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**Albert-László Barabási/Network Science Institute Executive Summary**

**Repurposing Drugs to Attack COVID-19**

**Faculty Expert:** Albert-László Barabási, Robert Gray Dodge Professor of Network Science and Distinguished Professor of Physics; Director of the Center for Complex Network Research

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As the COVID-19 pandemic intensifies, researchers are working to develop pharmaceutical drugs that slow the virus’s reach, heal the ill, and may offer a vaccine. But what if promising therapies already exist? Scientists are racing to identify approved and experimental drugs that may benefit patients, and network medicine is our most powerful platform to identify candidate therapies.

Northeastern’s Albert-László Barabási, Robert Gray Dodge Professor of Network Science, Distinguished Professor of Physics, and Director of the Center for Complex Network Research, has assembled a multidisciplinary team to use network medicine to hunt for a COVID-19 treatment. With traditional lengthy drug development pipelines now impracticable, Barabási is exploring repurposing approved drugs with known toxicity and side effects that may have a therapeutic effect on COVID-19 patients. To do so, he requires funding to scrutinize how the virus invades healthy cells, pinpoint drugs to treat the virus, and validate drugs using artificial intelligence/machine learning bioinformatics and trials.

**Deciphering the Viral Process**

In March, the Barabási Lab began re-curating its past work on the human interactome, an intracellular and intercellular network of protein interaction. Less than 10 days after starting, the team identified 40 medications that target the cellular areas where COVID-19 works. The virus latches on to a healthy cell’s proteins, then disrupts functions within that cell and generates millions more copies of itself. The lab developed a network model of the 332 proteins targeted by COVID-19, and examined how the virus’s perturbing activity might affect tissues and organs. For example, using this model to examine how COVID-19 binds with host proteins, the lab predicted that the virus could attack cells in the brain—which may explain why early symptoms in people with COVID-19 include loss of the senses of smell and taste.

After forecasting the cellular progression of COVID-19, Barabási began looking for drugs and experimental compounds that could fight the virus by targeting proteins in its network vicinity.

**Uncovering Potential Treatments**

* Barabási is working with Harvard Medical School researchers to comb through data on approved and experimental drugs that could be repurposed to treat COVID-19.
* **Computation**—To better grasp how COVID-19 hijacks healthy cells, the team must have data processed and analyzed by cloud services, as well as by supercomputers at Lawrence Livermore National Laboratory that apply advanced AI/ML bioinformatics tools to locate candidate therapies.
* **Network modeling**—Virtually every human disease spreads through a cellular network, and COVID-19 does so quickly as it invades a healthy cell. With additional support, Barabási will be able to add post-doctoral researchers who will use 3D modeling to better understand the virus’s spread.
* **Experimental validation**—The team will identify drugs that could be repurposed against COVID-19, test them in healthy human cells, and observe how they target areas where the virus works.