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System Upgrade on Fri,
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offline for less than an
hour but the E-
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Computational Methods for Understanding Bacterial and ...

Computational
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genomes Ying Xu , J.
Peter Gogarten Over
500 prokaryotic
genomes have been
sequenced to date, and

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thousands more have
been planned for the
next few years.

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characteristics of
prokaryotic genomes

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--Genes in prokaryotic
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Over 500 prokaryotic
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sequenced to date, and
thousands more have
been planned for the
next few years. While
these genomic
sequence data provide
unprecedented
opportunities for ...

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Understanding ...**

Abstract Recent advances in high-throughput RNA sequencing (RNA-seq) have enabled tremendous leaps forward in our understanding of bacterial transcriptomes. However, computational methods for analysis of

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bacterial transcriptome data have not kept pace with the large and growing data sets generated by RNA-seq technology.

Computational analysis of bacterial RNA-Seq data ...

Abstract Recent advances in high-throughput RNA sequencing (RNA-seq) have enabled tremendous leaps forward in our

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understanding of
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However,
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generated by RNA-seq
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Nucleic ...**

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using electrochemistry
paired with
computational or
mathematical modeling
to enhance and deepen
the understanding of
these systems. This
review is organized by
groups of
computational
methods, discussing
the scientific
advancements that
lead to the current
modeling frameworks
and future directions
for the field of

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microbial
electrochemistry.

**Editors' Choice—Review—Exploration of
Computational ...**

Various computational methods commonly used in the chemistry and biology fields prove to be useful in studying microbial electrochemical systems. Their implementation open for further advancements in the

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field of microbial
electrochemical
systems, both from a
fundamental and
applicative point of
view.

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**Editors' Choice—Review—Exploration of
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Metagenomics
provides the genetic
basis for understanding
the interplay between
uncultured bacteria,
their phage and the
environment. In

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particular, viral metagenomes (viromes) are providing new insight into phage-encoded host genes (i.e. auxiliary metabolic genes; AMGs) that reprogram host metabolism during infection.

Computational prospecting the great viral unknown | FEMS ...

Microorganisms play a vital role in various

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ecosystems and
characterizing
interactions between
them is an essential
step towards
understanding the
organization and
function of microbial
communities.

Computational
prediction has recently
become a widely used
approach to
investigate microbial
interactions.

Predicting microbial

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**interactions through
computational ...**

Computational
methods for culture-
independent
disambiguation of
wgMLST types in
biological samples with
multiple related
bacterial strains
Investigators will
develop computational
tools to differentiate
and analyze different
types of DNA mixed in
one sample.

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**Innovative Projects:
Broad Agency
Announcement (BAA**

...

First, the currently known riboswitches are primarily bacterial.

Thus, if riboswitches can be targeted specifically, the potential for undesired off-target interactions with human molecules is lessened. Second, riboswitches have evolved to bind small molecules with high

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affinity and specificity.

... Computational Methods for Understanding ... Archaeal

**Riboswitch - an
overview |**

ScienceDirect Topics

An understanding of the tools, databases, computational methods, and available pipelines used to generate genome annotations is necessary to assess their accuracy and

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their appropriateness for downstream applications. In this chapter we focus on the computational methods that have been developed for annotating bacterial and archaeal genomes.

Bioinformatics and Data Analysis in Microbiology

Using experimental and computational methods, researchers reveal workings of

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bacterial defense
system. Researchers
have uncovered new
insights into how
bacteria respond to
stress. When deprived
of...

Advances In **Understanding** **antibiotic**

resistance: Using
experimental ...

Our group develops
computational
methods for
understanding the
dynamics, interactions

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and conservation of complex biological systems. As new high-throughput biological data sources become available, they hold the promise of revolutionizing molecular biology by providing a large-scale view of cellular activity.

Joint/Adjunct Faculty | Computational & Systems Biology

The past two decades of analytical efforts

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have highlighted how much more remains to be learned about the human genome and, particularly, its complex involvement in promoting disease development and progression. While numerous computational tools exist for the assessment of the functional and pathogenic effects of genome variants, their precision is far from

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satisfactory,
particularly for ...

**Computational
Approaches for
Unraveling the
Effects of ...**

These data-driven
computational
methods have drawn
on the increasing
availability of large
clinical and
neuroimaging datasets.
The models themselves
provide new utility and
key insights into

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Advances In
Bioinformatics

disease, including fine-grained patient assessment (and clinical trial recruitment!) and improved understanding of disease mechanisms.

Computational modelling for understanding mechanisms of ...

Integrans are genomic elements that mediate horizontal gene transfer by inserting

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and removing genetic material using site-specific recombination. Integrons are commonly found in bacterial genomes, where they maintain a large and diverse set of genes that plays an important role in adaptation and evolution. Previous studies have started to characterize the wide range of biological functions ...

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