

References

- [1] Quinn T Ostrom, Haley Gittleman, Gabrielle Truitt, Alexander Boscia, Carol Kruchko, and Jill S Barnholtz-Sloan. Cbtrus statistical report: primary brain and other central nervous system tumors diagnosed in the united states in 2011–2015. *Neuro-oncology*, 20(suppl_4):iv1–iv86, 2018.
- [2] Quinn T Ostrom, Haley Gittleman, Jordonna Fulop, Max Liu, Rachel Blanda, Courtney Kromer, Yingli Wolinsky, Carol Kruchko, and Jill S Barnholtz-Sloan. Cbtrus statistical report: primary brain and central nervous system tumors diagnosed in the united states in 2008-2012. *Neuro-oncology*, 17(suppl_4):iv1–iv62, 2015.
- [3] Quinn T Ostrom, Haley Gittleman, Peter Liao, Chaturia Rouse, Yanwen Chen, Jacqueline Dowling, Yingli Wolinsky, Carol Kruchko, and Jill Barnholtz-Sloan. Cbtrus statistical report: primary brain and central nervous system tumors diagnosed in the united states in 2007–2011. *Neuro-oncology*, 16(suppl_4):iv1–iv63, 2014.
- [4] Michael Weller, Wolfgang Wick, Ken Aldape, Michael Brada, Mitchell Berger, Stefan M Pfister, Ryo Nishikawa, Mark Rosenthal, Patrick Y Wen, Roger Stupp, et al. Glioma. *Nature reviews Disease primers*, 1(1):1–18, 2015.
- [5] Gregory N Fuller and Bernd W Scheithauer. The 2007 revised world health organization (who) classification of tumours of the central nervous system: newly codified entities. *Brain pathology*, 17(3):304–307, 2007.
- [6] Felix Sahm, David Reuss, Christian Koelsche, David Capper, Jens Schittenhelm, Stephanie Heim, David TW Jones, Stefan M Pfister, Christel Herold-Mende, Wolfgang Wick, et al. Farewell to oligoastrocytoma: in situ molecular genetics favor classification as either oligodendroglioma or astrocytoma. *Acta neuropathologica*, 128(4):551–559, 2014.

- [7] Kewal K Jain. A critical overview of targeted therapies for glioblastoma. *Frontiers in oncology*, 8:419, 2018.
- [8] Hiroko Ohgaki and Paul Kleihues. Epidemiology and etiology of gliomas. *Acta neuropathologica*, 109(1):93–108, 2005.
- [9] Pei Yang, Yongzhi Wang, Xiaoxia Peng, Gan You, Wei Zhang, Wei Yan, Zhaoshi Bao, Yinyan Wang, Xiaoguang Qiu, and Tao Jiang. Management and survival rates in patients with glioma in china (2004–2010): a retrospective study from a single-institution. *Journal of neuro-oncology*, 113(2):259–266, 2013.
- [10] Elizabeth B Claus, Kyle M Walsh, John K Wiencke, Annette M Molinaro, Joseph L Wiemels, Joellen M Schildkraut, Melissa L Bondy, Mitchel Berger, Robert Jenkins, and Margaret Wrensch. Survival and low-grade glioma: the emergence of genetic information. *Neurosurgical focus*, 38(1):E6, 2015.
- [11] Navodini Wijethilake, Dulani Meedeniya, Charith Chitraranjan, and Indika Perera. Survival prediction and risk estimation of glioma patients using mrna expressions. In *2020 IEEE 20th International Conference on Bioinformatics and Bioengineering (BIBE)*, pages 35–42. IEEE, 2020.
- [12] Ping Wang, Yan Li, and Chandan K Reddy. Machine learning for survival analysis: A survey. *ACM Computing Surveys (CSUR)*, 51(6):1–36, 2019.
- [13] L Ganau, M Paris, GK Ligarotti, and M Ganau. Management of gliomas: overview of the latest technological advancements and related behavioral drawbacks. *Behavioural neurology*, 2015, 2015.
- [14] SE Metcalfe and R Grant. Biopsy versus resection for malignant glioma. *The Cochrane database of systematic reviews*, (3):CD002034–CD002034, 2001.
- [15] N Upadhyay and AD3473894 Waldman. Conventional mri evaluation of gliomas. *The British journal of radiology*, 84(special_issue_2):S107–S111, 2011.

- [16] P Kalavathi and VB Surya Prasath. Methods on skull stripping of mri head scan images—a review. *Journal of digital imaging*, 29(3):365–379, 2016.
- [17] Andriy Fedorov, Reinhard Beichel, Jayashree Kalpathy-Cramer, Julien Finet, Jean-Christophe Fillion-Robin, Sonia Pujol, Christian Bauer, Dominique Jennings, Fiona Fennessy, Milan Sonka, et al. 3d slicer as an image computing platform for the quantitative imaging network. *Magnetic resonance imaging*, 30(9):1323–1341, 2012.
- [18] Stefan Bauer, Thomas Fejes, and Mauricio Reyes. A skull-stripping filter for itk. *Insight Journal*, 2012, 2013.
- [19] Jiangwei Lao, Yinsheng Chen, Zhi-Cheng Li, Qihua Li, Ji Zhang, Jing Liu, and Guangtao Zhai. A deep learning-based radiomics model for prediction of survival in glioblastoma multiforme. *Scientific reports*, 7(1):1–8, 2017.
- [20] N Wijethilake, M Islam, and H Ren. Radiogenomics model for overall survival prediction of glioblastoma. *Medical & Biological Engineering & Computing*, 58:1767–1777, 2020.
- [21] Navodini Wijethilake, Mobarakol Islam, Dulani Meedeniya, Charith Chitraranjan, Indika Perera, and Hongliang Ren. Radiogenomics of glioblastoma: Identification of radiomics associated with molecular subtypes. In *Machine Learning in Clinical Neuroimaging and Radiogenomics in Neuro-oncology*, pages 229–239. Springer, 2020.
- [22] Florent Tixier, Hyemin Um, Dalton Bermudez, Aditi Iyer, Aditya Apte, Maya S Graham, Kathryn S Nevel, Joseph O Deasy, Robert J Young, and Harini Veeraraghavan. Preoperative mri-radiomics features improve prediction of survival in glioblastoma patients over mgmt methylation status alone. *Oncotarget*, 10(6):660, 2019.
- [23] Paul A. Yushkevich, Joseph Piven, Heather Cody Hazlett, Rachel Gimpel Smith, Sean Ho, James C. Gee, and Guido Gerig. User-guided 3D ac-



- tive contour segmentation of anatomical structures: Significantly improved efficiency and reliability. *Neuroimage*, 31(3):1116–1128, 2006.
- [24] Yunguan Fu, Nina Montaña Brown, Shaheer U. Saeed, Adrià Casamitjana, Zachary M. C. Baum, Rémi Delaunay, Qianye Yang, Alexander Grimwood, Zhe Min, Stefano B. Blumberg, Juan Eugenio Iglesias, Dean C. Barratt, Ester Bonmati, Daniel C. Alexander, Matthew J. Clarkson, Tom Vercauteren, and Yipeng Hu. Deepreg: a deep learning toolkit for medical image registration. *Journal of Open Source Software*, 5(55):2705, 2020.
- [25] Brian B Avants, Nick Tustison, and Gang Song. Advanced normalization tools (ants). *Insight j*, 2(365):1–35, 2009.
- [26] Mark Jenkinson, Christian F Beckmann, Timothy EJ Behrens, Mark W Woolrich, and Stephen M Smith. Fsl. *Neuroimage*, 62(2):782–790, 2012.
- [27] Bruce Fischl. Freesurfer. *Neuroimage*, 62(2):774–781, 2012.
- [28] Maarouf A Hammoud, Raymond Sawaya, Weiming Shi, Peter F Thall, and Norman E Leeds. Prognostic significance of preoperative mri scans in glioblastoma multiforme. *Journal of neuro-oncology*, 27(1):65–73, 1996.
- [29] Jonathan Long, Evan Shelhamer, and Trevor Darrell. Fully convolutional networks for semantic segmentation. In *Proceedings of the IEEE conference on computer vision and pattern recognition*, pages 3431–3440, 2015.
- [30] Olaf Ronneberger, Philipp Fischer, and Thomas Brox. U-net: Convolutional networks for biomedical image segmentation. In *International Conference on Medical image computing and computer-assisted intervention*, pages 234–241. Springer, 2015.
- [31] Fabian Isensee, Philipp Kickingereder, Wolfgang Wick, Martin Bendszus, and Klaus H Maier-Hein. Brain tumor segmentation and radiomics survival prediction: Contribution to the brats 2017 challenge. In *International MICCAI Brainlesion Workshop*, pages 287–297. Springer, 2017.

- [32] Lucas Fidon, Sebastien Ourselin, and Tom Vercauteren. Generalized wasserstein dice score, distributionally robust deep learning, and ranger for brain tumor segmentation: Brats 2020 challenge. *arXiv preprint arXiv:2011.01614*, 2020.
- [33] Andriy Myronenko. 3d mri brain tumor segmentation using autoencoder regularization. In *International MICCAI Brainlesion Workshop*, pages 311–320. Springer, 2018.
- [34] Zeyu Jiang, Changxing Ding, Minfeng Liu, and Dacheng Tao. Two-stage cascaded u-net: 1st place solution to brats challenge 2019 segmentation task. In *International MICCAI Brainlesion Workshop*, pages 231–241. Springer, 2019.
- [35] Sangeetha Saman and Swathi Jamjala Narayanan. Survey on brain tumor segmentation and feature extraction of mr images. *International Journal of Multimedia Information Retrieval*, 8(2):79–99, 2019.
- [36] Mobarakol Islam, V Jeya Maria Jose, and Hongliang Ren. Glioma Prognosis: Segmentation of the Tumor and Survival Prediction Using Shape, Geometric and Clinical Information. In Alessandro Crimi, Spyridon Bakas, Hugo Kuijf, Farahani Keyvan, Mauricio Reyes, and Theo van Walsum, editors, *Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries*, pages 142–153, Cham, 2019. Springer International Publishing.
- [37] Parita Sanghani, Beng Ti Ang, Nicolas Kon Kam King, and Hongliang Ren. Overall survival prediction in glioblastoma multiforme patients from volumetric, shape and texture features using machine learning. *Surgical oncology*, 27(4):709–714, 2018.
- [38] Xue Feng, Nicholas J Tustison, Sohil H Patel, and Craig H Meyer. Brain tumor segmentation using an ensemble of 3d u-nets and overall survival prediction using radiomic features. *Frontiers in Computational Neuroscience*, 14:25, 2020.

- [39] Li Sun, Songtao Zhang, Hang Chen, and Lin Luo. Brain tumor segmentation and survival prediction using multimodal mri scans with deep learning. *Frontiers in neuroscience*, 13:810, 2019.
- [40] Joost JM Van Griethuysen, Andriy Fedorov, Chintan Parmar, Ahmed Hosny, Nicole Aucoin, Vivek Narayan, Regina GH Beets-Tan, Jean-Christophe Fillion-Robin, Steve Pieper, and Hugo JWL Aerts. Computational radiomics system to decode the radiographic phenotype. *Cancer research*, 77(21):e104–e107, 2017.
- [41] W Han, L Qin, C Bay, X Chen, K-H Yu, N Miskin, A Li, X Xu, and G Young. Deep transfer learning and radiomics feature prediction of survival of patients with high-grade gliomas. *American Journal of Neuroradiology*, 41(1):40–48, 2020.
- [42] Karen Simonyan and Andrew Zisserman. Very deep convolutional networks for large-scale image recognition. *arXiv preprint arXiv:1409.1556*, 2014.
- [43] Ken Chatfield, Karen Simonyan, Andrea Vedaldi, and Andrew Zisserman. Return of the devil in the details: Delving deep into convolutional nets. *arXiv preprint arXiv:1405.3531*, 2014.
- [44] Guotai Wang, Wenqi Li, Sébastien Ourselin, and Tom Vercauteren. Automatic brain tumor segmentation using cascaded anisotropic convolutional neural networks. In *International MICCAI brainlesion workshop*, pages 178–190. Springer, 2017.
- [45] Özgün Çiçek, Ahmed Abdulkadir, Soeren S Lienkamp, Thomas Brox, and Olaf Ronneberger. 3d u-net: learning dense volumetric segmentation from sparse annotation. In *International conference on medical image computing and computer-assisted intervention*, pages 424–432. Springer, 2016.
- [46] Elodie Puybureau, Guillaume Tochon, Joseph Chazalon, and Jonathan Fabrizio. Segmentation of gliomas and prediction of patient overall survival: a

- simple and fast procedure. In *International MICCAI Brainlesion Workshop*, pages 199–209. Springer, 2018.
- [47] Lina Chato, Erik Chow, and Shahram Latifi. Wavelet transform to improve accuracy of a prediction model for overall survival time of brain tumor patients based on mri images. In *2018 IEEE International Conference on Healthcare Informatics (ICHI)*, pages 441–442. IEEE, 2018.
- [48] Zeina A Shboul, Mahbubul Alam, Lasitha Vidyaratne, Linmin Pei, Mohamed I Elbakary, and Khan M Iftekharuddin. Feature-guided deep radiomics for glioblastoma patient survival prediction. *Frontiers in Neuroscience*, 13, 2019.
- [49] Hao Dong, Guang Yang, Fangde Liu, Yuanhan Mo, and Yike Guo. Automatic brain tumor detection and segmentation using u-net based fully convolutional networks. In *annual conference on medical image understanding and analysis*, pages 506–517. Springer, 2017.
- [50] Dong Nie, Han Zhang, Ehsan Adeli, Luyan Liu, and Dinggang Shen. 3d deep learning for multi-modal imaging-guided survival time prediction of brain tumor patients. In *International conference on medical image computing and computer-assisted intervention*, pages 212–220. Springer, 2016.
- [51] Mobarakol Islam, V S Vibashan, V Jeya Maria Jose, Navodini Wijethilake, Uppal Utkarsh, and Hongliang Ren. Brain Tumor Segmentation and Survival Prediction Using 3D Attention UNet. In Alessandro Crimi and Spyridon Bakas, editors, *Brainlesion: Glioma, Multiple Sclerosis, Stroke and Traumatic Brain Injuries*, pages 262–272, Cham, 2020. Springer International Publishing.
- [52] Mariarosaria Incoronato, Marco Aiello, Teresa Infante, Carlo Cavaliere, Anna Maria Grimaldi, Peppino Mirabelli, Serena Monti, and Marco Salvatore. Radiogenomic analysis of oncological data: a technical survey. *International journal of molecular sciences*, 18(4):805, 2017.

- [53] Alhasan Alkuhlani, Mohammad Nassef, and Ibrahim Farag. Multistage feature selection approach for high-dimensional cancer data. *Soft Computing*, 21(22):6895–6906, 2017.
- [54] Christian Hartmann, Bettina Hentschel, Marcos Tatagiba, Johannes Schramm, Oliver Schnell, Clemens Seidel, Robert Stein, Guido Reifemberger, Torsten Pietsch, Andreas Von Deimling, et al. Molecular markers in low-grade gliomas: predictive or prognostic? *Clinical Cancer Research*, 17(13):4588–4599, 2011.
- [55] Shuguang Zuo, Xinhong Zhang, and Liping Wang. A rna sequencing-based six-gene signature for survival prediction in patients with glioblastoma. *Scientific reports*, 9(1):1–10, 2019.
- [56] Junmin Xian, Quanzhong Zhang, Xiwen Guo, Xiankun Liang, Xinhua Liu, and Yugong Feng. A prognostic signature based on three non-coding rna s for prediction of the overall survival of glioma patients. *FEBS open bio*, 9(4):682–692, 2019.
- [57] Wen-Jing Zeng, Yong-Long Yang, Zheng-Zheng Liu, Zhi-Peng Wen, Yan-Hong Chen, Xiao-Lei Hu, Quan Cheng, Jian Xiao, Jie Zhao, and Xiao-Ping Chen. Integrative analysis of dna methylation and gene expression identify a three-gene signature for predicting prognosis in lower-grade gliomas. *Cellular Physiology and Biochemistry*, 47(1):428–439, 2018.
- [58] Pooya Mobadersany, Safoora Yousefi, Mohamed Amgad, David A Gutman, Jill S Barnholtz-Sloan, José E Velázquez Vega, Daniel J Brat, and Lee AD Cooper. Predicting cancer outcomes from histology and genomics using convolutional networks. *Proceedings of the National Academy of Sciences*, 115(13):E2970–E2979, 2018.
- [59] Saima Rathore, Muhammad Aksam Iftikhar, and Zissimos Mourelatos. Prediction of overall survival and molecular markers in gliomas via anal-



- ysis of digital pathology images using deep learning. *arXiv preprint arXiv:1909.09124*, 2019.
- [60] Jingwei Zhao, Le Wang, Daliang Kong, Guozhang Hu, and Bo Wei. Construction of novel dna methylation-based prognostic model to predict survival in glioblastoma. *Journal of Computational Biology*, 2019.
- [61] Wei-Zhen Gao, Lie-Mei Guo, Tian-Qi Xu, Yu-Hua Yin, and Feng Jia. Identification of a multidimensional transcriptome signature for survival prediction of postoperative glioblastoma multiforme patients. *Journal of translational medicine*, 16(1):368, 2018.
- [62] Haley Gittleman, Andrew E Sloan, and Jill S Barnholtz-Sloan. An independently validated survival nomogram for lower-grade glioma. *Neuro-oncology*, 22(5):665–674, 2020.
- [63] Niha Beig, Salendra Singh, Kaustav Bera, Prateek Prasanna, Gagandeep Singh, Jonathan Chen, Anas SaeedBamashmos, Addison Barnett, Kyle Hunter, Volodymyr Statsevych, et al. Sexually dimorphic radiogenomic models identify distinct imaging and biological pathways that are prognostic of overall survival in glioblastoma. *Neuro-oncology*, 2020.
- [64] Roderick JA Little and Donald B Rubin. *Statistical analysis with missing data*, volume 793. John Wiley & Sons, 2019.
- [65] L Ladha and T Deepa. Feature selection methods and algorithms. *International journal on computer science and engineering*, 3(5):1787–1797, 2011.
- [66] Lei Yu and Huan Liu. Feature selection for high-dimensional data: A fast correlation-based filter solution. In *Proceedings of the 20th international conference on machine learning (ICML-03)*, pages 856–863, 2003.
- [67] Jingwei Zhao, Le Wang, Daliang Kong, Guozhang Hu, and Bo Wei. Construction of novel dna methylation-based prognostic model to predict sur-

- vival in glioblastoma. *Journal of Computational Biology*, 27(5):718–728, 2020.
- [68] Isabelle Guyon, Jason Weston, Stephen Barnhill, and Vladimir Vapnik. Gene selection for cancer classification using support vector machines. *Machine learning*, 46(1-3):389–422, 2002.
- [69] Ian T Jolliffe and Jorge Cadima. Principal component analysis: a review and recent developments. *Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences*, 374(2065):20150202, 2016.
- [70] Alex J Smola and Bernhard Schölkopf. A tutorial on support vector regression. *Statistics and computing*, 14(3):199–222, 2004.
- [71] Kyrre E Emblem, Marco C Pinho, Frank G Zöllner, Paulina Due-Tonnessen, John K Hald, Lothar R Schad, Torstein R Meling, Otto Rapalino, and Atle Bjornerud. A generic support vector machine model for preoperative glioma survival associations. *Radiology*, 275(1):228–234, 2015.
- [72] Luke Macyszyn, Hamed Akbari, Jared M Pisapia, Xiao Da, Mark Attiah, Vadim Pigrish, Yingtao Bi, Sharmistha Pal, Ramana V Davuluri, Laura Roccograndi, et al. Imaging patterns predict patient survival and molecular subtype in glioblastoma via machine learning techniques. *Neuro-oncology*, 18(3):417–425, 2015.
- [73] Faisal M Khan and Valentina Bayer Zubek. Support vector regression for censored data (svrc): a novel tool for survival analysis. In *2008 Eighth IEEE International Conference on Data Mining*, pages 863–868. IEEE, 2008.
- [74] E Marubini, A Morabito, and MG Valsecchi. Prognostic factors and risk groups: some results given by using an algorithm suitable for censored survival data. *Statistics in medicine*, 2(2):295–303, 1983.
- [75] A Ciampi, RS Bush, M Gospodarowicz, and JE Till. An approach to classifying prognostic factors related to survival experience for non-hodgkin's

- lymphoma patients: Based on a series of 982 patients: 1967–1975. *Cancer*, 47(3):621–627, 1981.
- [76] Louis Gordon and Richard A Olshen. Tree-structured survival analysis. *Cancer treatment reports*, 69(10):1065–1069, 1985.
- [77] Antonio Ciampi, Johanne Thiffault, Jean-Pierre Nakache, and Bernard Asselain. Stratification by stepwise regression, correspondence analysis and recursive partition: a comparison of three methods of analysis for survival data with covariates. *Computational statistics & data analysis*, 4(3):185–204, 1986.
- [78] A Ciampi. Recursive partition and amalgamation (recpam) for censored survival data: criteria for tree selection. *Statistical Software Newsletter*, 14(2):78–81, 1988.
- [79] Walter J Curran Jr, Charles B Scott, John Horton, James S Nelson, Alan S Weinstein, A Jennifer Fischbach, Chu H Chang, Marvin Rotman, Sucha O Asbell, Robert E Krisch, et al. Recursive partitioning analysis of prognostic factors in three radiation therapy oncology group malignant glioma trials. *JNCI: Journal of the National Cancer Institute*, 85(9):704–710, 1993.
- [80] Glenn Bauman, Knut Lote, David Larson, Lukas Stalpers, Christopher Leighton, Barbara Fisher, William Wara, David Macdonald, Larry Stitt, and J Gregory Cairncross. Pretreatment factors predict overall survival for patients with low-grade glioma: a recursive partitioning analysis. *International Journal of Radiation Oncology* Biology* Physics*, 45(4):923–929, 1999.
- [81] H. J. Cho and S. Hong. Median regression tree for analysis of censored survival data. *IEEE Transactions on Systems, Man, and Cybernetics - Part A: Systems and Humans*, 38(3):715–726, 2008.
- [82] María L Gandía-González, Sebastián Cerdán, Laura Barrios, Pilar López-Larrubia, Pablo G Feijoó, Alexis Palpan Jr, José M Roda, and Juan So-

- livera. Assessment of overall survival in glioma patients as predicted by metabolomic criteria. *Frontiers in Oncology*, 9:328, 2019.
- [83] J Ross Quinlan et al. Bagging, boosting, and c4. 5. In *AAAI/IAAI, Vol. 1*, pages 725–730, 1996.
- [84] Leo Breiman. Random forests. *Machine learning*, 45(1):5–32, 2001.
- [85] Bradley Efron. Tibshirani,(1993), an introduction to the bootstrap. *Monographs on Statistics and Applied Probability. Chapman & Hall/CRC*, 1, 1960.
- [86] Pierre Geurts, Damien Ernst, and Louis Wehenkel. Extremely randomized trees. *Machine learning*, 63(1):3–42, 2006.
- [87] Hemant Ishwaran, Udaya B Kogalur, Eugene H Blackstone, Michael S Lauer, et al. Random survival forests. *The annals of applied statistics*, 2(3):841–860, 2008.
- [88] Yoon Seong Choi, Sung Soo Ahn, Jong Hee Chang, Seok-Gu Kang, Eui Hyun Kim, Se Hoon Kim, Rajan Jain, and Seung-Koo Lee. Machine learning and radiomic phenotyping of lower grade gliomas: improving survival prediction. *European Radiology*, pages 1–9, 2020.
- [89] Yoav Freund and Robert E Schapire. A decision-theoretic generalization of on-line learning and an application to boosting. In *European conference on computational learning theory*, pages 23–37. Springer, 1995.
- [90] Jerome H Friedman. Greedy function approximation: a gradient boosting machine. *Annals of statistics*, pages 1189–1232, 2001.
- [91] Torsten Hothorn, Peter Bühlmann, Sandrine Dudoit, Annette Molinaro, and Mark J Van Der Laan. Survival ensembles. *Biostatistics*, 7(3):355–373, 2006.
- [92] Jun Zhu, Jianfei Chen, Wenbo Hu, and Bo Zhang. Big learning with bayesian methods. *National Science Review*, 4(4):627–651, 2017.

- [93] Simon Rabinowicz, Arjen Hommersom, Raphaela Butz, and Matt Williams. A prognostic model of glioblastoma multiforme using survival bayesian networks. In *Conference on Artificial Intelligence in Medicine in Europe*, pages 81–85. Springer, 2017.
- [94] Mu Zhou, Baishali Chaudhury, Lawrence O Hall, Dmitry B Goldgof, Robert J Gillies, and Robert A Gatenby. Identifying spatial imaging biomarkers of glioblastoma multiforme for survival group prediction. *Journal of Magnetic Resonance Imaging*, 46(1):115–123, 2017.
- [95] Vinicius Bonato, Veerabhadran Baladandayuthapani, Bradley M Broom, Erik P Sulman, Kenneth D Aldape, and Kim-Anh Do. Bayesian ensemble methods for survival prediction in gene expression data. *Bioinformatics*, 27(3):359–367, 2011.
- [96] Stephen P Luttrell. A bayesian analysis of self-organizing maps. *Neural Computation*, 6(5):767–794, 1994.
- [97] Pedro Henriques Abreu, Miriam Seoane Santos, Miguel Henriques Abreu, Bruno Andrade, and Daniel Castro Silva. Predicting breast cancer recurrence using machine learning techniques: a systematic review. *ACM Computing Surveys (CSUR)*, 49(3):1–40, 2016.
- [98] Sun-Mi Lee and Patricia A Abbott. Bayesian networks for knowledge discovery in large datasets: basics for nurse researchers. *Journal of biomedical informatics*, 36(4-5):389–399, 2003.
- [99] Nir Friedman, Dan Geiger, and Moises Goldszmidt. Bayesian network classifiers. *Machine learning*, 29(2-3):131–163, 1997.
- [100] Mu Zhou, Lawrence O Hall, Dmitry B Goldgof, Robert J Gillies, and Robert A Gatenby. Survival time prediction of patients with glioblastoma multiforme tumors using spatial distance measurement. In *Medical Imaging 2013: Computer-Aided Diagnosis*, volume 8670, page 86702O. International Society for Optics and Photonics, 2013.



- [101] Stephen R Piccolo and Lewis J Frey. Clinical and molecular models of glioblastoma multiforme survival. *International journal of data mining and bioinformatics*, 7(3):245, 2013.
- [102] Frank Rosenblatt. The perceptron: a probabilistic model for information storage and organization in the brain. *Psychological review*, 65(6):386, 1958.
- [103] Warren S McCulloch and Walter Pitts. A logical calculus of the ideas immanent in nervous activity. *The bulletin of mathematical biophysics*, 5(4):115–133, 1943.
- [104] David Faraggi and Richard Simon. A neural network model for survival data. *Statistics in medicine*, 14(1):73–82, 1995.
- [105] Travers Ching, Xun Zhu, and Lana X Garmire. Cox-nnet: an artificial neural network method for prognosis prediction of high-throughput omics data. *PLoS computational biology*, 14(4):e1006076, 2018.
- [106] Safoora Yousefi, Fatemeh Amrollahi, Mohamed Amgad, Chengliang Dong, Joshua E Lewis, Congzheng Song, David A Gutman, Sameer H Halani, Jose Enrique Velazquez Vega, Daniel J Brat, et al. Predicting clinical outcomes from large scale cancer genomic profiles with deep survival models. *Scientific reports*, 7(1):1–11, 2017.
- [107] Edward L Kaplan and Paul Meier. Nonparametric estimation from incomplete observations. *Journal of the American statistical association*, 53(282):457–481, 1958.
- [108] David R Cox. Regression models and life-tables. *Journal of the Royal Statistical Society: Series B (Methodological)*, 34(2):187–202, 1972.
- [109] Justin Bo-Kai Hsu, Tzu-Hao Chang, Gilbert Aaron Lee, Tzong-Yi Lee, and Cheng-Yu Chen. Identification of potential biomarkers related to glioma survival by gene expression profile analysis. *BMC medical genomics*, 11(7):34, 2019.

- [110] Lingchen Wang, Zhengwei Yan, Xiaona He, Cheng Zhang, Huiqiang Yu, and Quqin Lu. A 5-gene prognostic nomogram predicting survival probability of glioblastoma patients. *Brain and behavior*, 9(4):e01258, 2019.
- [111] Tong Yang, Ping Mao, Xianhai Chen, Xuan Niu, Gaofeng Xu, Xiaobin Bai, and Wanfu Xie. Inflammatory biomarkers in prognostic analysis for patients with glioma and the establishment of a nomogram. *Oncology letters*, 17(2):2516–2522, 2019.
- [112] Farnoosh Abbas-Aghababazadeh, Qian Li, and Brooke L Fridley. Comparison of normalization approaches for gene expression studies completed with high-throughput sequencing. *PloS one*, 13(10), 2018.
- [113] Amalia Annest, Roger E Bumgarner, Adrian E Raftery, and Ka Yee Yeung. Iterative bayesian model averaging: A method for the application of survival analysis to high-dimensional microarray data. *BMC bioinformatics*, 10(1):72, 2009.
- [114] Tianqi Chen and Carlos Guestrin. Xgboost: A scalable tree boosting system. In *Proceedings of the 22nd acm sigkdd international conference on knowledge discovery and data mining*, pages 785–794, 2016.
- [115] Liudmila Prokhorenkova, Gleb Gusev, Aleksandr Vorobev, Anna Veronika Dorogush, and Andrey Gulin. Catboost: unbiased boosting with categorical features. In *Advances in neural information processing systems*, pages 6638–6648, 2018.
- [116] Iresha Rubasinghe and Dulani Meedeniya. Ultrasound nerve segmentation using deep probabilistic programming. *Journal of ICT Research and Applications*, 13(3):241–256, 2019.
- [117] Eli Bingham, Jonathan P Chen, Martin Jankowiak, Fritz Obermeyer, Neeraj Pradhan, Theofanis Karaletsos, Rohit Singh, Paul Szerlip, Paul Horsfall, and Noah D Goodman. Pyro: Deep universal probabilistic pro-

- gramming. *The Journal of Machine Learning Research*, 20(1):973–978, 2019.
- [118] F. Pedregosa, G. Varoquaux, A. Gramfort, V. Michel, B. Thirion, O. Grisel, M. Blondel, P. Prettenhofer, R. Weiss, V. Dubourg, J. Vanderplas, A. Passos, D. Cournapeau, M. Brucher, M. Perrot, and E. Duchesnay. Scikit-learn: Machine learning in Python. *Journal of Machine Learning Research*, 12:2825–2830, 2011.
- [119] Terry M Therneau. *A Package for Survival Analysis in R*, 2020. R package version 3.2-3.
- [120] Zheng Zhao, Kenan Zhang, Qiangwei Wang, Guanzhang Li, Fan Zeng, Ying Zhang, Fan Wu, Ruichao Chai, Zheng Wang, Chuanbao Zhang, et al. Chinese glioma genome atlas (cgga): A comprehensive resource with functional genomic data for chinese glioma patients. *bioRxiv*, 2020.
- [121] Kaiming He, Xiangyu Zhang, Shaoqing Ren, and Jian Sun. Deep residual learning for image recognition. In *Proceedings of the IEEE conference on computer vision and pattern recognition*, pages 770–778, 2016.
- [122] Christian Szegedy, Wei Liu, Yangqing Jia, Pierre Sermanet, Scott Reed, Dragomir Anguelov, Dumitru Erhan, Vincent Vanhoucke, and Andrew Rabinovich. Going deeper with convolutions. In *Proceedings of the IEEE conference on computer vision and pattern recognition*, pages 1–9, 2015.
- [123] Mingxing Tan and Quoc V Le. Mixconv: Mixed depthwise convolutional kernels. *arXiv*, pages arXiv–1907, 2019.
- [124] Hang Zhang, Chongruo Wu, Zhongyue Zhang, Yi Zhu, Zhi Zhang, Haibin Lin, Yue Sun, Tong He, Jonas Mueller, R Manmatha, et al. Resnest: Split-attention networks. *arXiv preprint arXiv:2004.08955*, 2020.
- [125] Xiangyu Zhang, Xinyu Zhou, Mengxiao Lin, and Jian Sun. Shufflenet: An extremely efficient convolutional neural network for mobile devices. In *Pro-*

- ceedings of the IEEE conference on computer vision and pattern recognition*, pages 6848–6856, 2018.
- [126] Diederik P Kingma and Jimmy Ba. Adam: A method for stochastic optimization. *arXiv preprint arXiv:1412.6980*, 2014.
- [127] Tsung-Yi Lin, Priya Goyal, Ross Girshick, Kaiming He, and Piotr Dollár. Focal loss for dense object detection. In *Proceedings of the IEEE international conference on computer vision*, pages 2980–2988, 2017.
- [128] Bjorn Barz and Joachim Denzler. Deep learning on small datasets without pre-training using cosine loss. In *The IEEE Winter Conference on Applications of Computer Vision*, pages 1371–1380, 2020.
- [129] Christian Szegedy, Vincent Vanhoucke, Sergey Ioffe, Jon Shlens, and Zbigniew Wojna. Rethinking the inception architecture for computer vision. In *Proceedings of the IEEE conference on computer vision and pattern recognition*, pages 2818–2826, 2016.
- [130] Rafael Müller, Simon Kornblith, and Geoffrey E Hinton. When does label smoothing help? In *Advances in Neural Information Processing Systems*, pages 4694–4703, 2019.
- [131] Yu Zhang and Qiang Yang. A survey on multi-task learning. *IEEE Transactions on Knowledge and Data Engineering*, 2021.
- [132] Yan Li, Jie Wang, Jieping Ye, and Chandan K Reddy. A multi-task learning formulation for survival analysis. In *Proceedings of the 22nd ACM SIGKDD International Conference on Knowledge Discovery and Data Mining*, pages 1715–1724, 2016.
- [133] Hongyi Zhang, Moustapha Cisse, Yann N Dauphin, and David Lopez-Paz. mixup: Beyond empirical risk minimization. *arXiv preprint arXiv:1710.09412*, 2017.

- [134] Mobarakol Islam, VS Vibashan, and Hongliang Ren. Ap-mtl: Attention pruned multi-task learning model for real-time instrument detection and segmentation in robot-assisted surgery. In *2020 IEEE International Conference on Robotics and Automation (ICRA)*, pages 8433–8439. IEEE, 2020.
- [135] Zhao Chen, Vijay Badrinarayanan, Chen-Yu Lee, and Andrew Rabinovich. Gradnorm: Gradient normalization for adaptive loss balancing in deep multitask networks. In *International Conference on Machine Learning*, pages 794–803. PMLR, 2018.
- [136] Roel GW Verhaak, Katherine A Hoadley, Elizabeth Purdom, Victoria Wang, Yuan Qi, Matthew D Wilkerson, C Ryan Miller, Li Ding, Todd Golub, Jill P Mesirov, et al. Integrated genomic analysis identifies clinically relevant subtypes of glioblastoma characterized by abnormalities in *pdgfra*, *idh1*, *egfr*, and *nf1*. *Cancer cell*, 17(1):98–110, 2010.
- [137] Steve Pieper, Michael Halle, and Ron Kikinis. 3d slicer. In *2004 2nd IEEE international symposium on biomedical imaging: nano to macro (IEEE Cat No. 04EX821)*, pages 632–635. IEEE, 2004.
- [138] Abhijit Guha Roy, Nassir Navab, and Christian Wachinger. Concurrent spatial and channel ‘squeeze & excitation’ in fully convolutional networks. In *International Conference on Medical Image Computing and Computer-Assisted Intervention*, pages 421–429. Springer, 2018.
- [139] Kouros M Naeini, Whitney B Pope, Timothy F Cloughesy, Robert J Harris, Albert Lai, Ascia Eskin, Reshmi Chowdhury, Heidi S Phillips, Phioanh L Nghiemphu, Yalda Behbahanian, et al. Identifying the mesenchymal molecular subtype of glioblastoma using quantitative volumetric analysis of anatomic magnetic resonance images. *Neuro-oncology*, 15(5):626–634, 2013.
- [140] Laura Follia, Giulio Ferrero, Giorgia Mandili, Marco Beccuti, Daniele Giordano, Rosella Spadi, Maria Antonietta Satolli, Andrea Evangelista, Hi-



- royuki Katayama, Wang Hong, et al. Integrative analysis of novel metabolic subtypes in pancreatic cancer fosters new prognostic biomarkers. *Frontiers in oncology*, 9:115, 2019.
- [141] Evgenia Dimitriadou, Kurt Hornik, Friedrich Leisch, David Meyer, Andreas Maintainer, friedrich Leisch@ci, Ac Tuwien, and At. The e1071 package. 08 2006.
- [142] Mark Hall, Eibe Frank, Geoffrey Holmes, Bernhard Pfahringer, Peter Reutemann, and Ian H. Witten. The WEKA data mining software: an update. *SIGKDD Explorations*, 11(1):10–18, 2009.
- [143] Chuan Guo, Geoff Pleiss, Yu Sun, and Kilian Q Weinberger. On calibration of modern neural networks. *arXiv preprint arXiv:1706.04599*, 2017.
- [144] Mahdi Pakdaman Naeini, Gregory Cooper, and Milos Hauskrecht. Obtaining well calibrated probabilities using bayesian binning. In *Twenty-Ninth AAAI Conference on Artificial Intelligence*, 2015.
- [145] Jeremy Nixon, Michael W Dusenberry, Linchuan Zhang, Ghassen Jerfel, and Dustin Tran. Measuring calibration in deep learning. In *CVPR Workshops*, pages 38–41, 2019.
- [146] Arsenii Ashukha, Alexander Lyzhov, Dmitry Molchanov, and Dmitry Vetrov. Pitfalls of in-domain uncertainty estimation and ensembling in deep learning. *arXiv preprint arXiv:2002.06470*, 2020.
- [147] Max-Heinrich Laves, Sontje Ihler, Karl-Philipp Kortmann, and Tobias Ortmaier. Well-calibrated model uncertainty with temperature scaling for dropout variational inference. *arXiv preprint arXiv:1909.13550*, 2019.
- [148] Scott M Lundberg and Su-In Lee. A unified approach to interpreting model predictions. In *Advances in neural information processing systems*, pages 4765–4774, 2017.

- [149] Daniel Smilkov, Nikhil Thorat, Been Kim, Fernanda Viégas, and Martin Wattenberg. Smoothgrad: removing noise by adding noise. *arXiv preprint arXiv:1706.03825*, 2017.
- [150] Mukund Sundararajan, Ankur Taly, and Qiqi Yan. Axiomatic attribution for deep networks. *arXiv preprint arXiv:1703.01365*, 2017.
- [151] Jie Ren, Meiqing Lou, Jinlong Shi, Yajun Xue, and Daming Cui. Identifying the genes regulated by *idh1* via gene-chip in glioma cell u87. *International journal of clinical and experimental medicine*, 8(10):18090, 2015.
- [152] Shanrong Zhao, Wai-Ping Fung-Leung, Anton Bittner, Karen Ngo, and Xuejun Liu. Comparison of rna-seq and microarray in transcriptome profiling of activated t cells. *PloS one*, 9(1):e78644, 2014.
- [153] Li Fei-Fei, Rob Fergus, and Pietro Perona. One-shot learning of object categories. *IEEE transactions on pattern analysis and machine intelligence*, 28(4):594–611, 2006.
- [154] JA1 Carrillo, A Lai, PL Nghiemphu, HJ Kim, HS Phillips, S Kharbanda, P Moftakhar, S Lalaezari, W Yong, BM Ellingson, et al. Relationship between tumor enhancement, edema, *idh1* mutational status, mgmt promoter methylation, and survival in glioblastoma. *American Journal of Neuroradiology*, 33(7):1349–1355, 2012.
- [155] David A Gutman, Lee AD Cooper, Scott N Hwang, Chad A Holder, JingJing Gao, Tarun D Aurora, William D Dunn Jr, Lisa Scarpace, Tom Mikkelsen, Rajan Jain, et al. Mr imaging predictors of molecular profile and survival: multi-institutional study of the tcga glioblastoma data set. *Radiology*, 267(2):560–569, 2013.
- [156] Yuan-Feng Gao, Xiao-Yuan Mao, Tao Zhu, Chen-Xue Mao, Zhi-Xiong Liu, Zhi-Bin Wang, Ling Li, Xi Li, Ji-Ye Yin, Wei Zhang, et al. Col3a1 and snap91: novel glioblastoma markers with diagnostic and prognostic value. *Oncotarget*, 7(43):70494, 2016.

- [157] Sandrine Rorive, Xavier Moles Lopez, Calliope Maris, Anne-Laure Trepant, Sébastien Sauvage, Niloufar Sadeghi, Isabelle Roland, Christine De-caestecker, and Isabelle Salmon. Timp-4 and cd63: new prognostic biomarkers in human astrocytomas. *Modern pathology*, 23(10):1418–1428, 2010.
- [158] Qianghu Wang, Baoli Hu, Xin Hu, Hoon Kim, Massimo Squatrito, Lisa Scarpace, Ana C deCarvalho, Sali Lyu, Pengping Li, Yan Li, et al. Tumor evolution of glioma-intrinsic gene expression subtypes associates with immunological changes in the microenvironment. *Cancer cell*, 32(1):42–56, 2017.

