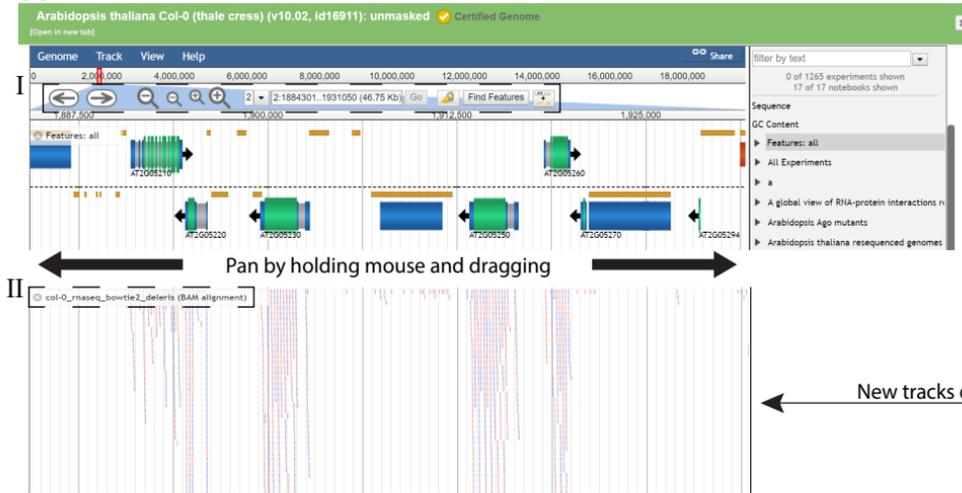
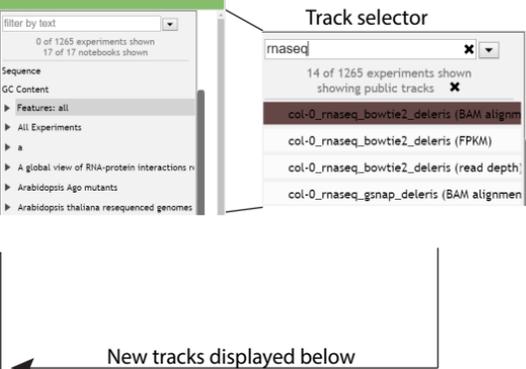


A



B



Introductory view of EPIC-CoGe. (A) An EPIC-CoGe screenshot displaying a segment of *Arabidopsis thaliana* Chromosome 1. Features (i.e., gene models) are shown, with green indicating exonic DNA, blue indicating non-coding or DNA associated with transposable elements (TEs), and gold bars indicating known TEs or repetitive elements. The user can pan across the chromosome by clicking and holding the mouse while dragging, or by hitting the left and right arrows in the main menu bar (Black dashed box denoted by “I”). The user can also increase or decrease the magnification, switch chromosomes, or hide track IDs in this menu bar. Search features are discussed in the text. Additional tracks can be loaded by clicking on them in the track selector shown in (B). Additional tracks will be loaded below your current tracks in the order in which they are selected. Tracks can be rearranged simply by clicking on the track ID (dashed box denoted by “II”) and dragging above or below the track of interest.

A

B

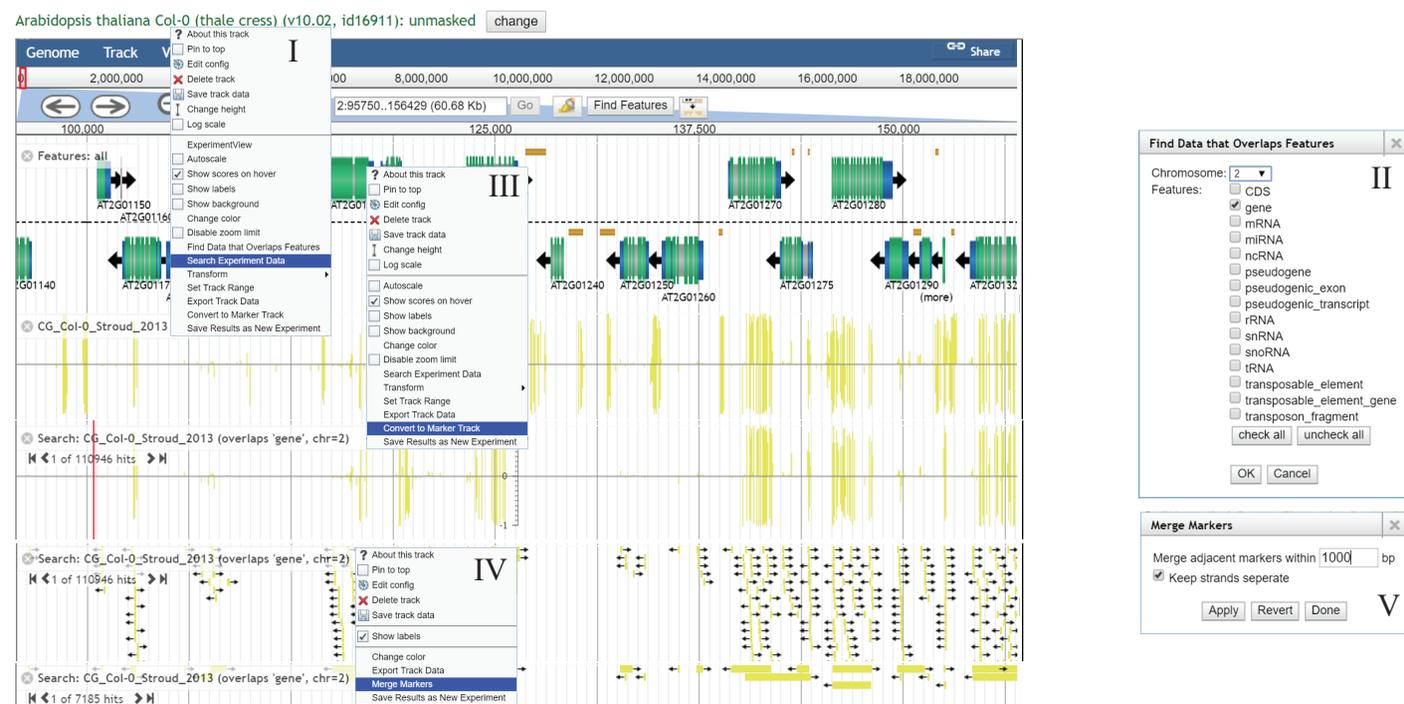
C

D

Search features within EPIC-CoGe. (A) Searching within the track selector. The user can search through the track selector to find any features or experiments associated with the genome being viewed. The total number of experiments and notebooks (both public and privately associated with the user) are indicated directly below the search box (indicated by the black arrow on the left). Users can search for data by name (e.g., rnaseq) and by data type (e.g., bam alignment). The user can also filter by particular criteria (i.e., public or private tracks; black arrow on the right) by clicking on the drop down menu next to the search box. (B) Searching within the viewer. Users can search for particular features based on their ID by clicking on the “Find Features” button within the main viewer (red arrow). This pops up a window that allows the user to enter a search criteria (e.g., “AT2G05210”). In addition, the user can search within a track by clicking on the drop down menu on the track ID. Search options will be listed in the drop down menu (e.g., find types of SNPs). (C) Searching through quantitative data. For certain types of quantitative data such as RNA-seq FPKM data, the user can search the data to find only those data points that fit a user defined criteria. After clicking on the drop down menu and selecting “Search Experimental Data”, a new window will pop up that allows the user to search for the highest value, the lowest value, or a range of values along a particular chromosome. Search results are returned as a new track that can be saved to the user’s CoGe notebook. (D) Identifying data that overlaps features. The user can also identify data that overlaps with certain features (e.g., SNPs that overlap miRNAs). This search function is also found through the drop down menu next to the track ID.



D



Comparing datasets by on-the-fly analyses. Dataset comparisons can be made within EPIC-CoGe, with the results returned as a new searchable and saveable track. By dragging and dropping one track on top of another while holding the control/command key, the user can determine where the query dataset overlaps (A) or does not overlap (B) the subject dataset. Searches are always performed in a query-centric manner so that the query data is returned in the new track. For instance, the user can determine where SNP data overlaps with transcriptional data. By using the SNP data as query, SNPs that overlap with expression data will be returned in the search results (A). To simplify datasets the user can also merge the two tracks (C), resulting in one track with both types of data. (D) When identifying large-scale patterns from many data points (such as epigenetic data), it is possible to simplify the data even further. For example, following a search of methylation data (in yellow) for just peaks that overlap with genes (I and II), there are still a large number of peaks that can be difficult to parse by eye. To simplify this data further, convert the search results to a marker track (III), then merge adjacent markers based on a user defined distance (V). This results in directional data that can quickly be examined. The user can then save these new data tracks in a CoGe notebook or export them to their own computer.

CoGe Search database advanced My Data Tools Help

Arabidopsis thaliana Col-0 (thale cress) (v10.02, id16911): unmasked [change](#)

Genome Track View Help Share filter by text

Details <https://genomeevolution.org/coge/FeatAnno.pl?dsg=16911;chr=1;start=125134;stop=125226>

Position: 125134-125226

CDS

Name(s): FID:306206480, **AT1G01320.1**, AT1G01320.1-Protein

CoGe Links: [CoGeBlast](#), [Fasta](#), [GenomeView](#), [SynFind](#), [FeatView](#)

Length: 5394 nt

Location: Chr 1 121,582-130,099 (-1) :: complement[[join\(121582..123501,123579..123669,123785..123897,123992..124123,124211..124394,124499..all.faa \(v10.02\)](#)]

Dataset: Arabidopsis thaliana Col-0 (thale cress) (v10.02) gid: 16911

Genome: Arabidopsis thaliana Col-0 (thale cress)

Organism: Arabidopsis thaliana Col-0 (thale cress)

Genomic Sequence: unmasked

DNA content: GC: 44.62% AT: 55.38%

Wobble content: GC: 39.1% AT: 60.9%

Additional Metadata

BEST Arabidopsis thaliana protein match is: [Tetratricopeptide repeat \(TPR\)-like superfamily protein \(TAIR:AT4G28080.1\)-](#)

CONTAINS InterPro DOMAIN/s: [Tetratricopeptide-like helical \(InterPro:IPR011990\)](#), [Tetratricopeptide repeat-containing \(InterPro:IPR013026\)](#), [T](#)

EXPRESSED DURING: 14 growth stages-

EXPRESSED IN: 24 plant structures-

FUNCTIONS IN: binding-

LOCATED IN: cellular_component unknown-

note: [Tetratricopeptide repeat \(TPR\)-like superfamily protein-](#)

Short Description: [Tetratricopeptide repeat \(TPR\)-like superfamily protein-](#)

Features: all

AT1G01010

AT1G01020 AT1G01010

Adam

SNPs Ecotype CA

ATRNaseq (rea

CG_Ago3 markers

AT At1NC At%ZORNaseq AT%Z0test

elements shown
books shown

A-protein interacto

l_methylation

mutants

tants

resequenced geno

aliana

Connecting EPIC-CoGe to the CoGe family of tools. Clicking on features within the EPIC-CoGe browser causes a popup to appear with information about that feature (shown). That feature can be easily ported to other CoGe tools by clicking on the CoGe links (arrow).

This box searches only this space. The box at the upper right searches the entire iPlant wiki.

 Search

- Genome Browser in an iframe

CoGe Interoperability / CoGe Interoperability Home
Genome Browser in an iframe

Created by elyons on Feb 04, 2017

Instant genome Browser:

This example uses an iframe to load CoGe's genome browser. Nothing is being hosted on the server and uses one line of HTML:

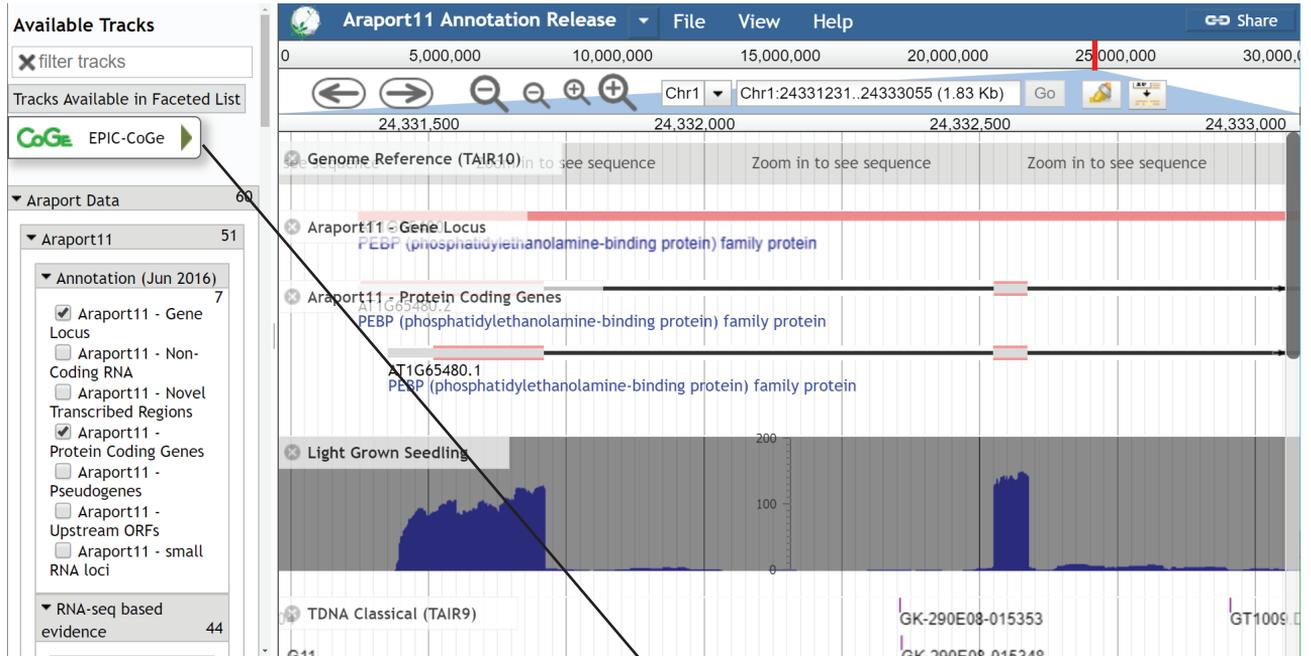
```
< iframe src = "https://genomeevolution.org/coge/GenomeView.pl?gid=16911&embed=1" style = " width : 100% ; height : 100% " ></ iframe >
```

The screenshot displays the CoGe Genome Browser interface. At the top, there are navigation tabs for 'Genome', 'Track', 'View', and 'Help', along with a 'Share' button. Below these is a genomic scale from 5,000,000 to 30,000,000. The main area shows several tracks: 'Features: all' with green arrows representing genes (e.g., AT1G01010, AT1G01040, AT1G01073, AT1G01115, AT1G01180, AT1G01210, AT1G01305, AT1G01355, AT1G01046, AT1G01110, AT1G01160, AT1G01020, AT1G01030, AT1G01060, AT1G01050, AT1G01090, AT1G01140, AT1G01183, AT1G01250, AT1G01320, AT1G01340, AT1G01270), and 'Atha_seedlings (BAM alignment) (coverage depth)' with red vertical bars. A dialog box titled 'Welcome to EPIC-CoGe' is open, listing features like filtering tracks, managing experiments, and exporting data. The dialog also includes a checkbox for 'Show this message when EPIC-CoGe is loaded' and an 'OK' button.

<https://pods.iplantcollaborative.org/wiki/display/CI/Genome+Browser+in+an+iframe>

Embedding EPIC-CoGe into your webpage using an iframe. An example tutorial on how to embed EPIC-CoGe into your webpage. Link to the tutorial is shown below. Additional documentation can be found here: https://genomeevolution.org/wiki/index.php/Embedding_CoGe_JBrowse_in_your_website

https://apps.araport.org/jbrowse/?data=arabidopsis&loc=Chr1%3A24330450..24333884&tracks=TAIR10_gene%2CAraport11_Loci%2CAraport11_gene_models%2CLight_tophat&highlight=



Select Tracks Help

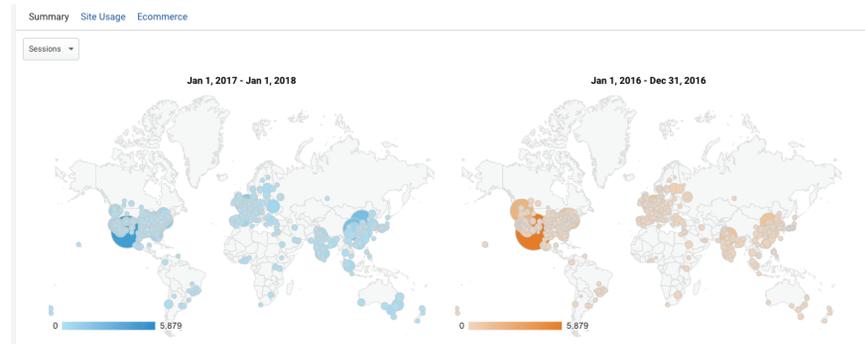
27 tracks

<input type="checkbox"/>	ID	Name	Gene Mutant	Description	Protocol	Processing	Pubmed ID	Lab Name	Platform	Samples	Data Source
<input type="checkbox"/>	1005	CHH_seedling-g-Col-0_Zemach_2_013	seedling-Col-0	CHH	BS-seq		PubMed	Zilberman Lab	Illumina HiSeq 2000	GSM1093629	CoGe
<input type="checkbox"/>	1013	MNase_Col-0_Zemach_2_013	Col-0	MNase	MNase-seq		PubMed	Zilberman Lab	Illumina Genome Analyzer II	GSM1014126	CoGe

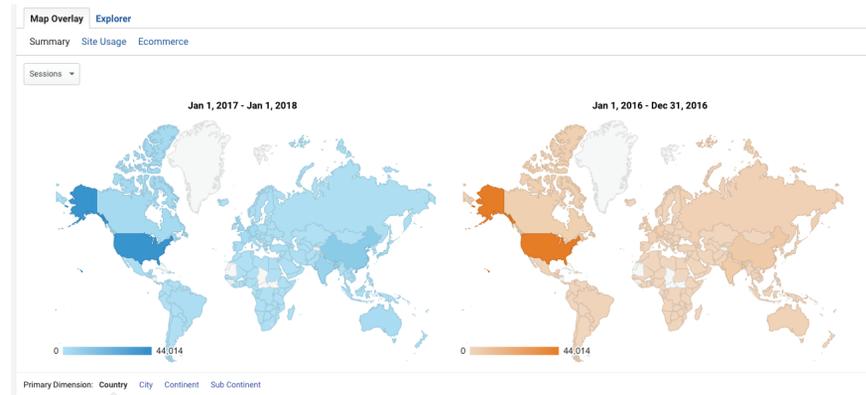
CoGe's REST API at work. Public genome and experimental datasets stored in CoGe can be displayed in your own genome browser by using CoGe's REST API. Shown is a screenshot of Araport11's genome browser with an EPIC-CoGe link. By clicking on the EPIC-CoGe link, a window pops up with information about the publicly available datasets that can be imported into the genome browser. A link to the Araport genome browser is shown. Documentation to CoGe's REST API can be found here:

https://docs.google.com/document/d/1GXOPIVvyTwoGR2IRjDNmdd2nj_6d8db7jx9hG8RxTDc/edit

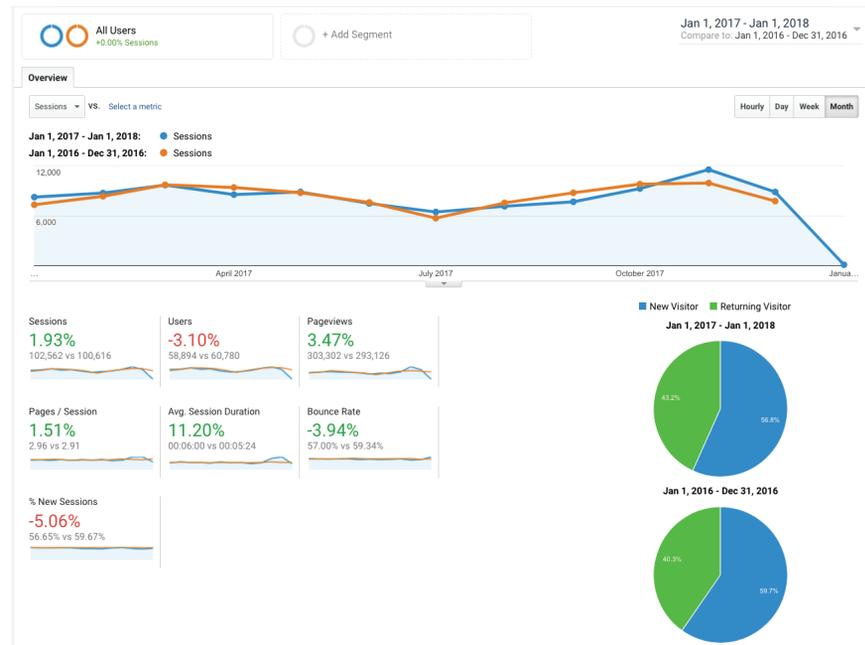
A



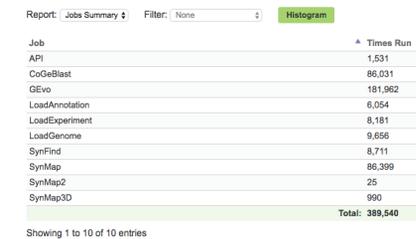
B



C



D



E



CoGe usage over the last two years. (A) Google Analytics report on CoGe usage over the past two years per city and (B) per country. (C) Monthly usage reports show that over the past two years CoGe has had approximately 100,000 sessions, 300,000 page views, and 60,000 users from nearly every country in the world. (D) Internal analytics tracking CoGe usage by application and (E) the number of genomes and experiments loaded into CoGe in the last five years.