

CAnine CuTaneous Cancer Histology Dataset (CATCH)

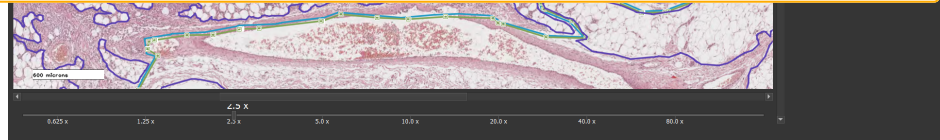
Summary

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We present a large-scale dataset of 350 histologic samples of seven different canine cutaneous tumors. All samples were obtained through

surgical resection due to neoplastic indicators and were selected retrospectively from the biopsy archive of the Institute for Veterinary Pathology of the Freie Universität Berlin according to sufficient tissue preservation and presence of characteristic histologic features for the corresponding tumor subtypes. Samples were stained with a routine Hematoxylin & Eosin dye and digitized with two Leica linear scanning systems at a resolution of 0.25 $\mu\text{m}/\text{pixel}$. Together with the 350 whole slide images, we provide a database consisting of 12,424 polygon annotations for six non-neoplastic tissue classes (epidermis, dermis, subcutis, bone, cartilage, and a joint class of inflammation and necrosis) and seven tumor classes (melanoma, mast cell tumor, squamous cell carcinoma, peripheral nerve sheath tumor, plasmacytoma, trichoblastoma, and histiocytoma).



The polygon annotations were generated using the open source software SlideRunner (<https://github.com/DeepPathology/SlideRunner>). Within SlideRunner, users can view whole slide images (WSIs) and zoom through their magnification levels. Using multiple clicks or click-and-drag, the pathologist annotated polygons for 13 classes (epidermis, dermis, subcutis, bone, cartilage, a joint class of inflammation and necrosis, melanoma, mast cell tumor, squamous cell carcinoma, peripheral nerve sheath tumor, plasmacytoma, trichoblastoma, and histiocytoma) on 287 WSIs. The remaining WSIs were annotated by three medical students in their 8th semester supervised by the leading pathologist who later reviewed these annotations for correctness and completeness.

Due to the large size of the dataset and the extensive annotations, it provides a good basis for segmentation and classification algorithms based on supervised learning. Previous work [1-4] has shown, that due to various homologies between the species, canine cutaneous tissue can serve as a model for human samples. Prouteau et al. have published an extensive comparison of the two species especially for cutaneous tumors and include homologies between canine and human oncology regarding "clinical and histological appearance, biological behavior, tumor genetics, molecular pathways and targets, and response to therapies" [1]. Ranieri et al. highlight that pet dogs and humans share many environmental risk factors and show the highest risk for cancer development at similar points of time respective to their life spans [2]. Both, Ranieri et al. and Pinho et al. highlight the potential of using insights from experiments on canine samples for developing human cancer treatments [2,3]. From a technical perspective, Aubreville et al. have shown that canine samples can be used to aid human cancer research through the use of transfer learning methods [4].

Potential users of the dataset can load the SQLite database into their custom installation of SlideRunner and adapt or extend the database with custom annotations. Furthermore, we converted the annotations to the COCO JSON format, which is commonly used by computer scientists for training neural networks. Its pixel-level annotations can be used for supervised segmentation algorithms as opposed to datasets that only provide clinical data on slide level.

References

1. Prouteau, Anaïs, and Catherine André. "Canine melanomas as models for human melanomas: Clinical, histological, and genetic comparison." *Genes* 10.7 (2019): 501. <https://doi.org/10.3390/genes10070501>
2. Ranieri, G., et al. "A model of study for human cancer: Spontaneous occurring tumors in dogs. Biological features and translation for new anticancer therapies." *Critical reviews in oncology/hematology* 88.1 (2013): 187-197. <https://doi.org/10.1016/j.critrevonc.2013.03.005>
3. Pinho, Salomé S., et al. "Canine tumors: a spontaneous animal model of human carcinogenesis." *Translational Research* 159.3 (2012): 165-172. <https://doi.org/10.1016/j.trsl.2011.11.005>
4. Aubreville, Marc, et al. "A completely annotated whole slide image dataset of canine breast cancer to aid human breast cancer research." *Scientific data* 7.1 (2020): 1-10. <https://doi.org/10.1038/s41597-020-00756-z>

Acknowledgements

The authors would like to thank everyone who contributed to the creation of this dataset through providing samples, annotations or technical support.

Data Access

Data Access

Data Type	Download all or Query/Filter	License
Tissue Slide Images (SVS, 522 GB)	Download Search (Download and apply the IBM-Aspera-Connect plugin to your browser to retrieve this faspex package)	CC BY 4.0
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Additional Resources for this Dataset

The following external resources have been made available by the data submitters. These are not hosted or supported by TCIA, but may be useful to researchers utilizing this collection.

- The polygon annotations were generated using the open source software SlideRunner (<https://github.com/DeepPathology/SlideRunner>).

Detailed Description

Detailed Description

Image Statistics	
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Modalities	Pathology
Number of Patients	282
Number of Images	350
Images Size (GB)	565.8

Citations & Data Usage Policy

Citations & Data Usage Policy

Users must abide by the [TCIA Data Usage Policy and Restrictions](#). Attribution should include references to the following citations:

Data Citation

Wilm, F., Fragoso, M., Marzahl, C., Bertram, C., Klopfleisch, R., Maier, A., Aubreville, M., & Breininger, K. (2022). **CAnine CuTaneous Cancer Histology Dataset (Version 1) [Data set]**. The Cancer Imaging Archive. <https://doi.org/10.7937/TCIA.2M93-FX66>

TCIA Citation

Clark K, Vendt B, Smith K, Freymann J, Kirby J, Koppel P, Moore S, Phillips S, Maffitt D, Pringle M, Tarbox L, Prior F. **The Cancer Imaging Archive (TCIA): Maintaining and Operating a Public Information Repository**. Journal of Digital Imaging, Volume 26, Number 6, December, 2013, pp 1045-1057. DOI: [10.1007/s10278-013-9622-7](https://doi.org/10.1007/s10278-013-9622-7)

Additional Publication Resources:

The Collection authors suggest the below will give context to this dataset:

- Prouteau, & André. (2019). Canine Melanomas as Models for Human Melanomas: Clinical, Histological, and Genetic Comparison. In Genes (Vol. 10, Issue 7, p. 501). MDPI AG. <https://doi.org/10.3390/genes10070501>
- Ranieri, G., Gadaleta, C. D., Patruno, R., Zizzo, N., Daidone, M. G., Hansson, M. G., Paradiso, A., & Ribatti, D. (2013). A model of study for human cancer: Spontaneous occurring tumors in dogs. Biological features and translation for new anticancer therapies. In Critical Reviews in Oncology/Hematology (Vol. 88, Issue 1, pp. 187–197). Elsevier BV. <https://doi.org/10.1016/j.critrevonc.2013.03.005>
- Pinho, S. S., Carvalho, S., Cabral, J., Reis, C. A., & Gärtner, F. (2012). Canine tumors: a spontaneous animal model of human carcinogenesis. In Translational Research (Vol. 159, Issue 3, pp. 165–172). Elsevier BV. <https://doi.org/10.1016/j.trsl.2011.11.005>
- Aubreville, M., Bertram, C. A., Donovan, T. A., Marzahl, C., Maier, A., & Klopfleisch, R. (2020). A completely annotated whole slide image dataset of canine breast cancer to aid human breast cancer research. In Scientific Data (Vol. 7, Issue 1). Springer Science and Business Media LLC. <https://doi.org/10.1038/s41597-020-00756-z>

Other Publications Using This Data

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