

BRAVE NEW ANALYTICS.

Changing the conventional perception of NGS analytical processing.

Abstract: Cloud-based architectures, with their inherent distribution of storage and computation, provide an ideal foundation for large-scale NGS analytics, where terabytes and petabytes of data must be stored and processed. By designing solutions that leverage the inherent scalability, capacity, performance, simplicity and cost-efficiency of cutting-edge cloud technology, researchers can access computational power unlike any currently available.

Utilizing cloud-based architectures that unify large quantities of affordable commodity systems with directly-attached storage, all working in concert, Ayrris™ provides a single-system view that transcends the performance and capacity of any single machine within the system.

The result is a system that combines three core technologies into a single unified platform.

- > High-Performance Computing System
- > Cloud Computing Platform
- > Complex Analytics Platform

Combining all three technologies together provides unified storage and computation in a system of unlimited flexibility and power at a truly affordable price.

REDUCE

costs through a reliable platform that doesn't require a dedicated staff to oversee

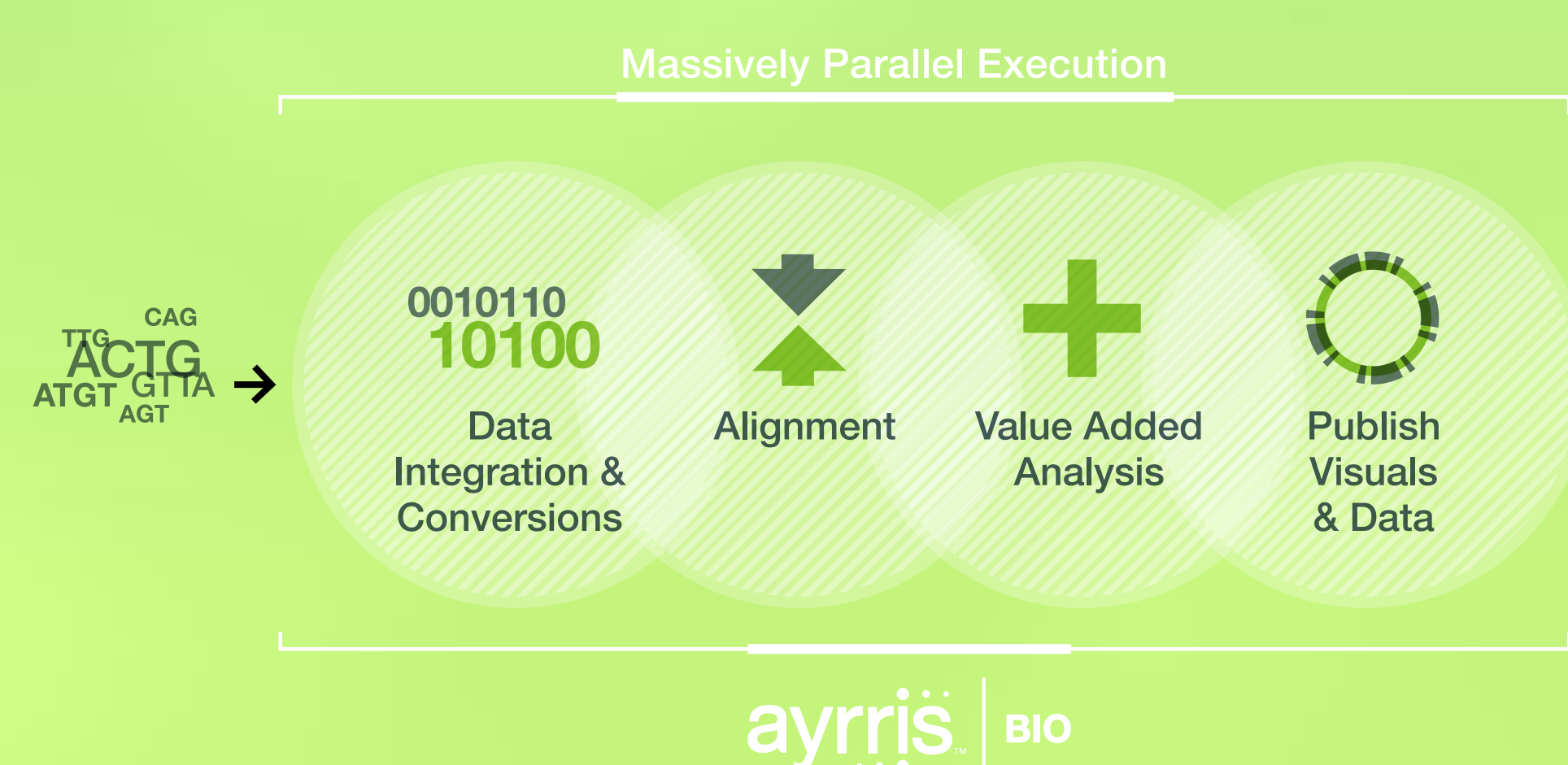
ANALYZE

at lightning speed through unprecedented data processing rates

ACHIEVE

quality and performance through scalable execution that can handle massive amounts of data

GENERIC PIPELINE OVERVIEW



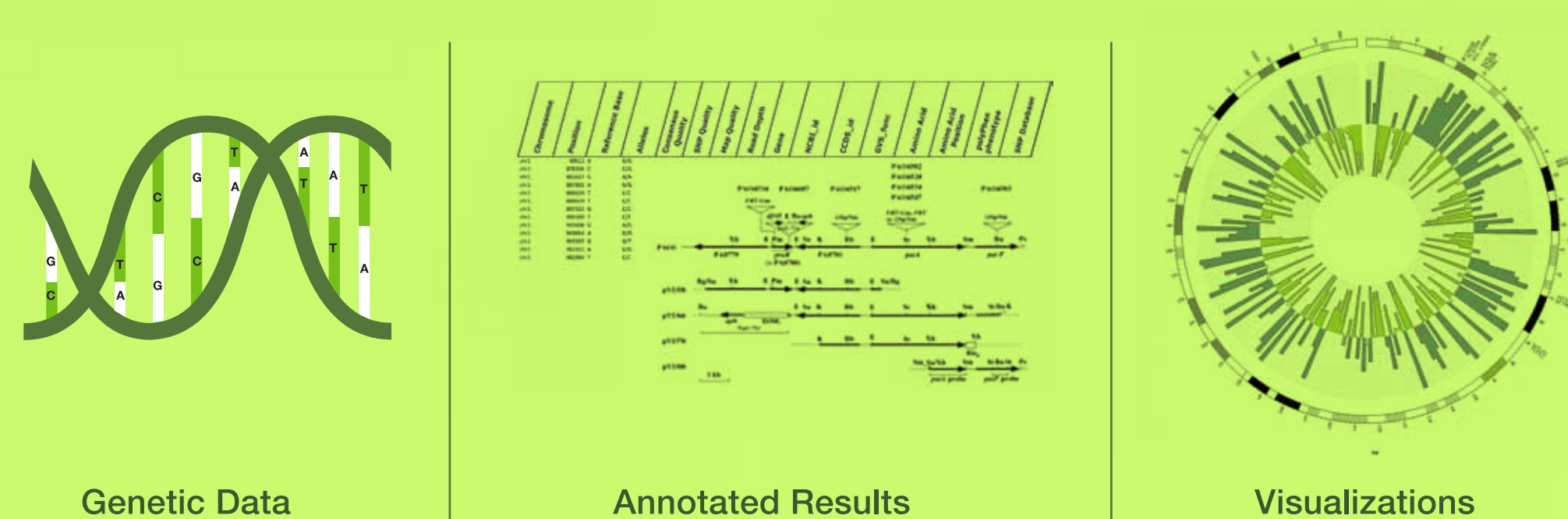
The Ayrris solution is delivered via automated analytical pipelines.

Ayrris uses cloud computing architectures to optimally deliver efficient NGS processing.

Pipeline steps can be built from common genomics tools such as:

- > Aligners (BWA, Tophat, Novoalign, Eland)
- > Tertiary Analysis (SAM Tools, Picard)
- > Annotation (Seattle Seq)
- > Visualization (Genome Browsers, Circos)

PIPELINE OUTPUT *Published Visuals & Data*



Exome/Whole Genome

- > De-dupped BAM file
- > SNPs
- > Rare variants
- > Indels
- > Variants

RNA-SEQ

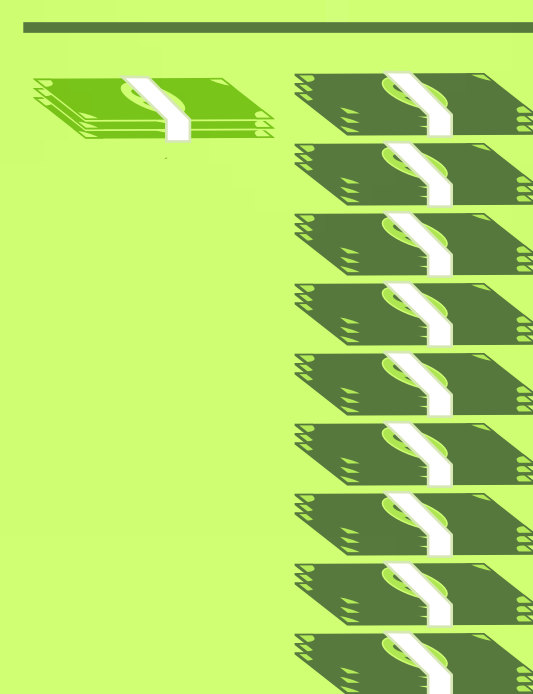
- > Aligned BAM file
- > BED file for junctions, insertions, deletions
- > Transcripts (TFG file)
- > Gene/Isoform (FPKM)
- > SNPs

EXOME NGS ANALYSIS RESULTS COMPARISON

AYRRIS/BIO Computational storage with optimized NGS pipelines

TRADITIONAL Storage array with computational clusters

\$100K vs \$1M
Infrastructure Cost



100 vs 1000
Core Efficiency



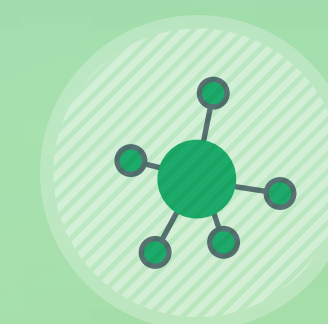
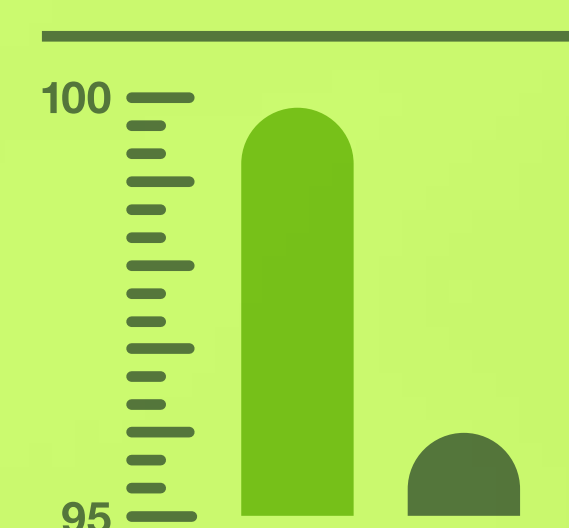
0.5 vs 20
Processing Hours



Week vs Months
Pipeline Construction



99.92% vs 96.00%
Accuracy



Dynamic software provisioning and membership

- > Manage 1000's of machines as a single entity
- > Dynamic scaling of resources



Advanced application execution built for scale and reliability

- > Dynamic workload management
- > Application-level fault tolerance



Scalable, reliable distributed file storage

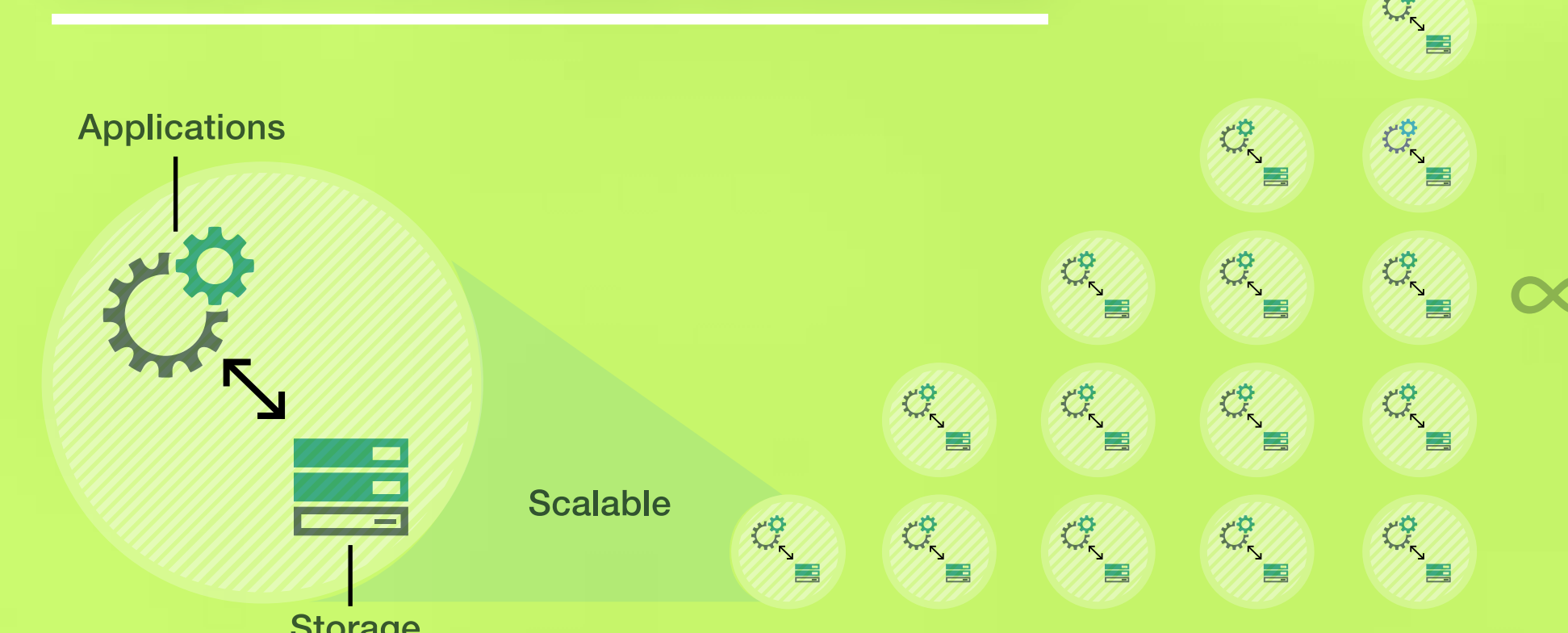
- > Massive scale on commodity technologies
- > Petabytes of data, billions of files and objects

CLOUD COMPUTING ARCHITECTURES

ANALYTICS

HIGH-PERFORMANCE COMPUTING

COMPUTATIONAL STORAGE



Bring the work to the data

Application and storage are brought together into a single integrated platform

- > Provides 10-100x performance gains with commodity technologies
- > Contrasts with traditional methods of computing with expensive storage and networking platforms

Deployment

- > Ayrris is available as an appliance or via Appistry's cloud
- > Prices starting at \$250/run