

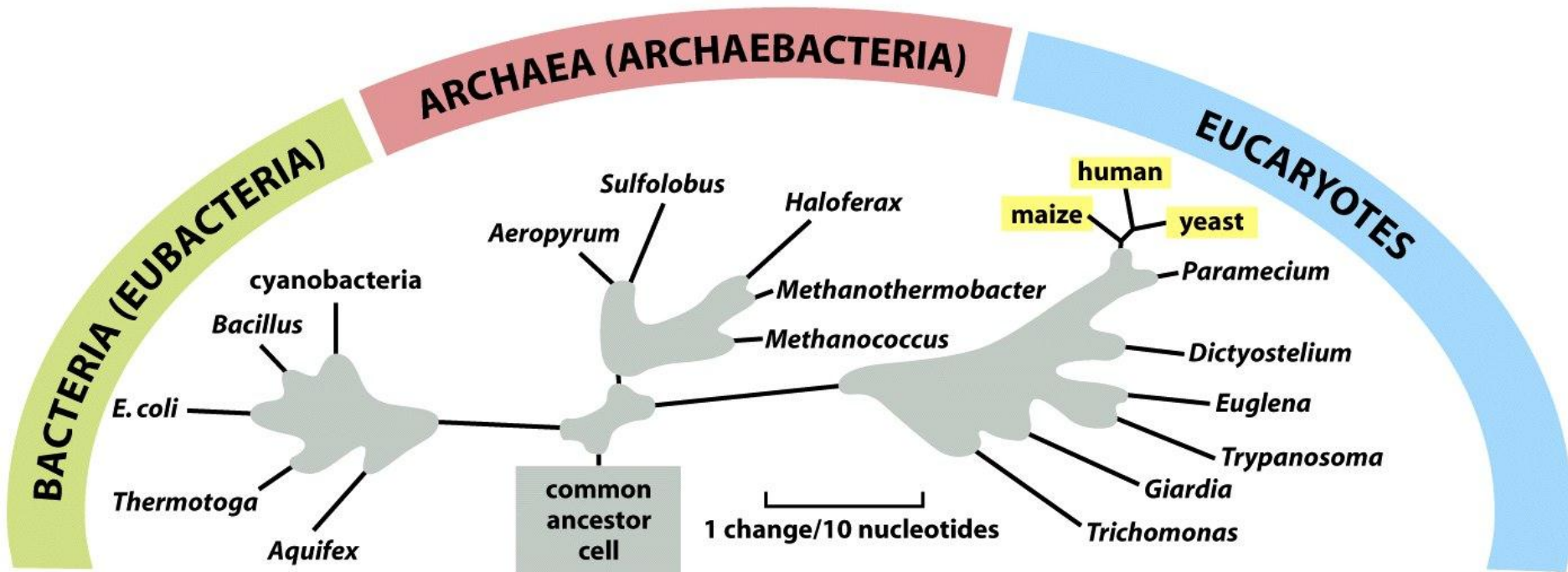
VERY LARGE SCALE OPERON PREDICTIONS VIA COMPARATIVE GENOMICS

USING MICROSOFT AZURE

Ehsan Tabari
University of NC Charlotte

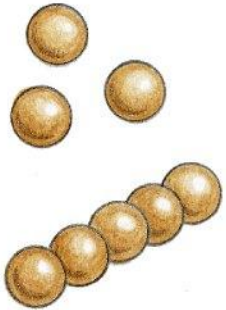
Life domains

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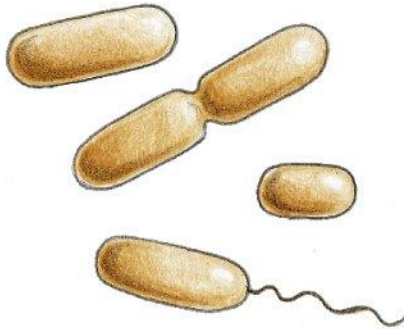


Prokaryotes

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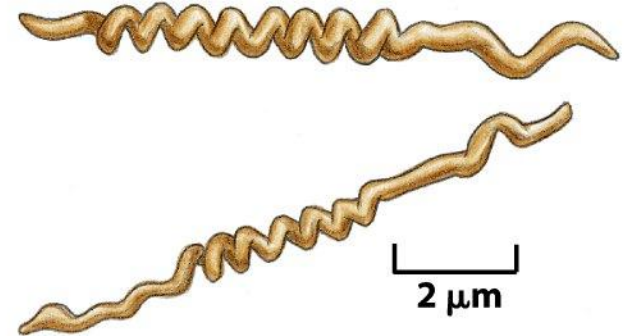
spherical cells
e.g., *Streptococcus*



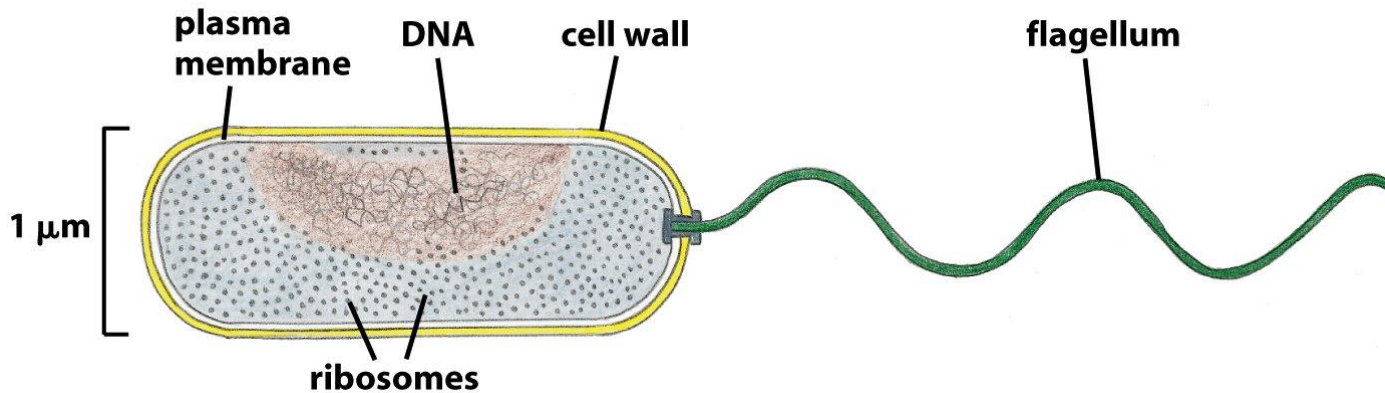
rod-shaped cells
e.g., *Escherichia coli*,
Vibrio cholerae



the smallest cells
e.g., *Mycoplasma*,
Spiroplasma

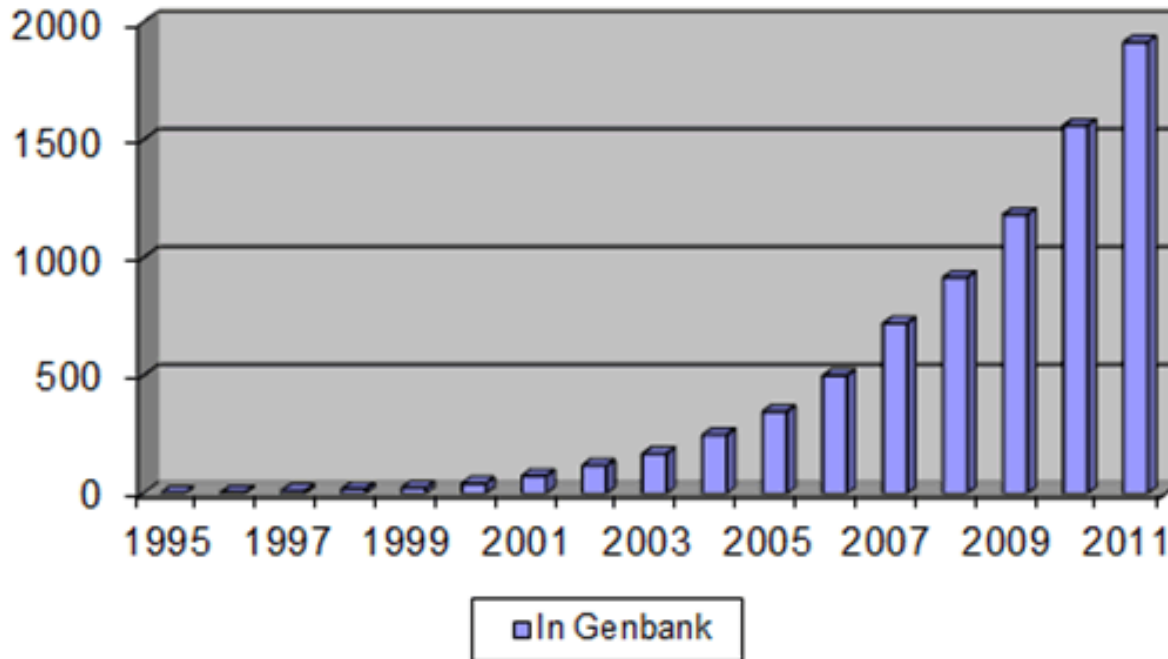


spiral cells
e.g., *Treponema pallidum*



Research in Life

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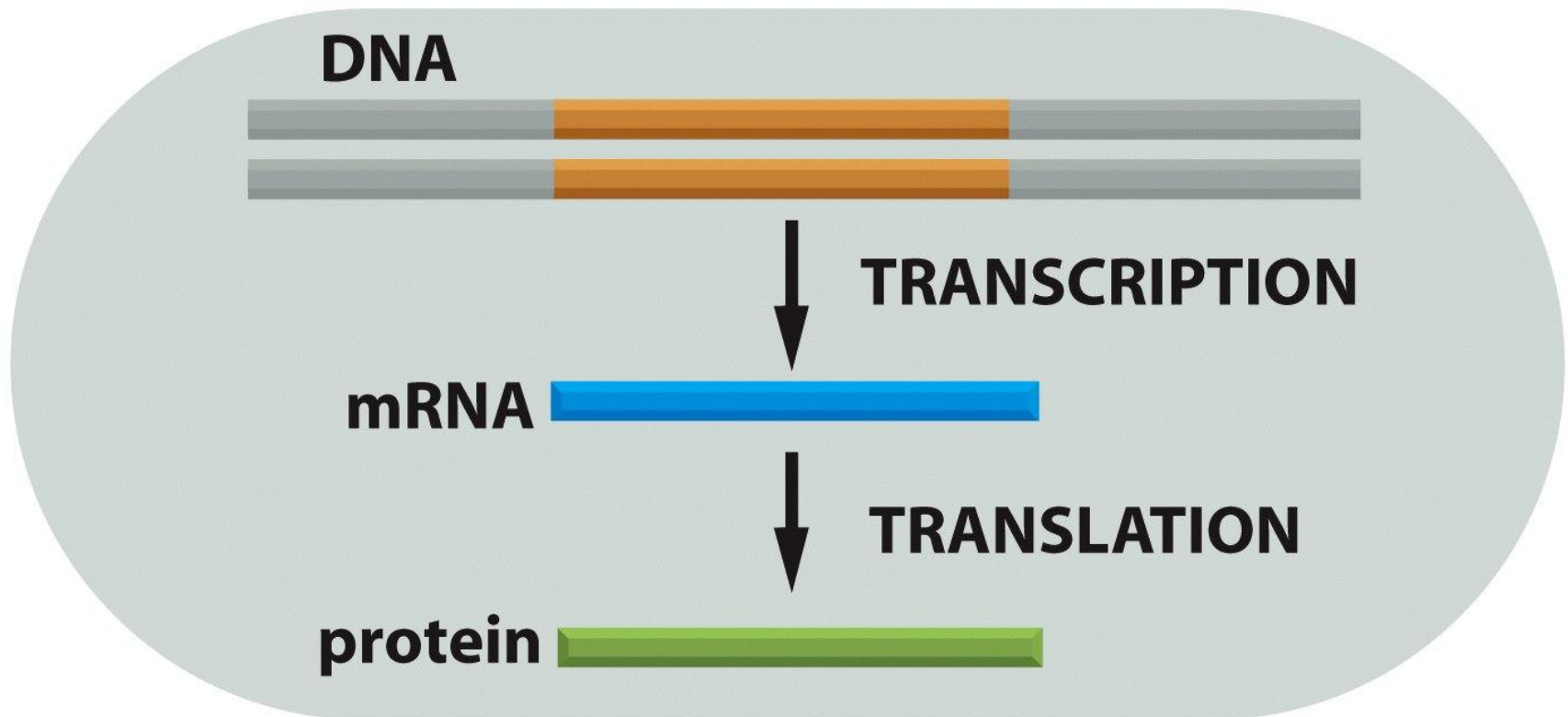


Domain	Currently Sequenced	In progress
BACTERIA	2,847	7,908
ARCHAEA	153	213
EUKARYOTES	173	2,385

Central Dogma of Biology

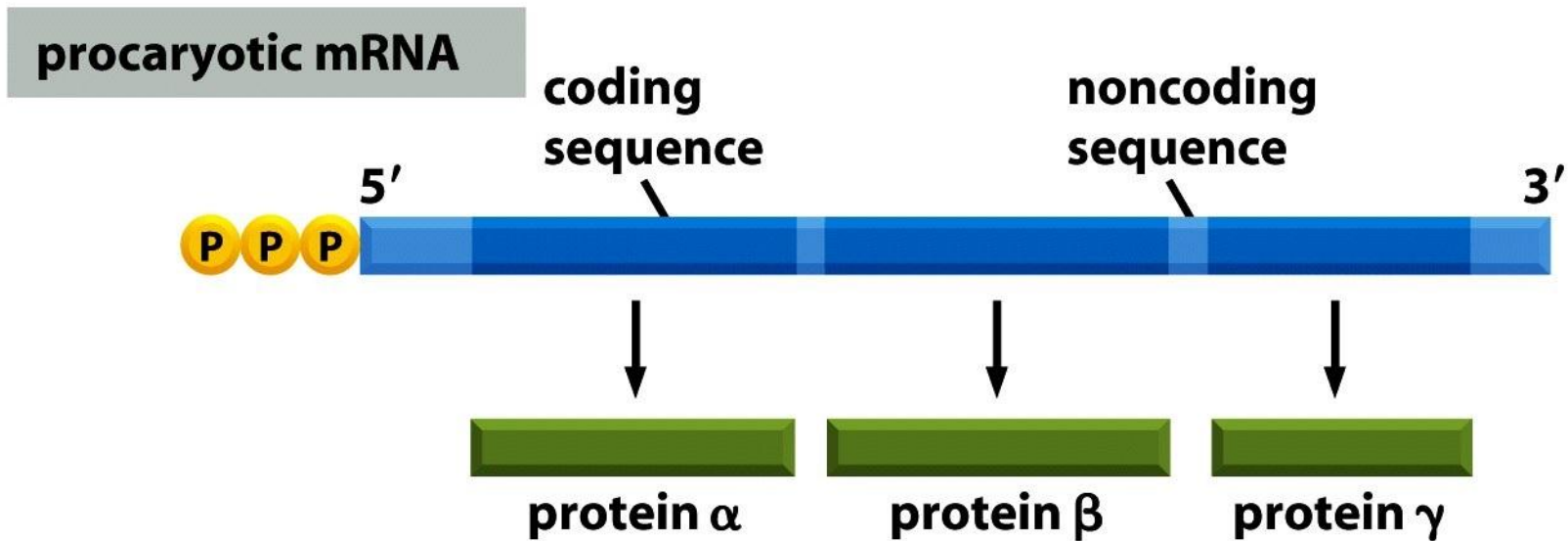
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PROCARYOTES



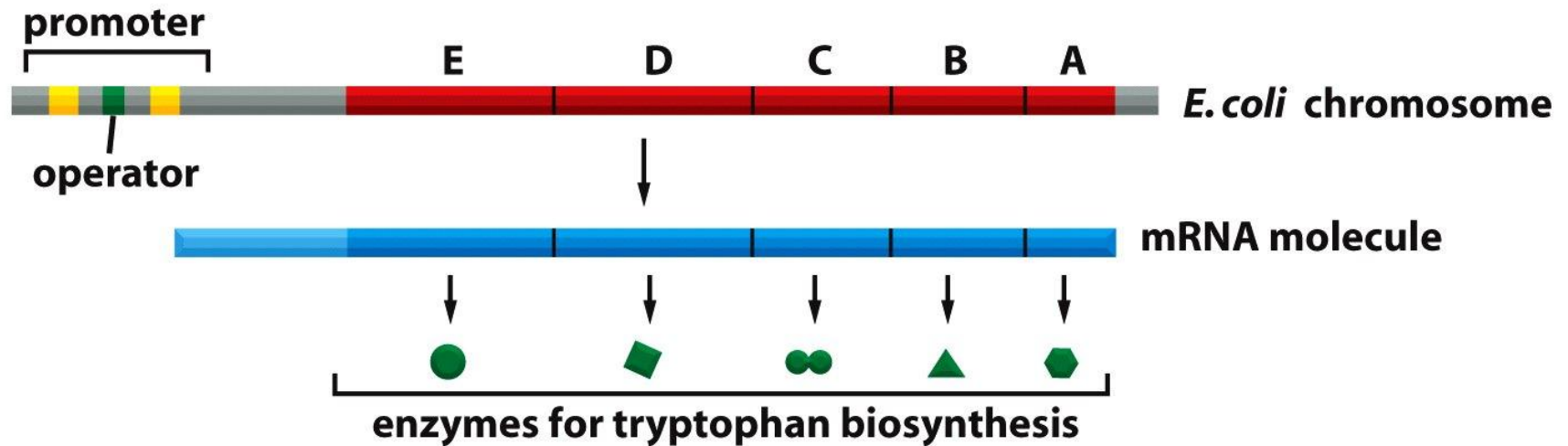
Operons

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Operons

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- Functional prediction
- Gene transcription
- Gene regulation

The Question

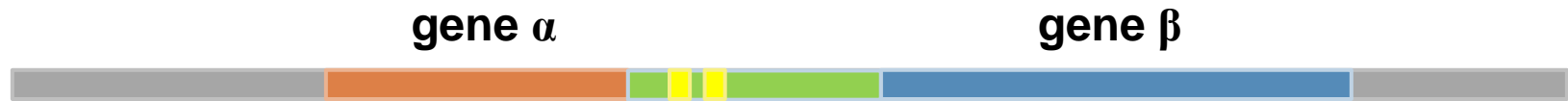
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- Gene pair in an operon?
- Prediction vs. Verification
- Features

Features

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- Intergenic Distance
- Transcription Factors
- Gene Pair Neighborhood Conservation
- Mutual Expression level
- Functional Similarities

Prokaryote s

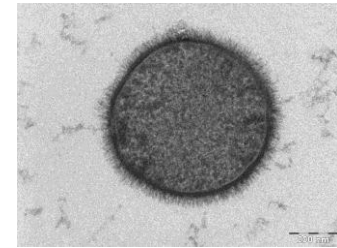
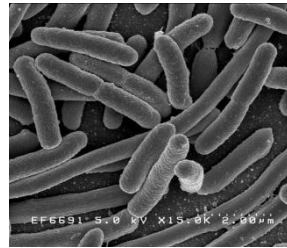
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- 1499 published genomes
 - Genome
 - Predicted genes



Model Organisms

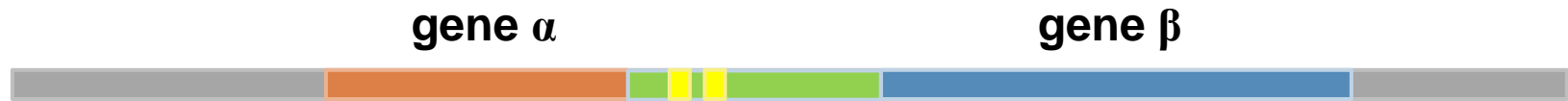
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	<i>Escherichia coli</i> K12 MG1655	<i>Bacillus subtilis</i> W168
Predicted Genes	4144	4176
Known Operons	843	166
Gene pairs in Operon	1588	387
	38.3%	9.3%

Features

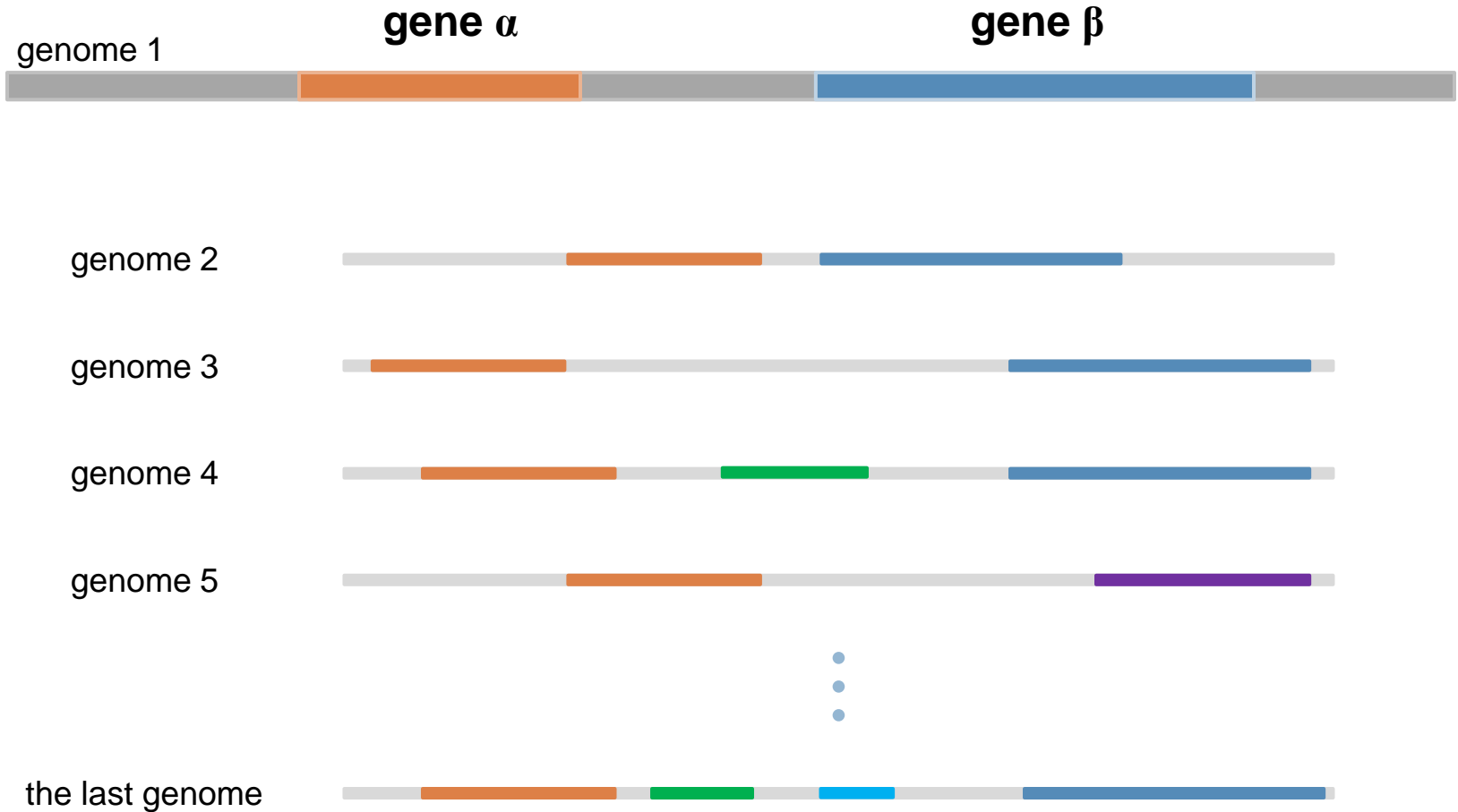
13



- Intergenic Distance
- Transcription Factors
- Gene Pair Neighborhood Conservation**
- Mutual Expression level
- Functional Similarities

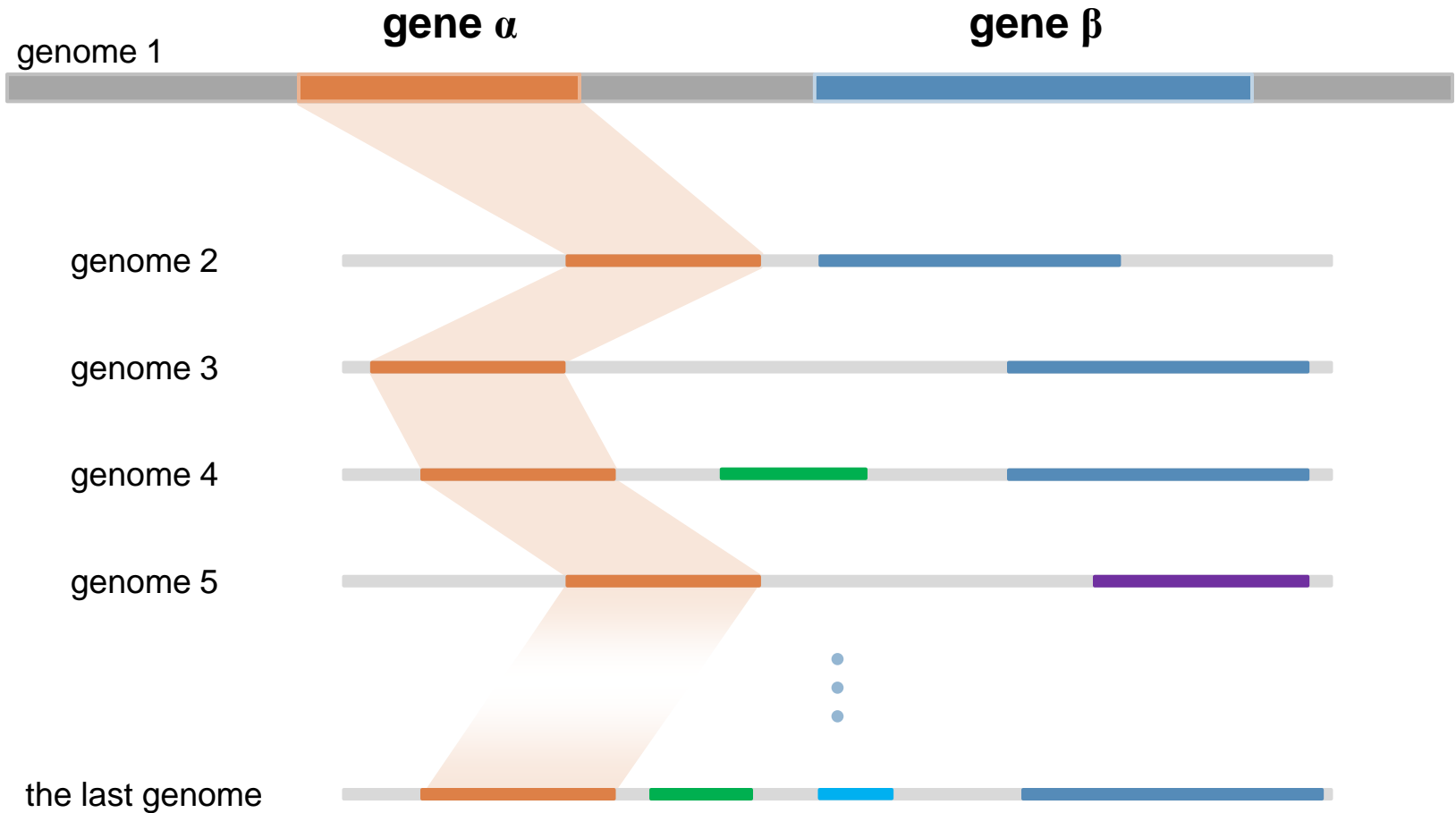
Gene neighborhood Conservation

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Orthologous Genes

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Gene Neighborhood Conservation

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- Find Orthologous genes
 - ▣ pairwise BLASTs
 - ▣ Processing results
- Calculate conservation values
 - for each gene pair of every genome

BLAST

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- String search tool
- Inexact gapped matches
- Search a query against a database
 - ▣ Search a gene in a genome
- Bidirectional BLAST hits to deduce orthology

On Cloud

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- How many?
 - ▣ $1499 \times 1498 = 2,245,502$
- Runtime of each BLAST?
 - ▣ 2 minutes
- How long will it take on a single computer?
 - ▣ $2.2M \times 2\text{min} = 3,118 \text{ days!}$

Azure Cloud

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- Windows Azure HPC Scheduler
 - Parametric Sweep

- 300 small size nodes
 - 1 CPU core
 - 2GB Memory

- 20TB of Azure Storage

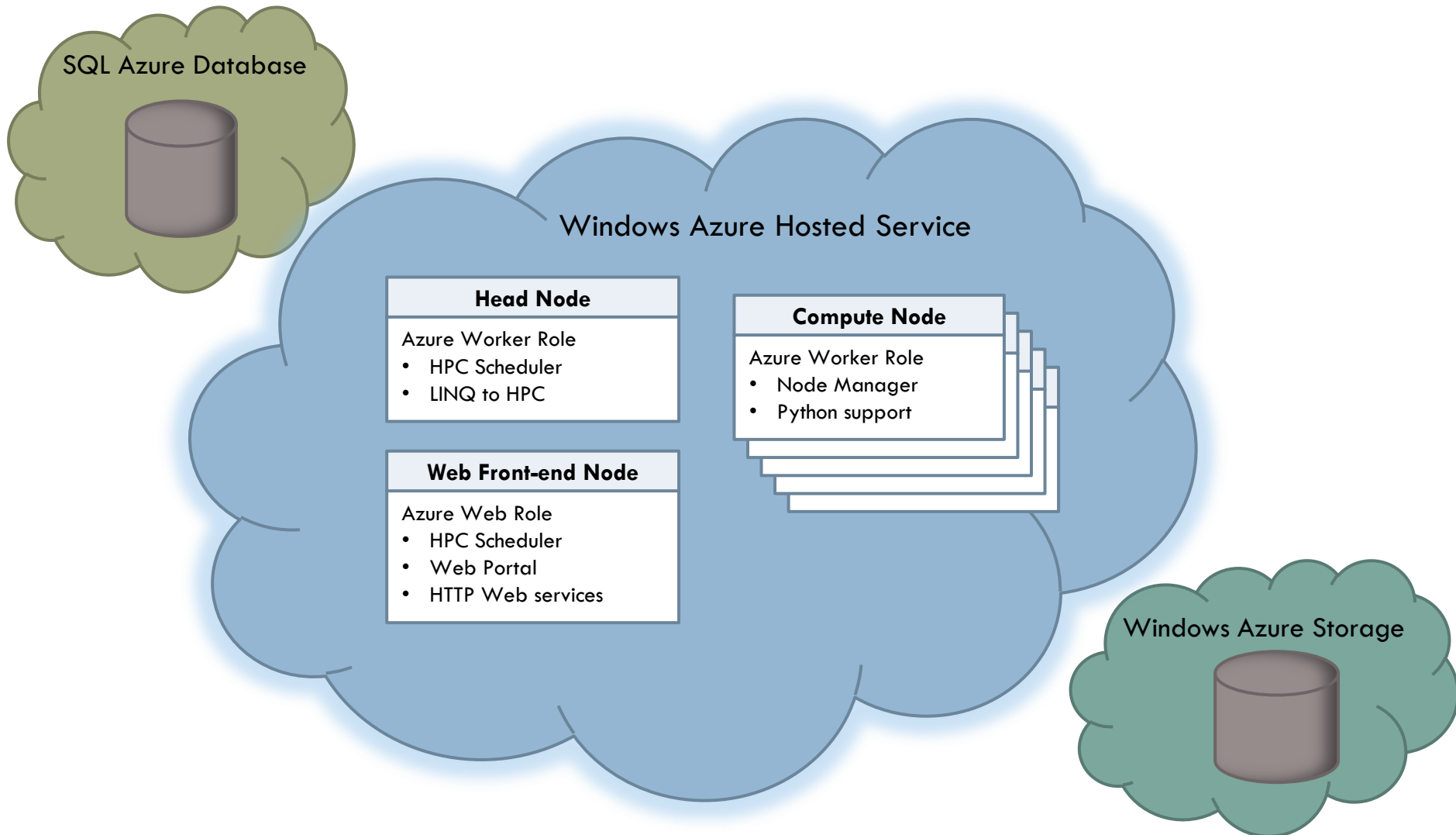
Windows Azure HPC Scheduler

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- Parametric Sweep
 - ▣ Embarrassingly parallel problems
- SOA Services
 - ▣ Distributed applications
- MPI Applications
 - ▣ Platform-independent standard

HPC Architecture

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Parametric Sweep BLAST

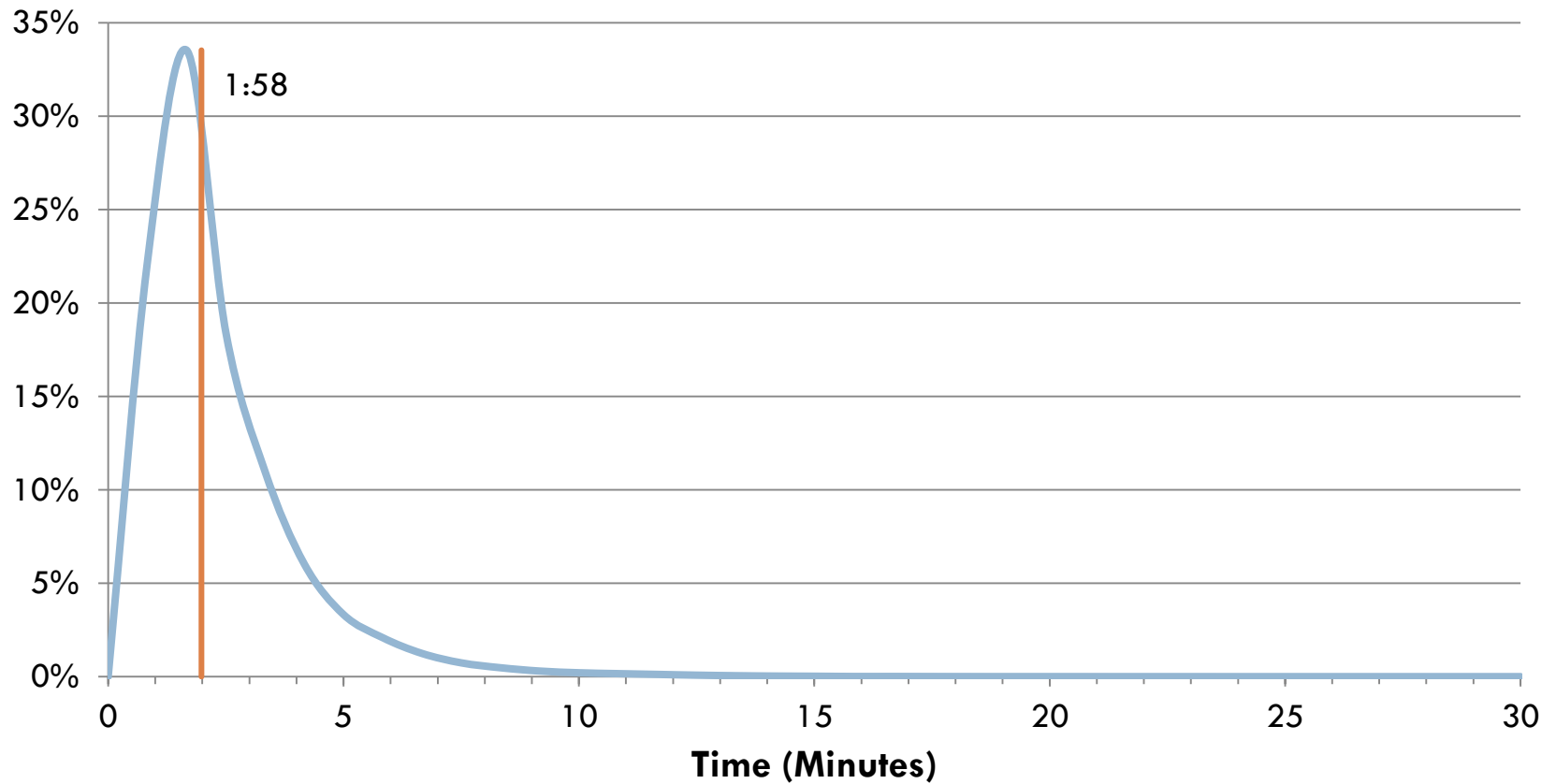
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- Deploy a hosted service
- Run
 - ▣ Downloads required data from storage account to the work node
 - ▣ Run BLAST
 - ▣ Uploads the results back to storage account
- Check Fails, log files, ...

Blast run time

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Blast Runtime



Storage

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- Genome
 - ▣ Including blast databases: 11.1 GB
- BLAST
 - ▣ 7.5 TB
- The rest
 - ▣ Calculated results: 25 GB

Total cost

25

- Computation
 - ▣ About \$9,000 in total

- Storage
 - ▣ About \$900 / month

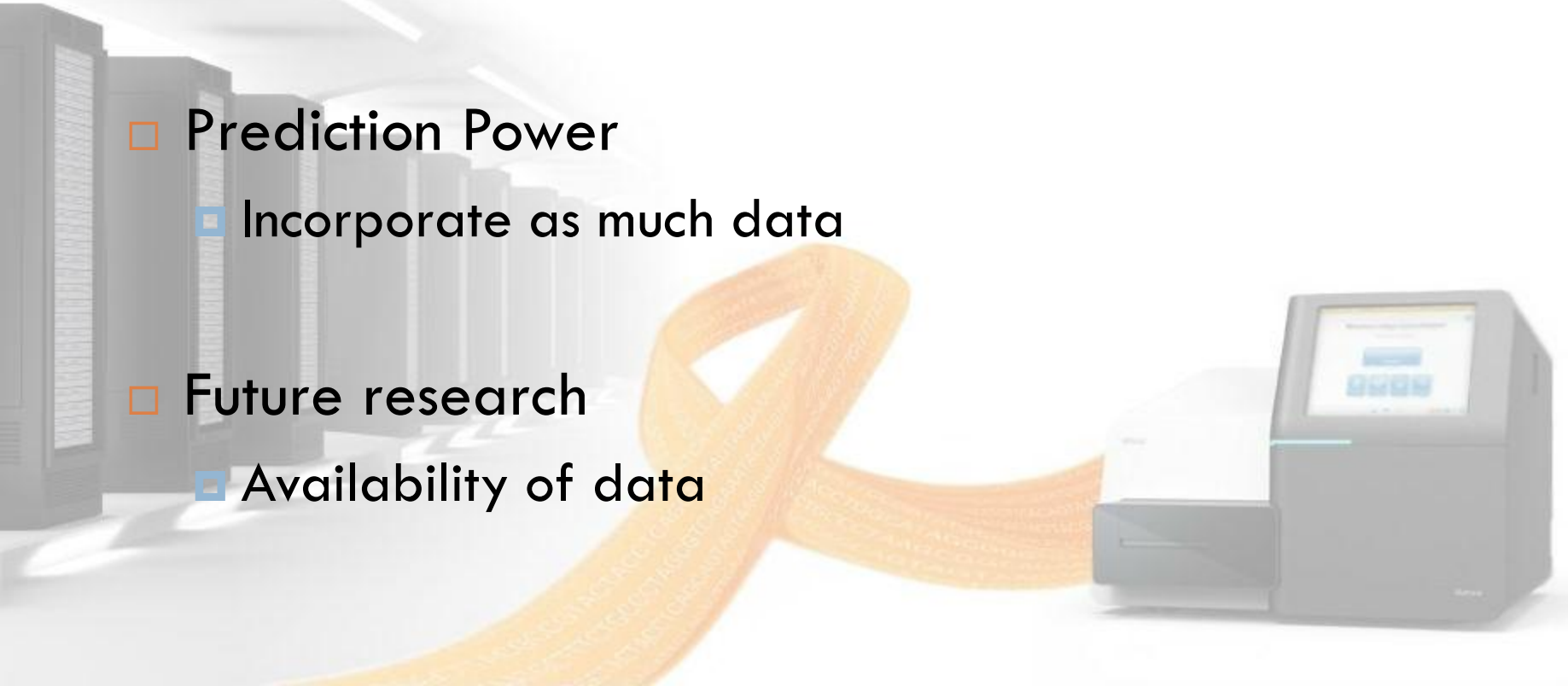
Importance

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- Computationally intensive research
 - Cost
 - Time

- Prediction Power
 - Incorporate as much data

- Future research
 - Availability of data



Thank You

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- Acknowledgments
 - Dr. ZhengChang Su
 - Bioinformatics @ UNC Charlotte
 - Microsoft support team

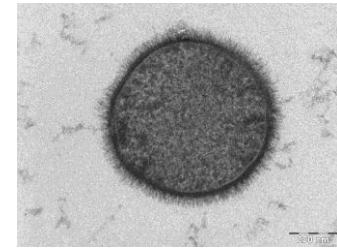
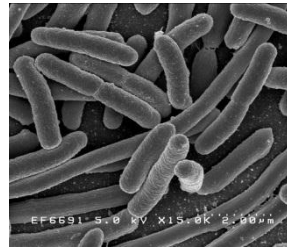


EXTRA SLIDES



Model Organisms

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Conservation

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Genome	2	3	4	5	6	...	1499
gene α	√	√	√	√	×		√
gene β	√	√	√	×	×		×
D_g	1/1	1/1	1/2				1/3

$$\log \frac{\sum_K \frac{1}{1 + D_g(g_i, g_j, K)}}{D_H(g_i, g_j)}$$