



Machine learning for early cancer detection

A machine learning method to train and validate algorithms to classify cancer risk based on a blood sample.

IP Status: PCT Application Filed; **Application #:** PCT/US2020/042196

Applications

- Screen dogs for risk of developing hemangiosarcoma
- Development for diagnostics of other dog cancers
- Development for diagnostics for human cancers
- Basic research on HSA and other cancers

Key Benefits & Differentiators

- **Minimally invasive:** Machine learning applied to analysis of a simple blood sample.
- **Sensitive and specific:** Biomarker identification differentiates dogs at risk for hemangiosarcoma from healthy animals, as well as from animals with other cancers or illnesses.
- **Useful in other species and cancers:** Machine learning approach can be applied to a variety of other cancers in dogs as well as humans to identify biomarkers in order to classify tumor risks and inform therapeutic approaches.

Machine learning to identify cancer risk

Hemangiosarcoma (HSA) is a common malignancy in dogs that is difficult to diagnose until late onset, often resulting in death unless identified in time for emergency surgery. Once the disease is found, there is no cure for it and it is rapidly fatal. No known test is available for circulating tumor cells (CTCs), or circulating tumor-associated cells (CTACs) in a subject. Dr. Jaime Modiano's lab at the University of Minnesota developed a method to identify CTC and CTAC cells (based on experimentally determined biomarkers) from a blood sample in order to predict the likelihood that the subject has one or more types of cancer, such as HSA.

Using machine learning, this method facilitates the differentiation of blood samples from 1) healthy dogs, 2) dogs with non-malignant pathology of the spleen, 3) dogs with HSA and 4) dogs with non-HSA tumors. Flow cytometric analysis of blood samples from each of these groups was carried out to train and validate machine learning algorithms based on markers (including alpha-v/beta-3 integrin, CD51/CD61, CD34, CD177, c-Kit among others) and cells size and granularity. Unknown samples from healthy dogs can then be classified into a defined "risk group" using these trained algorithms. This process has the potential to detect cancer in dogs in its earliest stages facilitating more effective intervention strategies. Importantly, this process could also be applied to other tumors and diseases in dogs as well as in humans.

Phase of Development

TRL: 3

Ongoing clinical study in dogs, including planned lifetime follow-up to establish accuracy of risk classification. .

Technology ID

2019-197

Category

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Researchers

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References

1. Lamerato-Kozicki AR, Helm KM, Jubala CM, Modiano JF(2006) , Canine hemangiosarcoma originates from hematopoietic precursors with potential for endothelial differentiation