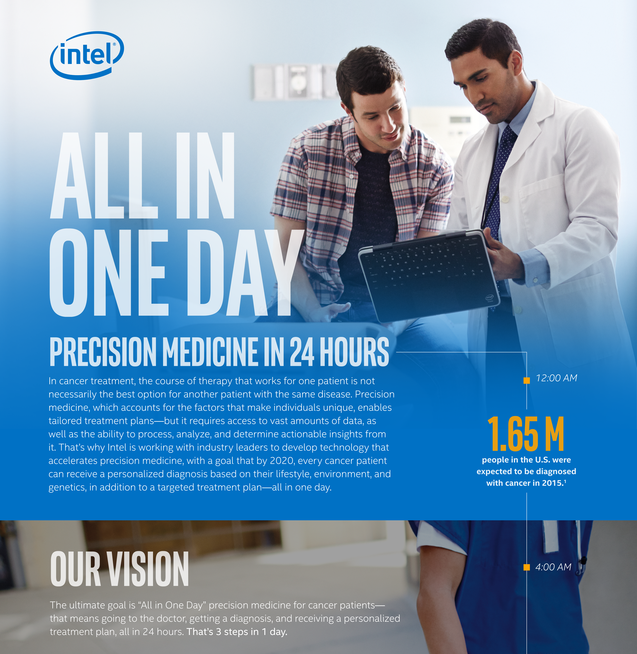

ALL IN ONE DAY

PRECISION MEDICINE IN 24 HOURS

In cancer treatment, the course of therapy that works for one patient is not necessarily the best option for another patient with the same disease. Precision medicine, which accounts for the factors that make individuals unique, enables tailored treatment plans—but it requires access to vast amounts of data, as well as the ability to process, analyze, and determine actionable insights from it. That's why Intel is working with industry leaders to develop technology that accelerates precision medicine, with a goal that by 2020, every cancer patient can receive a personalized diagnosis based on their lifestyle, environment, and genetics, in addition to a targeted treatment plan—all in one day.

12:00 AM

1.65 M

people in the U.S. were expected to be diagnosed with cancer in 2015.[1]

OUR VISION

The ultimate goal is "All in One Day" precision medicine for cancer patients—that means going to the doctor, getting a diagnosis, and receiving a personalized treatment plan, all in 24 hours. **That's 3 steps in 1 day.**

4:00 AM

8:00 AM

12:00 PM

1 Primary Sequencing
Patient visits doctor and individual genome sequencing is performed.

2 Secondary Analysis
Disease-causing genes and key pathways are identified through analytics.

3 Precision Medicine
Gene-targeted drugs, if available, are pinpointed, and collaborative knowledge bases of patient sequencing, treatment, and outcome data are consulted so that clinicians can recommend individualized treatments.

< 1%

of the cancer patient population is currently being sequenced for genomic research.[2]

THE OBSTACLES

Meeting the goal of "All in One Day" precision cancer care will require breakthroughs in multiple areas, including computing. There are **4 main technical challenges** to overcome before precision medicine can become the norm.

4:00 PM

Secure Sharing
Scientists and physicians need to be able to securely collaborate and learn from the large amounts of data available across distributed clinical and research sites while also protecting patient privacy and preserving each institution's intellectual property, but this is a challenge today.

96%

of cancer patient data is not easily accessible by the greater research community.[3]

Size
If, for just one patient, genomic sequencing generates about 1TB of raw data per year, then 1,000 patients would generate 1PB of data.[4] Moving datasets this large to a central location can often be impractical and regulatorily prohibitive.

It would take

20 DAYS

just to copy 1PB of data onto and off of disks for shipment to a central location for analytics.[5]

Speed
Accelerating both primary sequencing and secondary analysis processes is key to developing better patient outcomes. Right now, this can take weeks to complete.

8:00 PM

Scalability
The sheer volume of genomic sequencing data is outpacing the capabilities of current architectures.

1.65 million patients would create

~4EB

of genomic data.[1,4]

12:00 AM

OUR SOLUTION

Intel and world leaders in this space are addressing these challenges in **2 ways**.

TRANSFORMATIVE TOOLS

Intel and the Broad Institute are co-developing tools to accelerate biomedical research.

Cromwell is an open-standards-based integrated workflow orchestration engine that simplifies complex computational workflows and can launch genomic pipelines on private or public clouds in a portable and reproducible manner.

GenomicsDB is a database built for genomic data that can store vast amounts of patient variant data and perform fast processing at unprecedented scale.

The **Genome Analysis Toolkit (GATK)** is the industry-standard software package for analysis of high-throughput sequencing data. This pipeline is optimized to work with both Cromwell and GenomicsDB, with a primary focus on variant discovery and genotyping.

SECURE SHARING

The **Collaborative Cancer Cloud (CCC)** is a federated analytics platform—involving Oregon Health & Science University, the Dana-Farber Cancer Institute, and the Ontario Institute for Cancer Research—that uses Intel® technology to collectively analyze large amounts of patient genomic, imaging, and clinical data from each institute in a distributed way, all while preserving the privacy and security of the patient data at each site.

This offers huge potential to accelerate the ability of physicians and scientists to understand the root causes of cancer and develop targeted, molecular treatments with the goal of making "All in One Day" precision cancer care a reality by 2020.

Running GATK integrated with Cromwell and GenomicsDB in a cloud environment enabled the Broad Institute to accelerate variant calling on ~100 whole genome samples from

8 DAYS TO 18 HOURS.[6]

In partnership with industry leaders worldwide, Intel is developing the necessary architecture, tools, platforms, and solutions for life-saving advancements. And when precision medicine becomes the standard of care, we'll all be that much closer to seeing the "All in One Day" vision become a reality for cancer patients everywhere.

Explore precision medicine at
intel.com/healthcare/lifesciences

1. "Cancer Facts & Figures 2015." American Cancer Society, 2015. http://www.cancer.org/research/cancerfactsstatistics/cancerfactsfigures2015.

2. According to CDC, 32.8 million people were five-year cancer survivors and 14.1 million new cancer cases were diagnosed worldwide in 2012, for a total of 46.7 million people alive with cancer as of 2012. Based on data compiled from various sources by the National Human Genome Research Institute, global demand for Whole Genome Sequencing (WGS) in 2015 was estimated to be 400,000, which is less than 1% of the total number of people alive with cancer per CDC. For more information, visit http://www.cdc.gov/cancer/international/statistics.htm and http://www.genome.gov/27553526.

3. According to an article in the Wall Street Journal, citing Google Ventures, less than 4% of US Cancer patients are in clinical trials where data is made available for research, meaning that information about treatments and patient outcomes for 96% of patients who receive standard of care is not easily accessible. http://on.wsj.com/1smeQTO.

4. For optimum results Illumina recommends a minimum coverage of 30x for normal tissue and 60x coverage for tumor samples. http://bit.ly/1X1JYkk. FASTQ file containing all the normal tissue reads for whole genome sequencing at 30x coverage is approximately 200GB of data, and at 60x coverage for the tumor sample it would be approximately 400GB. If the patient is sequenced at least 2 times per year to capture changes in mutations, they would generate at least 1.2TB per year. http://bit.ly/1T5VKkA

5. With a 10Gbps transfer rate, 1.024PB (or 1,024TB) of data would take approximately 10 days and 10 hours to transfer from a data center to external disks/drives and an equivalent 10 days and 10 hours to transfer the data off the disks/drives onto a central location's data center storage. Estimated using online data transfer calculator at http://www.thecloudcalculator.com/calculators/file-transfer.html.

6. "Broad Institute, Intel work together to develop tools to accelerate biomedical research." Broad Institute, April 2016. http://bit.ly/1XN7xTi.