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## Big data GPU/CPU kernalisation pipeline for API based quantitative genetic assessments in field-based drone research

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The transition away from legacy BIOS firmware architectures provides an opportunity to increase the accuracy of large genomics platforms through advanced chipsets integrated with custom-built 4G/LTE broadcast base-stations that currently enable high speed data compression in remote locations. How these devices integrate phenotype data for selection of traits with respect to environmental variation in field trials requires efficient data capture, storage and real time GPU virtualisation of all connected devices. We propose a method utilizing unmanned drones with precision instrumentation for pre-processing and offline data capture systems with pre-flashed custom ROMs for phenotypic measurement based on Markov chains and probability functions making use of Gibb's sampling. Environmental datasets such as topography maps, soil type, and climate data is cross-referenced to accurately and efficiently select genetically in the field via the onboard CPU/ GPU cluster and cloud-based API's (solid state SSH super-computer CPU/GPU nuc SSH connection) kernel whilst online. Ultimately computation compression ratios, CPU and GPU facilitation of metascopic data clusters and embedded machine states, will determine much of the way forward in this space. However, the logistics required to "train" a drone via a neural network machine learning pipeline to accurately assess genotype in the field or, the management approach whether that be the desired outcome is now a reality. This research provides the preliminary pipeline using barley and yield, maturity, canopy-temperature, NDVI and stomata physiology as the plant characteristics to deliver a proof of concept (poster).

## **Biography**

Karl Svatos is a consultant for Scientific Aerospace; (autonomous drone and software development company), and innovation project manager for Pivotel Satellite; (IoT service provider throughout Australia and South East Asia). Karl specilalises in big data science, formatting, encryption, machine learning and custom kernel OS development. He achieved the Bachelor of Environmental Science with Honours in 2008 from the University of Western Australia (UWA). After brief stints in ministerial portfolios he turned his focus to environmental science specialising in 'big data' water modelling of nutrient fate scenarios. In 2010 he completed his Master's Degree at UWA in environmental science. More recently he discovered his passion in genetics and in investigating the role that environmental processes drive and contribute to the formation of heritable traits via horizontal gene transfer, rapid mutation and natural selection. He has been involved in the formulation of Hidden Markov Chains (HMV's) through Gibb's sampling using the Monte Carlo algorithm analysis of probability method. I like researching about the history of the command line and computer languages like FORTRAN, B, C, Python and R, and Turing machines from a "Prisoner's Dilemma POV. Karl started his PhD in 2016.

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