



### Touching lives around the globe

190 million patients

tracked with our patient monitors last year

Present in

100 countries

with 450+ products and services

homes every day

1,000,000

**100+ years** 

of **listening deeply** to customers to understand what really matters

100,000+

professionals are supported with **education** 

+970 million people

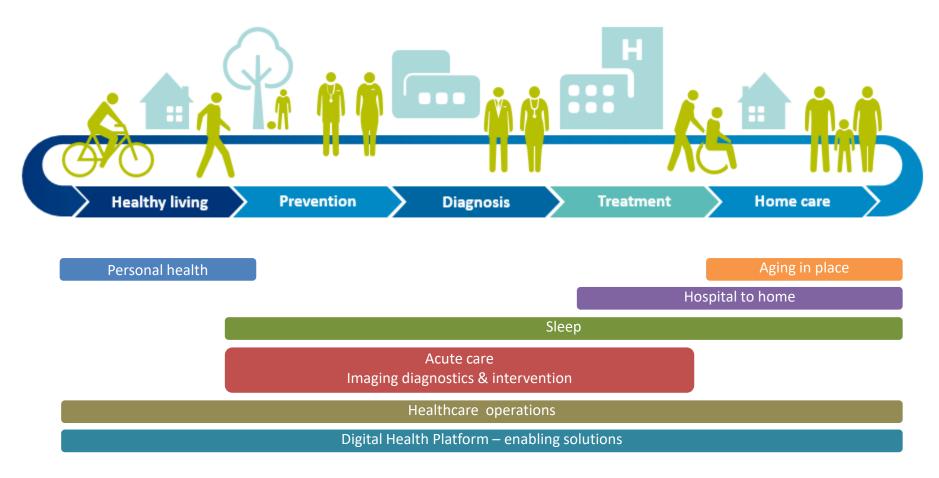
in emerging markets around the world now have **access** to Philips diagnostic imaging

10 petabytes

of data **managed** for health care providers



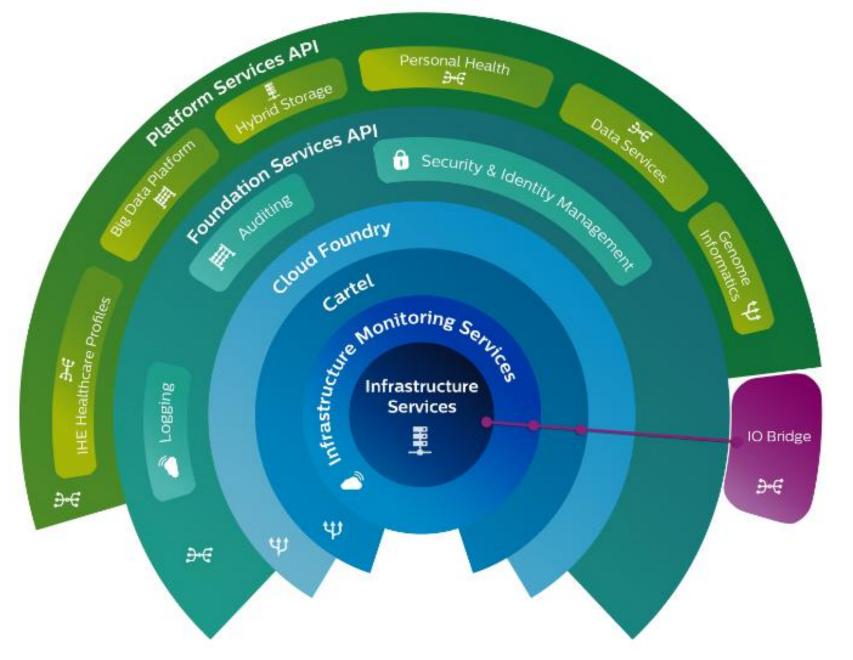
#### Solutions for the Health continuum





### **Philips Propositions**







### Genetic heterogeneity

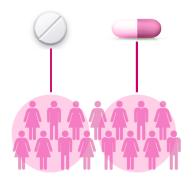
#### Current practice



One size fits all

### Genetic heterogeneity

#### Current practice



One size fits all



Genomically-enabled personalized medicine







Airplane View



Street View





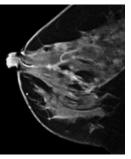


Airplane View

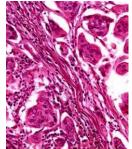


Street View

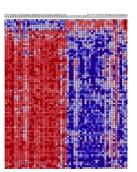
**Imaging Systems** 

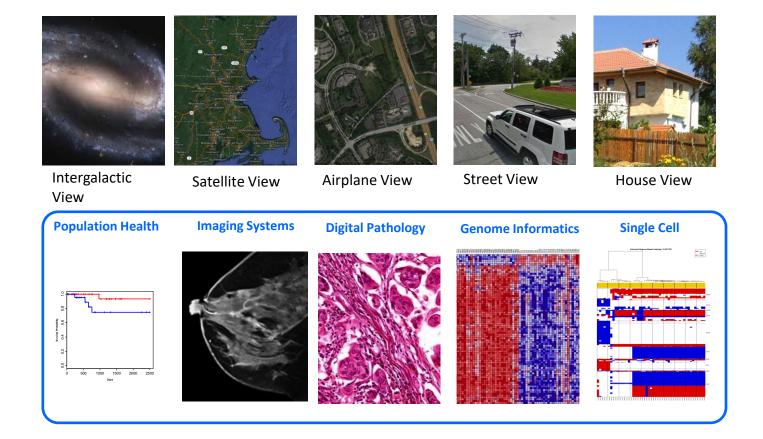


**Digital Pathology** 



**Genome Informatics** 

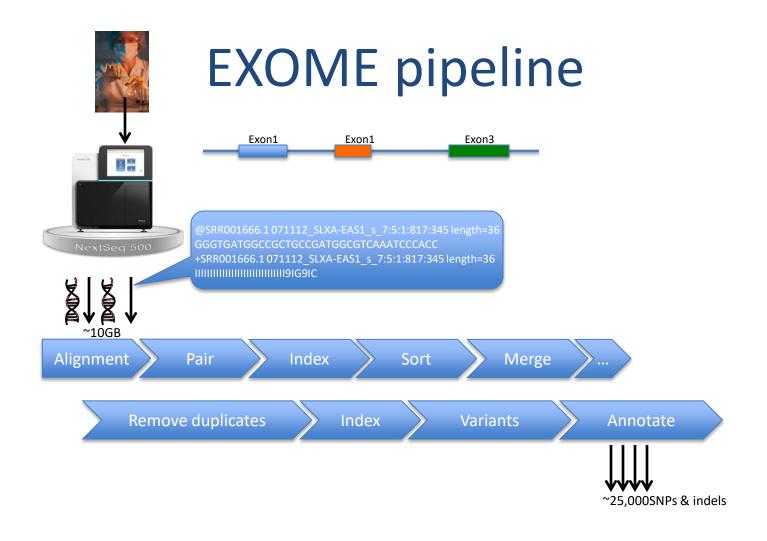




#### **HSDP Core Genomics Platform** Genomics for Infectious Genomics for Oncology Disease Genomic fingerprint: Phylogenetic tree mutations, fusions of an outbreak genomics Actionable information Transmission route **DNA Sequencing Technology** Molecular Epidemiology **Personalized Therapy** identifying infection selection for cancer spread patients Bacteria / Tumor prepared samples

Characterization	Storage (raw data)	Storage (processed data)	RAM	CPU (2.6GHz)	CPU (Philips)
Targeted exome 500 genes 500x	4-8GB	8-16GB	4-20GB	days	30mn
Whole exome 100x	20-40GB	4-80GB	4-20GB	weeks	6-8hr
Targeted 500 translocations 500x	4-8GB	8-16GB	4-20GB	days	1hr
Targeted transcriptome > 400x	2-4GB	4-8GB	1-4GB	days	1hr
Whole transcriptome 100x	10-20GB	20-40GB	4-20GB	days	2-8hr
Whole genome 30x normal 100x tumor	0.5-1TB	1-2TB	4-20GB	months	days





## Unaligned file MS6\_S13\_L001\_R1\_00 1\_fp.fastq

Protocol

truseq\_amplicon\_cancer \_panel\_afp1

Sequencing performed

2015-11-11,11:22:00

Aligned file
MS6\_S13\_L001.nb.refi
ned.bam

#### • Tools:

trimmomatic (0.33); fastQC (0.11.3); bwa (0.7.12-r1039); Samtools (1.2); GenomeAnalysisTK Variant file
MS6\_S13\_L001\_filtere
d.vcf

#### • Tools:

GenomeAnalysisTK.jar
-T UnifiedGenotyper-L
truseq\_amplicon\_can
cer\_panel\_afp1.bed

### Asynchronous processing API

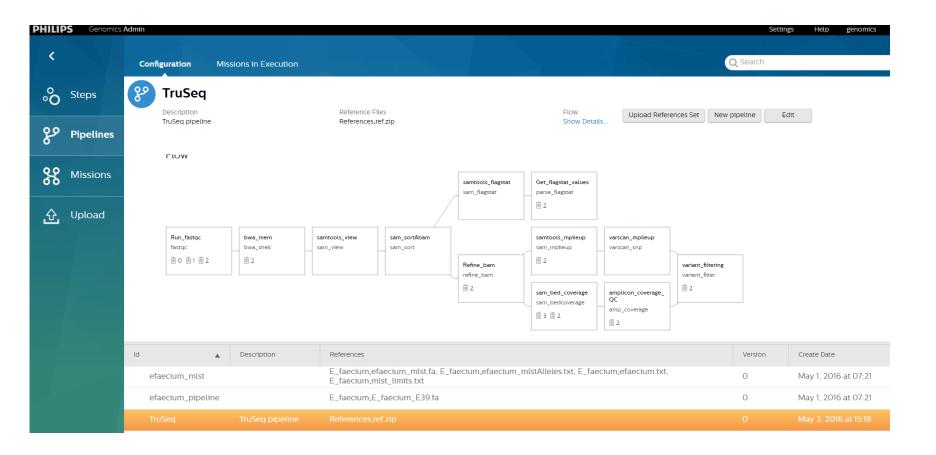


### **Gateway API**

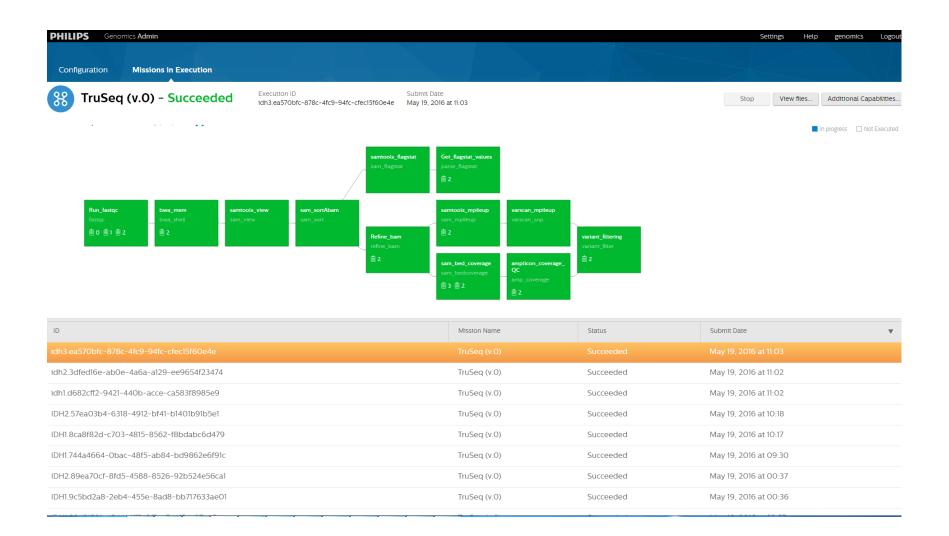
GET /genomics/Mission/{mission-id}
POST /genomics/MissionExecution
GET /genomics/MissionExecution/{mission-execution-id}
POST /genomics/MissionExecutions
POST /genomics/MissionExecution/\$qc-metrics
POST /genomics/MissionExecution/\$mlst
POST /genomics/MissionExecution/\$phylo-tree
GET /genomics/MissionExecution/{mission-execution-id}/\$phylo-tree
POST /genomics/MissionPackage
GET /genomics/MissionPackage/{package-id}
GET /genomics/MissionPackage/{package-id}/\$export
POST /genomics/MissionPackage/\$import
GET /genomics/BioSequence
POST /genomics/Pathogen/{pathogen-id}/{limits-filename}

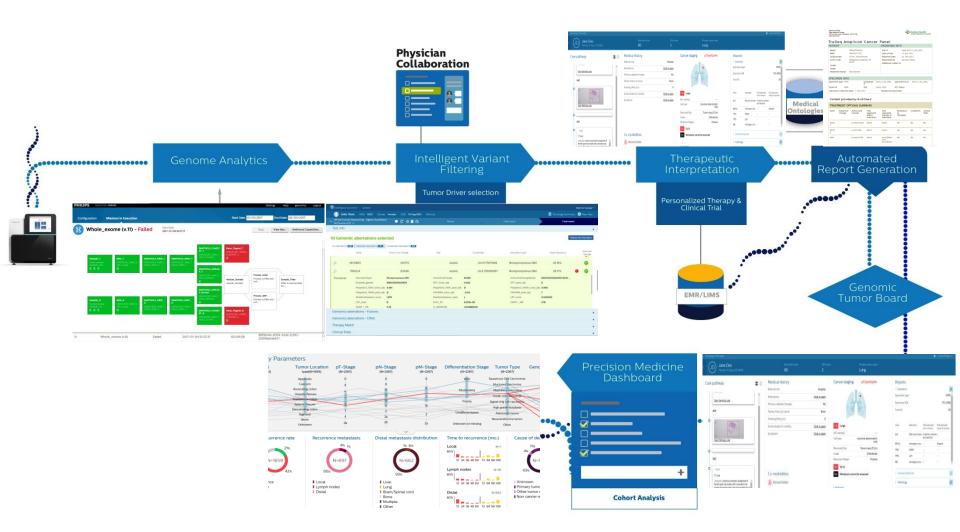


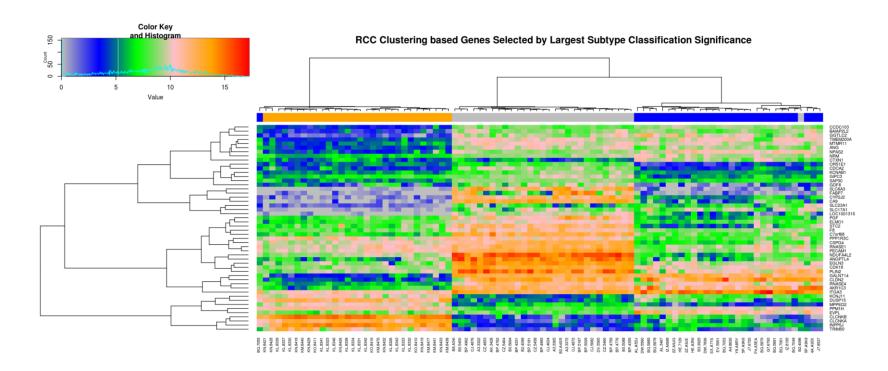
### **Pipeline Definition**



#### Mission Execution

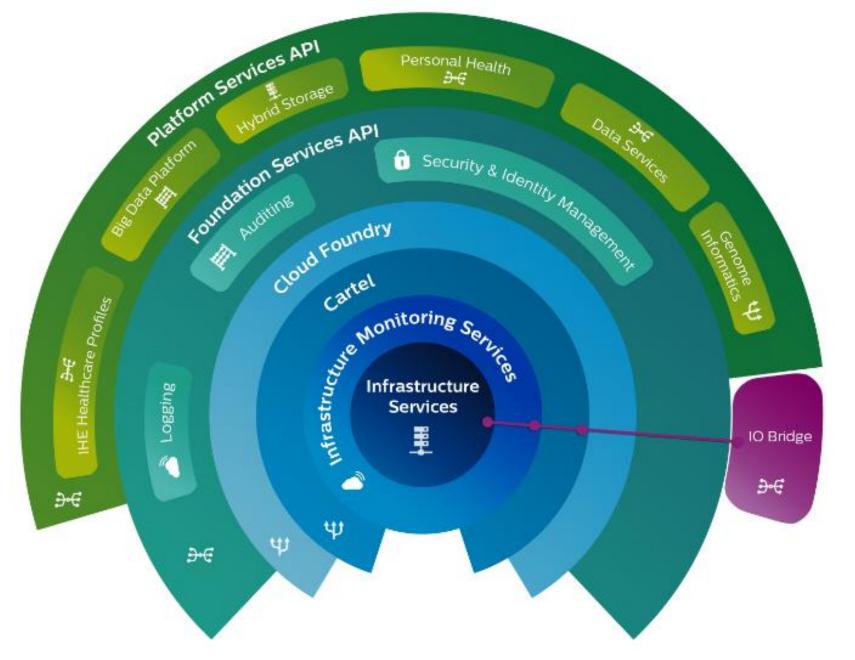






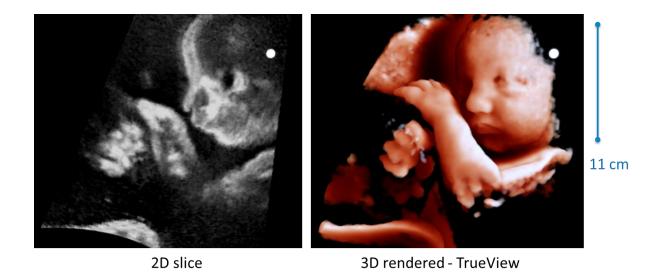
#### Confusion matrix:

	KICH	KIRC	KIRP	class.error
KICH	30.00	0.00	0.00	0.00
KIRC	0.00	29.00	1.00	0.03
KIRP	1.00	0.00	29.00	0.03

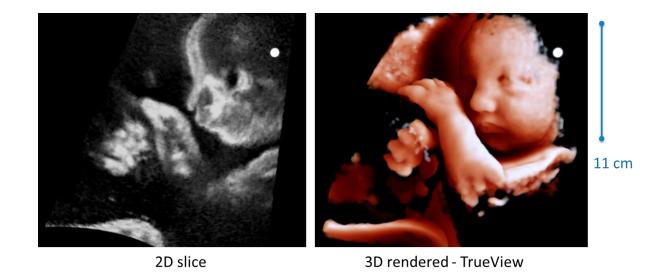


#### **PHILIPS**

#### **Ultrasound & Modelization**



#### **Ultrasound & Modelization**

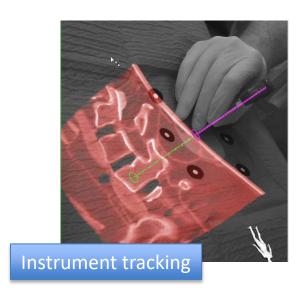


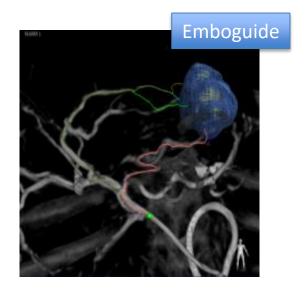


nuchal translucency

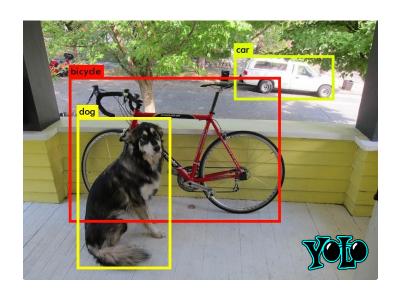
#### **Guided Therapy**





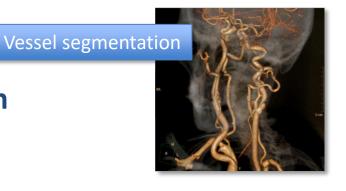


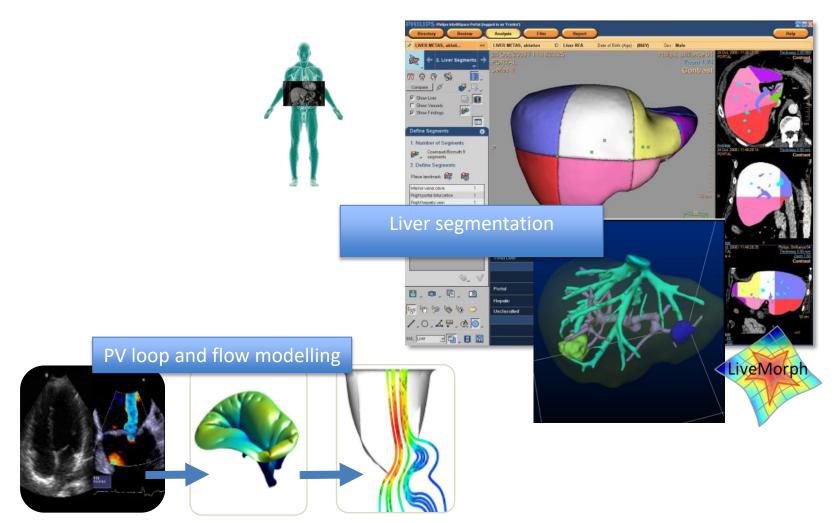
#### **Anatomical Awareness**

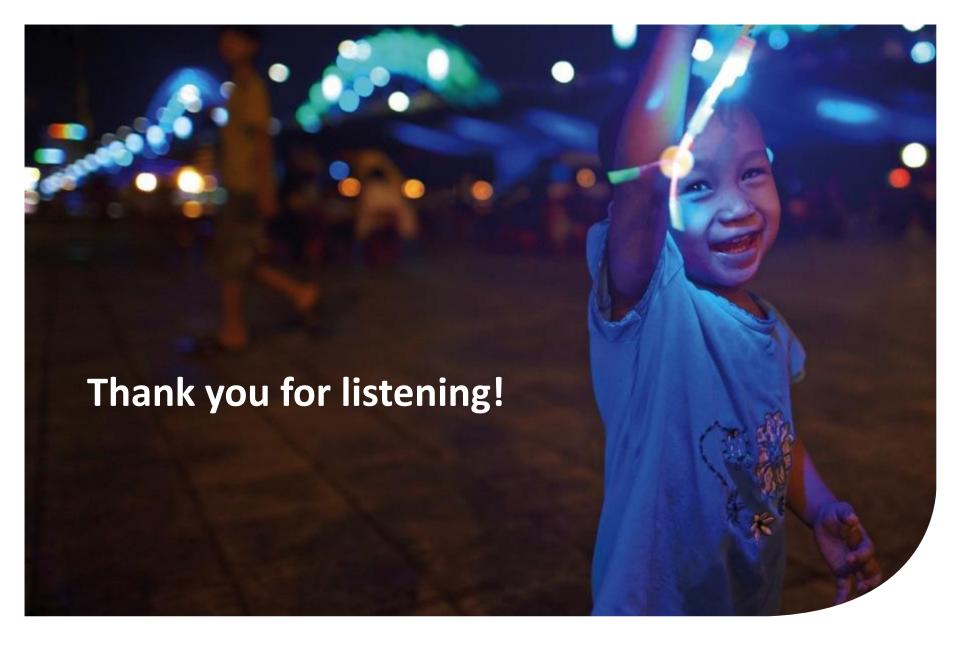


# **Anatomical Awareness** Head Chest Spine Liver Spleen L.kidney R.kidney Field of view Organ-level Sub-organ

# Organ Segmentation and Modelization







### **PHILIPS**