

Mathematician uses genetics in algorithm to find best drug targets for cancer

The way in which people receive cancer therapy is pretty much the same as it's been for decades: researchers determine the highest dose of a drug or treatment that does not cause unacceptable side effects; oncologists then administer that dose to patients on a standard timetable—usually daily tablets for oral chemotherapeutics and other pill-based regimens, infusions on a weekly schedule for injectable drugs and Monday-through-Friday treatments for radiation therapy.

Almost all current cancer therapies are given this way. And although the approach has undoubtedly extended countless patients' lives, given that more than \$80 billion is spent on cancer care in the US alone, it's worth asking: are these schedules really yielding the best results for patients? And could alternative timetables produce better outcomes?

Franziska Michor hopes to answer these questions. The 31-year-old mathematical biologist from the Dana-Farber Cancer Institute in Boston sits beneath a whiteboard of multicolor equations and schematic diagrams. To one side are computer printouts of her young toddler; on the other side are empty champagne bottles from bygone celebrations of her most important academic accomplishments. She plugs away at a desktop keyboard, modeling how tumors grow and evolve.

Read the full, original story: [The mathematician versus the malignancy](#)