**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 | 642 | 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 | 206 | 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 | 88 | 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. Datasets are ordered by the number of observations (second column, from smallest to largest). Censoring rate is rounded to 4 decimal places.