loprinzi,C.L. et al. (1994) Prospective evaluation of prognostic variables from patient-completed questionnaires. North Central Cancer Treatment Group. J. Clin. Oncol., 12, 601–607. |
| GE\_6 | 240 | 7401 | Omics | 0.4250 | Van Houwelingen,H.C. (2004) The Elements of Statistical Learning, Data Mining, Inference, and Prediction. Trevor Hastie, Robert Tibshirani and Jerome Friedman, Springer, New York, 2001. No. of pages: xvi 533. ISBN 0-387-95284-5. Statistics in Medicine, 23, 528–529. |
| GE\_2 | 295 | 4921 | Omics | 0.7322 | Beer,D.G. et al. (2002) Gene-expression profiles predict survival of patients with lung adenocarcinoma. Nat. Med., 8, 816–824. |
| PBC | 312 | 7 | Clinical | 0.5994 | Fleming,T.R. and Harrington,D.P. (2005) Counting Processes and Survival Analysis. Wiley Series in Probability and Statistics. |
| UNOS\_Kidney | 3000 | 101 | Clinical | 0.7350 | OPTN data (https://optn.transplant.hrsa.gov/) |
| ANZ | 3323 | 40 | Clinical | 0.8739 | ANZDATA (https://www.anzdata.org.au/) |

Data table showing the names of datasets used in this paper in the first column. Censoring rate is rounded to 4 decimal places.