

Regulatory Sequence Analysis Tools (RSAT)


- Since 1998 (15 years !)
- Initiated in Cuernavaca, Mexico
- yeast cis-regulatory elements



Jacques van Helden

RSAT improvements over the years

RSAT NeAT




New items 🔥

- Most popular tools
 - retrieve sequence
 - peak-motifs
 - oligo-analysis (words)
 - matrix-scan (quick)
- > view all tools
- Genomes and genes
 - Sequence tools
 - Matrix tools 🔥
 - Build control sets
- Motif discovery
 - Pattern matching
- Comparative genomics 🔥
 - NGS - ChIP-seq
 - Genetic variations 🔥
- Conversion/Utilities
 - Drawing
- SOAP Web services

Regulatory Sequence Analysis Tools

Welcome to **Regulatory Sequence Analysis Tools (RSAT)**.



This web site provides a series of modular computer programs specifically designed for the detection of regulatory signals in non-coding sequences. RSAT servers have been up and running since 1997. The project was initiated by **Jacques van Helden**, and is now pursued by the **RSAT team**.

This website is free and open to all users.

🔗 **Which program to use ?** A guide to our main tools for new users.

- 1 - Choose your type of data to analyse**
- 2 - Choose your biological question / analysis to perform**
- 3 - Relevant RSAT programs**


📖 Check **RSAT tutorial** at **ECCB'14** and **all training material**

📖 Learn how to use **Peak-motifs** with a **Nature Protocol** [\[view article\]](#)


📧 Stay Tuned !! **RSS feed** to all RSAT news.

★ Also try our **new programs** 🔥


🔗 Complete list of online tools is in the left menu



maintained by TAGC - Université Aix Marseille, France



maintained by Computational Genomics lab
CCG - UNAM, Cuernavaca, Mexico



maintained by plateforme ABIMS Roscoff, France



<http://rsat.eu>

- *Medina-Rivera*, Defrance*, Sand*, Herrmann, Castro-Mondragon, Delerce, Jaeger, Blanchet, Vincens, Caron, Staines, Contreras-Moreira, Artufel, Charbonnier-Khamvongsa, Hernandez, Thieffry, Thomas-Chollier#, van Helden#. **Nucleic Acids Research, 2015***
- *Thomas-Chollier, Darbo, Herrmann, Defrance, Thieffry, van Helden **Nature Protocols, 2012***
- *Thomas-Chollier, Defrance, Medina-Rivera, Sand, Herrmann, Thieffry, van Helden **Nucleic Acids Research, 2012***
- *Medina-Rivera, Abreu-Goodger, Thomas-Chollier, Salgado, Collado-Vides, van Helden **Nucleic Acids Research, 2011***
- *Sand, Thomas-Chollier, van Helden **Bioinformatics, 2009***
- *Thomas-Chollier*, Sand*, Turatsinze, Janky, Defrance, Vervisch, van Helden **Nucleic Acids Research, 2008***
- *Sand, Thomas-Chollier, Vervisch, van Helden **Nature Protocols, 2008***
- *Thomas-Chollier*, Turatsinze*, Defrance, van Helden **Nature Protocols, 2008***
- *van Helden, **Nucleic Acids Research, 2003***

RSAT in a nutshell

The screenshot shows the RSAT website interface. At the top, there's a navigation bar with 'RSAT' and 'NeAT'. Below it, a sidebar on the left lists various tool categories like 'Most popular tools', 'Genomes and genes', 'Sequence tools', etc. The main content area is titled 'Regulatory Sequence Analysis Tools' and contains a welcome message, a description of the site's purpose, and a list of tools categorized by biological question. The footer includes logos for 'RSAT Fungi', 'RSAT Prokaryotes', and 'RSAT Metazoa' along with their respective maintainers.

Regulatory Sequence Analysis Tools

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Which program to use ? A guide to our main tools for new users.

1 - Choose your type of data to analyse
List of gene names

2 - Choose your biological question / analysis to perform
Which regulatory elements are conserved in promoters of orthologs ? (only for prokaryotes and fungi)

3 - Relevant RSAT programs
footprint-scan

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RSAT Fungi maintained by TAGC - Université Aix Marseilles, France

RSAT Prokaryotes maintained by Computational Genomics lab CCG - UNAM, Cuernavaca, Mexico

RSAT Metazoa maintained by plateforme ABIMS Roscoff, France

Tasks

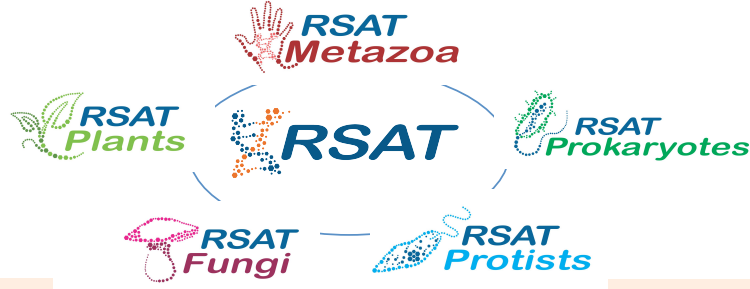
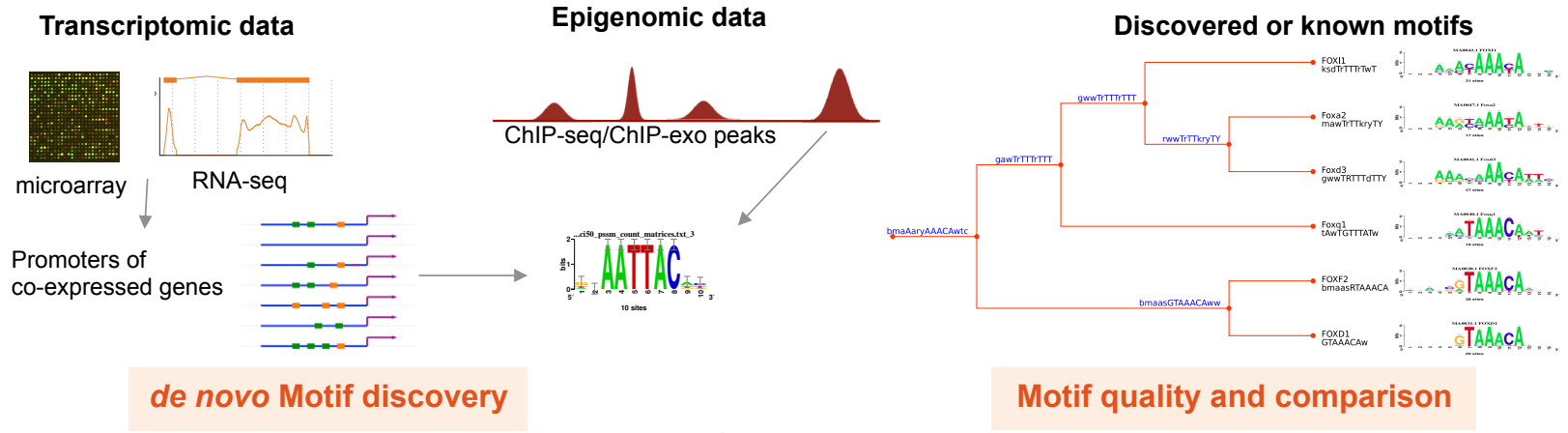
Sequence retrieval
de novo motif discovery
Pattern matching
Motif comparison
Vizualisation

User-friendly interface
Manuals
Demos

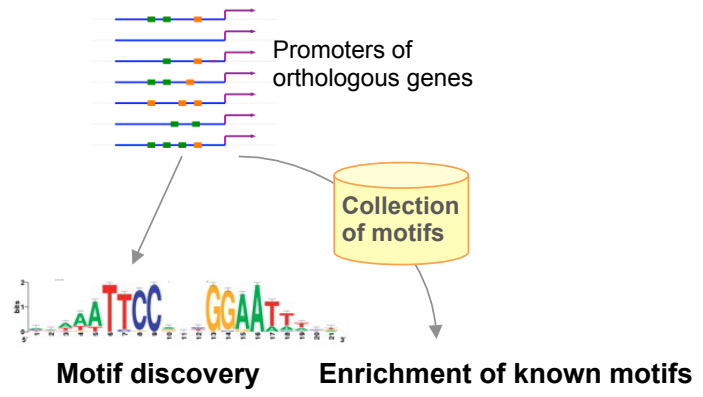
Programmatic access
Public SOAP Web services
Stand-alone (command-line)

Applications

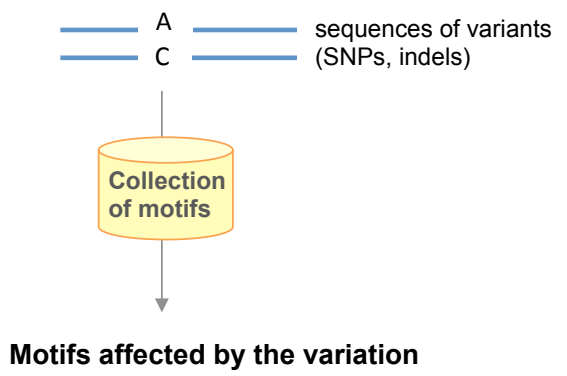
ChIP-seq peaks
Co-expression clusters
Phylogenetic footprints
Regulatory variations



Comparative genomics

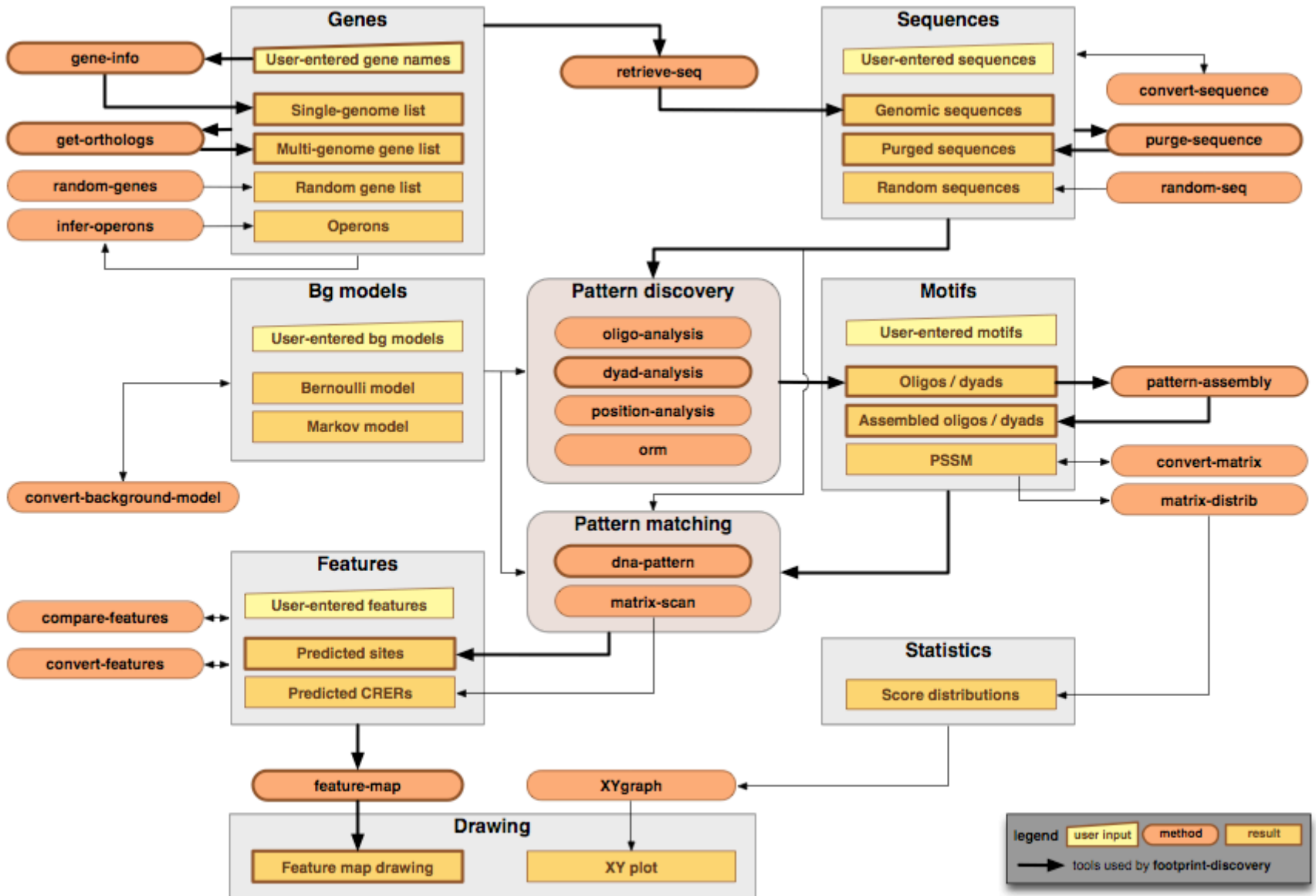


Regulatory variations



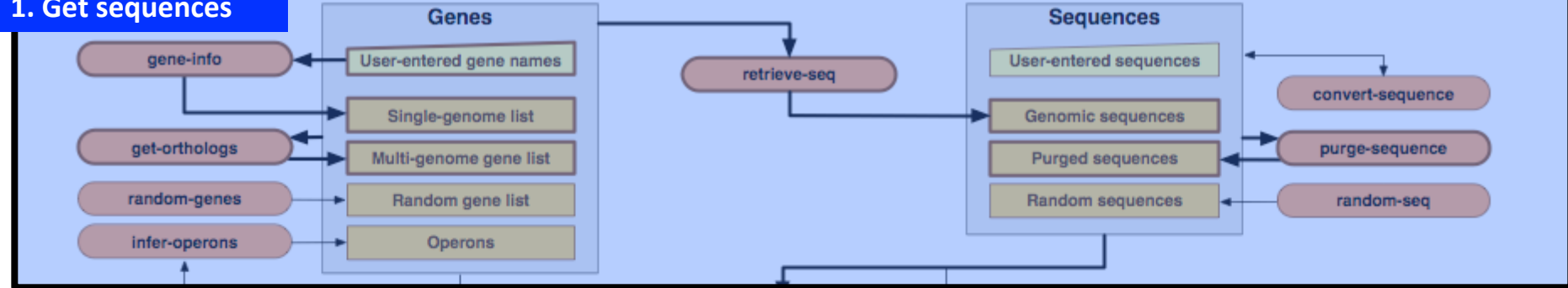
Medina-Rivera*, Defrance*, Sand*, Herrmann, Castro-Mondragon, Delerce, Jaeger, Blanchet, Vincens, Caron, Staines, Contreras-Moreira, Artufel, Charbonnier-Khamvongsa, Hernandez, Thieffry, Thomas-Chollier#, van Helden#. *Nucleic Acids Research*, 2015

Map of the tools

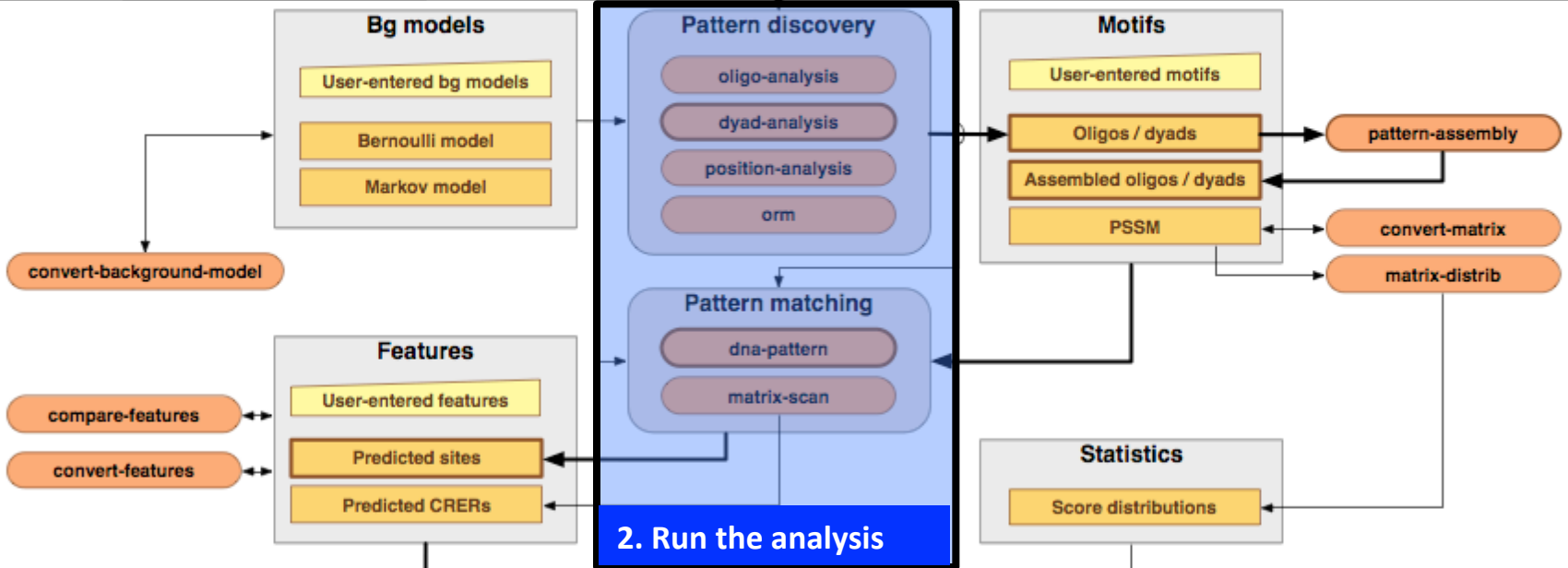


Common RSAT procedure

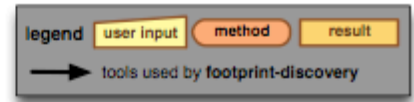
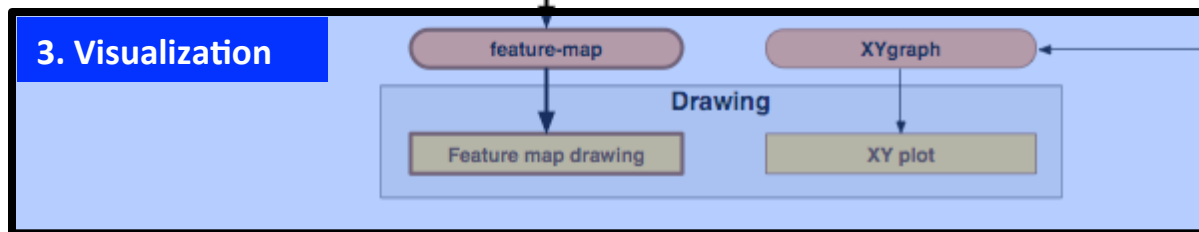
1. Get sequences



2. Run the analysis



3. Visualization



Using RSAT

RSAT NeAT

Regulatory Sequence Analysis Tools

Most popular tools

- retrieve sequence
- oligo-analysis (words)
- matrix-scan (matrices)
- random sequence

> view all tools

Genomes and genes

New!

- Sequence retrieval
- Pattern discovery
- Pattern matching
- Comparative genomics
- Conversion/Utilities
- Drawing
- Web services

New!

Help

- Map of the tools
- Introduction
- Tutorials
- Course
- Contact & Forum New!

Information

Feedback
Jacques van Helden

Sequence retrieval

- retrieve sequence
- retrieve EnsEMBL sequence New!
- purge sequence
- convert sequence
- random sequences

Expandable menus

2. Run the analysis

3. Visualization

Help: tutorials, forum

Information: publications,...

RSAT Web forms

RSA-tools - retrieve sequence

Tool name

Returns upstream, downstream or ORF sequences for a list of genes

Tool description

Remark: If you want to retrieve sequences from an organism that is in the [Ensembl](#) database, we recommend to use the [retrieve-ensembl-seq](#) program instead

Single organism Organism

Multiple organisms

Genes all selection

Upload gene list from file

Query contains only IDs (no synonyms)

Feature type CDS mRNA tRNA rRNA scRNA

Sequence type From To

Prevent overlap with neighbour genes (noorf)

Mask repeats (only valid for organisms with annotated repeats)

Admit imprecise positions

Sequence format

Sequence label

Tool parameters

Output

Go button (launches the analysis)
Demo button (fill in the form for test purposes)

Output server display email

[MANUAL TUTORIAL](#) [MAIL](#)

[Help](#)

Public servers



maintained by TAGC - Université Aix Marseilles, France



maintained by Computational Genomics lab
CCG - UNAM, Cuernavaca, Mexico



maintained by plateforme ABIMS Roscoff, France



maintained by Ecole Normale Supérieure Paris, France



maintained by Bruno Contreras Moreira, Spain



maintained by SLU Global Bioinformatics Center, Uppsala, Sweden

Learning how to use RSAT

? **Which program to use ?** A guide to our main tools for new users.

1 - Choose your type of data to analyse

Choose Data type ▾

2 - Choose your biological question / analysis to perform

Choose selection ▾

3 - Relevant RSAT programs

Choose selection ▾

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maintained by [SLU Global Bioinformatics Center](#), Uppsala, Sweden

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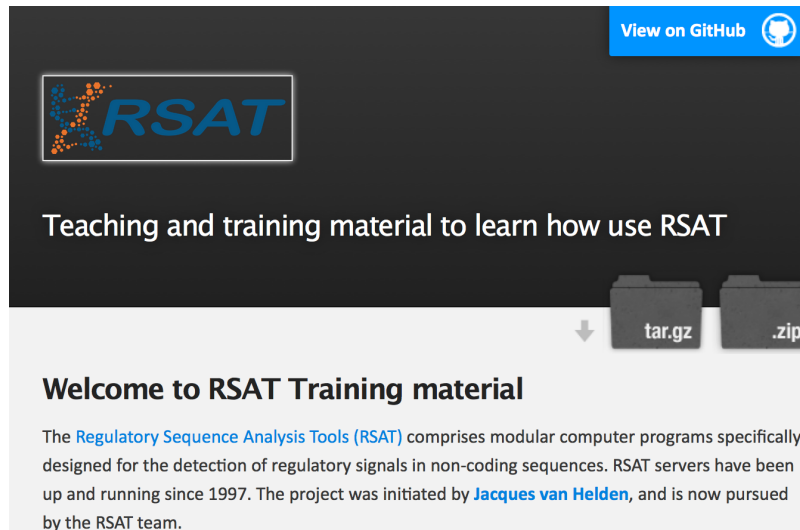
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Training material on GitHub



The screenshot shows the GitHub repository page for RSAT. At the top right, there is a blue button that says "View on GitHub" with the GitHub logo. Below this is the RSAT logo, which consists of the letters "RSAT" in a blue, stylized font with a cluster of orange and blue dots to the left. Underneath the logo, the text reads "Teaching and training material to learn how use RSAT". Below this text, there are two download buttons: one for "tar.gz" and one for ".zip", each with a downward arrow icon. At the bottom of the screenshot, there is a heading "Welcome to RSAT Training material" followed by a paragraph of text: "The [Regulatory Sequence Analysis Tools \(RSAT\)](#) comprises modular computer programs specifically designed for the detection of regulatory signals in non-coding sequences. RSAT servers have been up and running since 1997. The project was initiated by [Jacques van Helden](#), and is now pursued by the RSAT team."