Together we have reached the end. Two partners, two allies, two distributions that supported millions of innovators have reached their end-of-life (EOL). April will be remembered as the month where ROS Kinetic and Ubuntu Xenial reached EOL. ROS Kinetic is one of the most used, widely deployed and extensively contributed ROS distributions (1st with 1233 repos in ros/rosdistro). Released in 2016, it supported newer related components, notably Gazebo 7 and OpenCV 3, and this month has reached its end.

But the end has also brought opportunities, and today we will chat about them.

It’s so easy these days to set-up your own WiFi network. You order a router online, plug it into the electrical socket, define a password and you’re good to go. WiFi is fast, reliable and easy to use. But if you want to cover a wider area or connect hundreds of small devices it quickly becomes inefficient and expensive. Is the only way to go to your local mobile network operator and sign a contract? No! Thanks to open source technology, you can build your own LTE or 5G network.
I tweeted back at the start of April that I?m moving on from Canonical/Ubuntu.

Well, I left on April 30th, have had two weeks of ?funemployment?., and today I start my new gig.

[...]

In a bit of excellent timing, this week we?re running Influx Days - a virtual event focused on the impact of time series data. I?ll be learning along with everyone else who?s attending!

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Oxford University partners with Oracle to speed identification of deadly COVID-19 variants[5] [Ed: This is a privacy violation with a very aggressive company. How was this approved?]

Oracle and Oxford University are partnering to bring Oxford's Scalable Pathogen Pipeline Platform (SP3) to the global community to more quickly identify COVID-19 variants in what it calls the Global Pathogen Analysis System. COVID-19 variants have emerged as a serious threat to inoculation and public health initiatives in many regions of the world. Mutations don't generally weaken a virus, but do have the potential to make it stronger or easy to spread.

[...]

SP3 fetches data from public repositories of genome data and uses container technology like Docker to build workflows capable of examining new genome sequences against known pathogens to identify variants. While available as a cloud-hosted platform, it was (and is) traditionally designed to be deployed in private environments; its head node only needs to be an Ubuntu machine running 18.04 or higher, and can be installed with a simple bash command.

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Ubuntu

Source URL: http://www.tuxmachines.org/node/151263

Links: