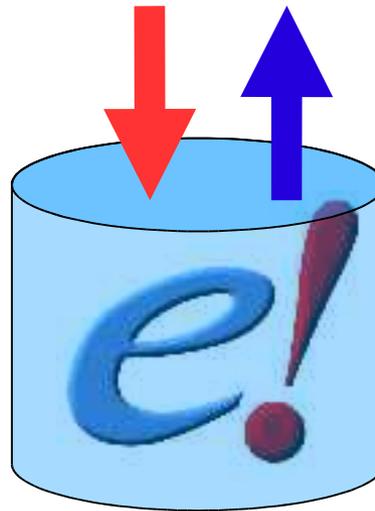


Ensembl and DAS



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Wellcome Trust Sanger Institute
April 2006

DAS and Ensembl

- DAS Essentials
- Ensembl as DAS server
- Adding DAS sources to Ensembl views
- DAS configuration in Ensembl
- DAS code in Ensembl
- Future development



DAS Essentials

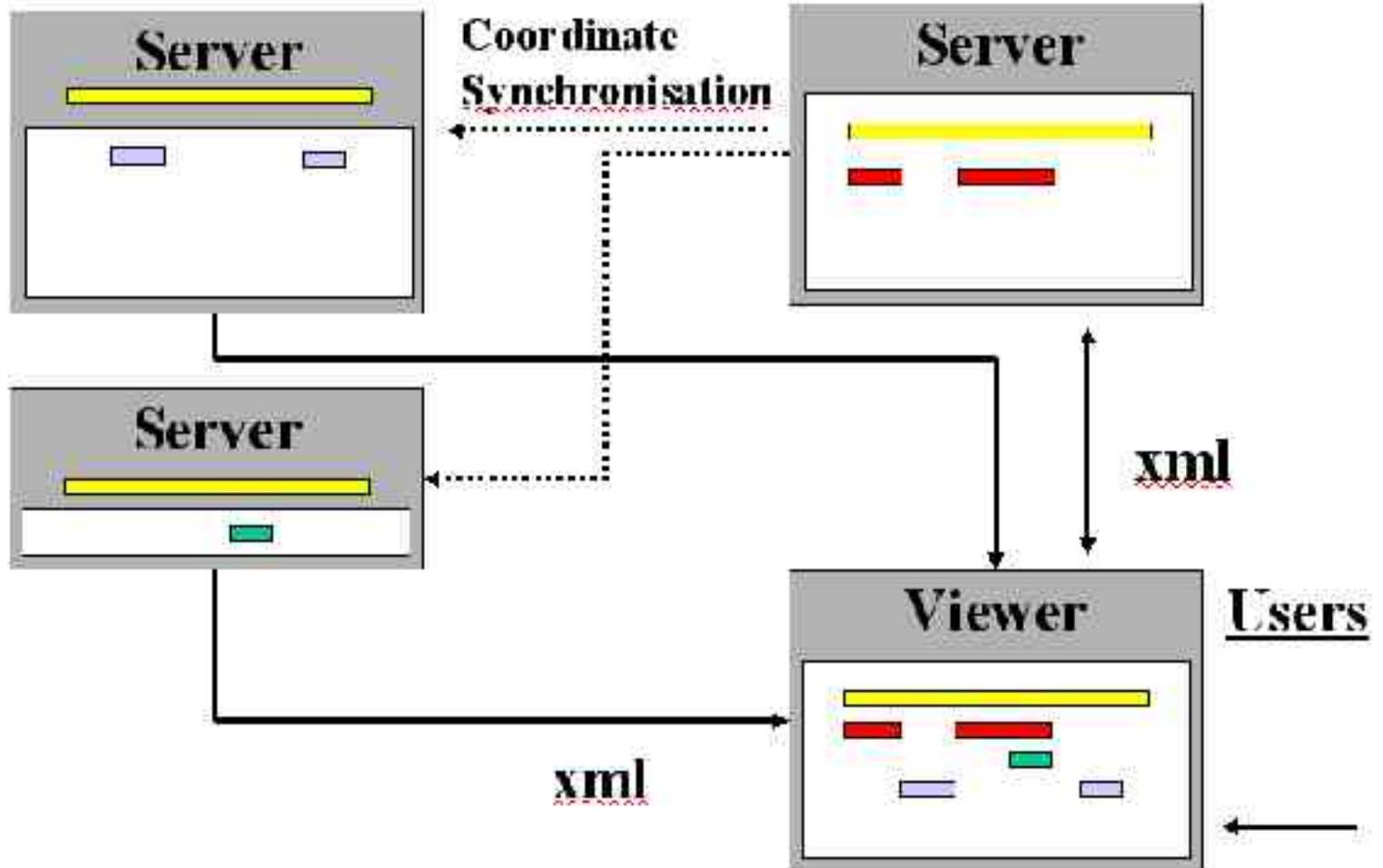
- Distributed Annotation System (DAS);
 - A server system for the sharing of Reference Sequences, and their annotations.
- DAS servers:
 - Reference server
 - Annotation server
- DAS requests:
 - dns
 - entry_points
 - dna
 - features
- Ensembl as DAS server:

<http://www.biodas.org/documents/spec.html>

Distributed Annotation System

External Contributors

Database providers



Ensembl

DAS Essentials

`features` - Get the annotations

http://www.ebi.ac.uk/das-srv/asd/das/atd_human/features?segment=13:3770000,3810000

```
<?xml version="1.0" standalone="yes"?>
<!DOCTYPE DASSET SYSTEM "http://www.biodas.org/dtd/dasgdf.dtd" >
<DASSET>
  <GDF version="1.0" href="http://www59-codel.ebi.ac.uk:9100/das/asd_human/features">
    <SEGMENT id="13" version="1.0" start="3770000" stop="3810000">
      <FEATURE id="5438:1.215740" label="6438:1.215740">
        <TYPE id="exon" reference="no" subparts="no" superparts="no">exon</TYPE>
        <START>3265804</START>
        <END>3258215</END>
        <ORIENTATION>--</ORIENTATION>
        <LINK href="http://www.ebi.ac.uk/asc_srv/Atd.cgi?ret=cd-TRANSCRIPT;origin=AT;product=
        <GROUP id="5438" label="ENSG00000133121 AT-1" />
      </FEATURE>
      <FEATURE id="5438:1.215741" label="6438:1.215741">
        <TYPE id="exon" reference="no" subparts="no" superparts="no">exon</TYPE>
        <START>3263887</START>
        <END>3253978</END>
        <ORIENTATION>--</ORIENTATION>
        <LINK href="http://www.ebi.ac.uk/asc_srv/Atd.cgi?ret=cd-TRANSCRIPT;origin=AT;product=
        <GROUP id="5438" label="ENSG00000133121 AT-1" />
      </FEATURE>
      <FEATURE id="5438:1.215742" label="6438:1.215742">
        <TYPE id="exon" reference="no" subparts="no" superparts="no">exon</TYPE>
        <START>3263475</START>
        <END>3253754</END>
        <ORIENTATION>--</ORIENTATION>
        <LINK href="http://www.ebi.ac.uk/asc_srv/Atd.cgi?ret=cd-TRANSCRIPT;origin=AT;product=
        <GROUP id="5438" label="ENSG00000133121 AT-1" />
      </FEATURE>
    </SEGMENT>
  </GDF>
</DASSET>
```

Ensembl as DAS server

- list of reference sources

<http://www.ensembl.org/das/dsn>

```

- <DSN>
  <SOURCE id= 'Homo_sapiens' version= 37_35j">Homo_sapiens</SOURCE>
  <MAPMASTER>http://www.ensembl.org/das/Homo_sapiens</MAPMASTER>
- <DESCRIPTION>
  Homo_sapiens Reference server based on NCBI35. Contains 111 entry points of the highest assembly tier.
</DESCRIPTION>
</DSN>
- <DSN>
  <SOURCE id= 'Macaca_mulatta' version= "37_1a">Macaca_mulatta</SOURCE>
  <MAPMASTER>http://www.ensembl.org/das/Macaca_mulatta</MAPMASTER>
- <DESCRIPTION>
  Macaca_mulatta Reference server based on MMUL_0_1. Contains 192158 entry points of the highest assembly tier.
</DESCRIPTION>
</DSN>
<DSN>
  <SOURCE id= 'Monodelphis_domestica' version= "37_2a">Monodelphis_domestica</SOURCE>
  <MAPMASTER>http://www.ensembl.org/das/Monodelphis_domestica</MAPMASTER>
- <DESCRIPTION>
  Monodelphis_domestica Reference server based on BROADO2. Contains 5078 entry points of the highest assembly tier.
</DESCRIPTION>
</DSN>

```



Ensembl as DAS server

- list of entry points

http://www.ensembl.org/das/Homo_sapiens.current.reference/entry_points

http://www.ensembl.org/das/Homo_sapiens.NCBI36.reference/entry_points

-<DASEP>

-<ENTRY_POINTS href="http://www.ensembl.org/das" version="1.0">

<SEGMENT id="1" start="1" stop="245522847" orientation="+">1</SEGMENT>

<SEGMENT id="10" start="1" stop="135113628" orientation="+">10</SEGMENT>

<SEGMENT id="10_NT_079544" start="1" stop="115275" orientation="-">10_NT_079544</SEGMENT>

<SEGMENT id="11" start="1" stop="134152384" orientation="+">11</SEGMENT>

<SEGMENT id="12" start="1" stop="132449811" orientation="+">12</SEGMENT>

<SEGMENT id="12_NT_091701" start="1" stop="166818" orientation="-">12_NT_091701</SEGMENT>

<SEGMENT id="13" start="1" stop="114142980" orientation="+">13</SEGMENT>

<SEGMENT id="13_NT_078092" start="1" stop="186858" orientation="-">13_NT_078092</SEGMENT>

<SEGMENT id="14" start="1" stop="106368585" orientation="+">14</SEGMENT>

<SEGMENT id="15" start="1" stop="100338915" orientation="+">15</SEGMENT>

<SEGMENT id="15_NT_079546" start="1" stop="139280" orientation="-">15_NT_079546</SEGMENT>

<SEGMENT id="15_NT_079547" start="1" stop="168820" orientation="-">15_NT_079547</SEGMENT>

<SEGMENT id="15_NT_079548" start="1" stop="119514" orientation="-">15_NT_079548</SEGMENT>

<SEGMENT id="15_NT_079549" start="1" stop="111861" orientation="-">15_NT_079549</SEGMENT>

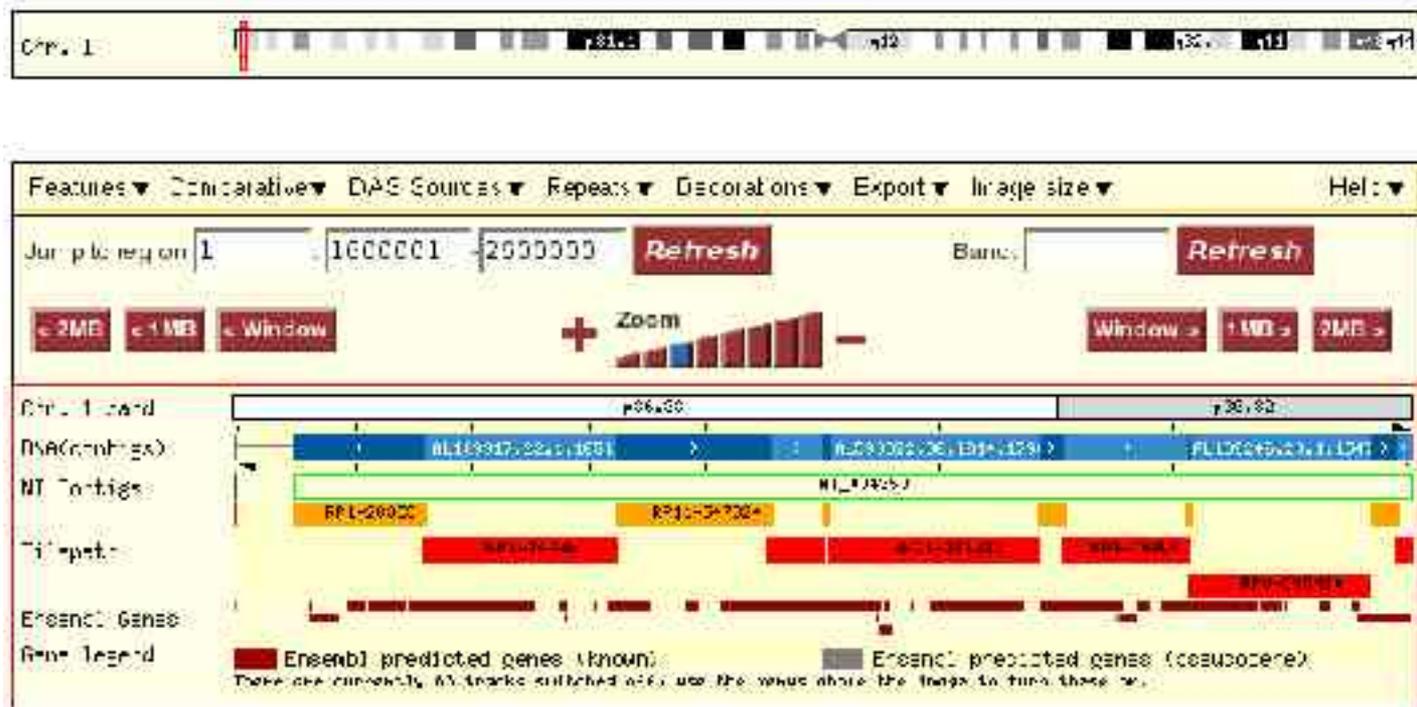
<SEGMENT id="15_NT_079553" start="1" stop="44888" orientation="-">15_NT_079553</SEGMENT>

<SEGMENT id="16" start="1" stop="88827254" orientation="+">16</SEGMENT>

Ensembl

Ensembl as DAS server

- Exploring assembly





Ensembl as DAS server

- Exploring assembly:

http://www.ensembl.org/das/Homo_sapiens.current.reference/features?segment=1:1,1000000

```
<DASGET>
<GFF>
- <SEGMENT id="1" start="1" stop="1000000">
  - <FEATURE id="1">
    <START>1<START>
    <STOP>1000000<STOP>
    <TYPE id="chromosome" category="component" reference="yes" superparts="no" subparts="yes">chromosome</TYPE>
    <TARGET id="1" start="1" stop="1000000">1</TARGET>
  </FEATURE>
  - <FEATURE id="supercontig:NT_077912">
    <START>557583<START>
    <STOP>511231<STOP>
    <TYPE id="supercontig" category="component" reference="yes" superparts="yes" subparts="yes">supercontig</TYPE>
    <TARGET id="NT_077912" start="1" stop="133649">supercontig:NT_077912</TARGET>
  </FEATURE>
  <FEATURE id="supercontig:NT_077913">
    <START>561232<START>
    <STOP>1000000<STOP>
    <TYPE id="supercontig" category="component" reference="yes" superparts="yes" subparts="yes">supercontig</TYPE>
    <TARGET id="NT_077913" start="1" stop="435764">supercontig:NT_077913</TARGET>
  </FEATURE>
  <FEATURE id="supercontig:NT_077402">
    <START>1<START>
    <STOP>167280<STOP>
```

Ensembl



Ensembl as DAS server

- Exploring assembly:
http://www.ensembl.org/das/Homo_sapiens.current.reference/features?segment=NT_077912

```

-<DASGFF>
-<GFF>
  <SEGMENT id="NT_077912" start="" stop="">
    -<FEATURE id="NT_077912">
      <START/>
      <STOP/>
      <TYPE id="supercontig" category="component" reference="yes" superparts="yes" subparts="yes">supercontig</TYPE>
      <TARGET id="NT_077912" start="" stop="">NT_077912</TARGET>
    </FEATURE>
    <FEATURE id="clone:AL732372.15">
      <START>1</START>
      <STOP>153649</STOP>
      <TYPE id="clone" category="component" reference="yes" superparts="yes" subparts="yes">clone</TYPE>
      <TARGET id="AL732372.15" start="1" stop="153649">clone:AL732372.15</TARGET>
    </FEATURE>
    -<FEATURE id="chromosome:1">
      <START>1</START>
      <STOP>153649</STOP>
      <TYPE id="chromosome" category="supercomponent" reference="yes" superparts="no" subparts="yes"/>
      <TARGET id="1" start="357383" stop="5112315">
    </FEATURE>
  </SEGMENT>
</GFF>
</DASGFF>

```

Ensembl



Ensembl as DAS server

- Exploring assembly:
http://www.ensembl.org/das/Homo_sapiens.current.reference/features?segment=AL732372.15.1.153649

```
- <DASGET>
- <GET>
  - <SEGMENT id="AL732372.15.1.153649" start="" stop="">
    - <FEATURE id="AL732372.15.1.153649">
      <START/>
      <STOP/>
      <TYPE id="contig" category="component" reference="yes" superparts="yes" subparts="no">contig</TYPE>
      <TARGET id="AL732372.15.1.153649" start="" stop="">AL732372.15.1.153649</TARGET>
    </FEATURE>
  - <FEATURE id="clone:AL732372.15">
    <START>1</START>
    <STOP>153649</STOP>
    <TYPE id="clone" category="supercomponent" reference="yes" superparts="yes" subparts="yes" />
    <TARGET id="AL732372.15" start="1" stop="153649" />
  </FEATURE>
</SEGMENT>
</GET>
</DASGET>
```

Ensembl



Ensembl

Ensembl as DAS server

- Exploring assembly:

http://www.ensembl.org/das/Homo_sapiens.current.karyotype/features?segment=22

```
- <SEGMENT id="22" start="1" stop="49591432">
  - <FEATURE id='p11.1'>
    <START>9607114</START>
    <STOP>11808744</STOP>
    <TYPE id='acen'>acen</TYPE>
    <METHOD id='ensembl'>ensembl</METHOD>
    <ORIENTATION/>
  </FEATURE>
  - <FEATURE id='p11.2'>
    <START>6604891</START>
    <STOP>9607113</STOP>
    <TYPE id='gvar'>gvar</TYPE>
    <METHOD id='ensembl'>ensembl</METHOD>
    <ORIENTATION/>
  </FEATURE>
  - <FEATURE id='p12'>
    <START>3002224</START>
    <STOP>6604890</STOP>
    <TYPE id='stalk'>stalk</TYPE>
    <METHOD id='ensembl'>ensembl</METHOD>
    <ORIENTATION/>
  </FEATURE>
```

e!

Ensembl

Adding DAS source to Ensembl



Ensembl

Adding DAS source to Ensembl

- **Switch on pre-configured server**
- **Set up your own server**
(ProServer, Dazzle, LDAS – see Ensembl docs)
- **Configure an existing server**
- **Upload your own data**
- **View your data**
- **Send your source to a colleague**
- **Web-based sources (Contigview & Cytoview only)**

Switch on a pre-configured source in geneview, protview, transview

Gene DAS Report

DAS Sources

- [AltaiBase](#) (Alternative splice database)
- [ALTtrans](#) (Alternative Transcript Diversity Database)
- [ArrayExpress](#) (Gene Expression Database)
- [GAD](#) (Genetic Association Database)
- [HGNC](#) (HUGO Gene Nomenclature Committee)
- [HUGO_text](#) (PubMedical mining via HUGO Databases)
- [Phenotypes](#) (Associated directly or via orthologues or protein families)
- [Protomap](#) (Global classification of proteins into hierarchical clusters)
- [Resourcerer](#) (Knowledgebase of biological processes)
- [UniProt](#) (Protein knowledge base)

Switch on a pre-configured source in contigview and cytoview

E Detailed view

The screenshot shows the Ensembl genome browser interface. On the left, there is a navigation pane with various tracks and filters. The main area displays a genomic map with tracks for 'GeneTrack', 'RepeatMasker', and 'RepeatMasker'. A 'Refresh' button is visible at the top right of the main area.

Set up your own DAS source

- ProServer
 - ♦ <http://www.sanger.ac.uk/Software/analysis/proserver/>
- Dazzle
 - ♦ <http://www.biojava.org/dazzle/>
- LDAS
 - ♦ <http://biodas.org/servers/LDAS.html>

and register with DAS Registry !

<http://das.sanger.ac.uk/registry>



DAS Registry

url	http://www.ebi.ac.uk/das-srv/uniprot/das/arkistotle/
unique id	DS_109
nickname	uniprot
display in DAS clients	<input type="checkbox"/> VSDICE <input checked="" type="checkbox"/> EMB-EMBL <input checked="" type="checkbox"/> DASsty
description	<p>The UniProt DAS Reference Server serves both sequence and feature data from UniProt/Swiss-Prot and UniProt/TrEMBL. In addition to this, feature links to InterPro for all the proteins in UniProt are provided, including basic information (position, etc) and a brief description) and internet addresses to the relevant data source. The following kinds of protein ID / Accession number can be used: UniProt Accession numbers e.g. Q36502 Swiss-Prot IDs e.g. A/Human TrEMBL IDs e.g. Q12368 IPI IDs e.g. IPI00016171 UniProt IDs e.g. LP00001250361 or a full description of the service, visit: http://www.ebi.ac.uk/uniprot-das/</p>
admin email	uniprot-das_AT_ebi.ac.uk
homepage	http://www.ebi.ac.uk/uniprot-das/
DAS capabilities	sequence features entry points stylesheet
Team Code	PROPRC
Coordinate Systems	UniProt, Protein Sequence
Registered at	2005.03.21
Last tested successfully at	2006.03.17
label(s)	EMBL, TrEMBL, UniProt
	send this das source to a friend
	validate server
	edit this server. (das source admin only)
	remove this server. (das source admin only)

EMBL



Configure an existing source

e!Ensembl Human Database View Class: Human

Ensembl v57c 11/15/2009 Help

Manage Sources

- Add Data Source
- Update your data



DAS sources

Name	DAS Server	Data Source	Coordinate System
 AHS Data	http://www.ebi.ac.uk/ena/ahs/ahsdata/	ahs_gene	EnsemblGene ID
 AHS Data	http://www.ebi.ac.uk/ena/ahs/ahsdata/	ahs_gene	EnsemblGene ID
 Array Express	http://www.ebi.ac.uk/ena/array-express/	array-express	HyperGenes-ProtAcc
 GAD	http://www.ebi.ac.uk/ena/gad/gaddata/	gad	HUGO ID
 HSCG	http://hygiene.gcf.ac.uk/HSCG/data/	HSCG	EnsemblGene ID
 HCCO_01	http://www.ebi.ac.uk/ena/hcco/hcco01/	hcco01	HUGO ID
 HEP Array	http://www.ebi.ac.uk/ena/hep/heparray/	hep_array	EnsemblGene ID
 Heparin	http://www.proteincentral.org/hsa/	protein	UniprotGene-ProtAcc
 Heparin	http://www.proteincentral.org/hsa/	GC_uniprot	UniprotGene-ProtAcc
 HEP Array	http://www.ebi.ac.uk/ena/hep/heparray/	hep_array	UniprotGene-ProtAcc
 HEP Array (DBP) VAF	http://www.ebi.ac.uk/ena/hep/heparray/	hep_array (DBP) VAF	EnsemblGene ID
 HEP Array	http://www.ebi.ac.uk/ena/hep/heparray/	HEP Array	HyperGenes-ProtAcc
 HEP Array	http://www.ebi.ac.uk/ena/hep/heparray/	HEP Array	HyperGenes-ProtAcc

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Ensembl

Configure an existing source

DAS Wizard Step 2 of 3: Data appearance

Coordinate System

- Ensembl Gene ID
- Ensembl Location
- Chromosome
- Contig
- Contig
- Contig
- NT Contig
- Ensembl Peptide ID
- Ensembl Transcript ID
- Entrez Gene ID
- HUGO ID
- IPI Accession
- IPI ID
- UniprotSwiss-Prot Name
- UniprotSwiss-Prot Acc

Enable on

- geneview
- intronview
- cytobandview
- proteinview
- cdnaview

Back **Next**

Configure an existing source

DAS Wizard Step 3 of 3: Display configuration

Name:	<input type="text" value="slingshot"/>
Track label:	<input type="text" value="slingshot"/>
Hide URL:	<input type="text"/>
Link track:	<input type="text"/>
Link URL:	<input type="text"/>
Track colour:	<input type="text" value="0.00"/>
Group features:	<input type="text" value="No"/>
Display on:	<input type="text" value="Both strands"/>
Max rows to display:	<input type="text" value="10 rows"/>
Label features:	<input type="text" value="Gene features"/>
Apply stylesheet:	<input type="text" value="No"/>
Use score:	<input type="text" value="No"/>

Configure an existing source

DAS sources

	Name	DAS Server	Data Source	Coordinate System
	NCBIsplice	http://www.ncbi.nlm.nih.gov/was/das	ncbi_splice	Ensembl Gene ID
	Alltrans	http://www.ebi.ac.uk/das/was/das	all_gene	Ensembl Gene ID
	ArrayExpress	http://www.ebi.ac.uk/das/arrayexpress/das	arrayexpress	UniProt Swiss-Prot Acc
	gaf	http://www.ebi.ac.uk/das/wgencode/das	gaf	HUGO ID
	HGN	http://www.genenames.org/HGN/das	HGN	Ensembl Gene ID
	HUGO_link	http://www.ebi.ac.uk/das/wgencode/das	linking	HUGO ID
	Phenotype	http://www.ebi.ac.uk/das/wgencode/das	phenotype	Ensembl Gene ID
	Protein	http://www.protein.org.uk/das	protein	UniProt Swiss-Prot Acc
	Proteome	http://www.proteome.org.uk/das	SK_human	UniProt Swiss-Prot Acc
	UniProt	http://www.ebi.ac.uk/das/uniprot/das	uniprot	UniProt Swiss-Prot Acc
	HydrexL_000129	http://www.ebi.ac.uk/das	HydrexL_000129	Ensembl Local ID
	TRILL-DAS	http://www.ebi.ac.uk/das/trill/das	TRILL	UniProt Swiss-Prot Acc
	UniProt	http://www.ebi.ac.uk/das/wgencode/das	linking	UniProt Swiss-Prot Acc



Upload your data

- File format:
 - annotation section

<http://www.sanger.ac.uk/Software/formats/GFF/>

- stylesheet section

http://www.ensembl.org/info/data/external_data/das/CSS_support.pdf

- Examples:

http://www.ensembl.org/info/data/external_data/das/das_upload_v1.euf

Ensembl



Upload your data

DAS Wizard Step 1 of 3: Data location

Please provide your data location

Please [READ THE UPLOAD INSTRUCTIONS CAREFULLY](#) before uploading any data. Your data must be formatted correctly before upload will work properly. The instructions page has detailed information about the data format.

Please read and understand the [Ensembl policy on uploaded data](#)

Email

Password
your email and password to ensure that nobody else can modify your annotation

Paste your data

or choose a file to upload

Upload File:

If you want to update an existing annotation on Ensembl DAS Server enter its Data Source Name and select your action

Data source

Action Overwrite append

Files marked with * are required

Ensembl

Upload your data

DAS Wizard Step 2 of 3: Data appearance

Successfully uploaded stylesheet
 Successfully uploaded 11 entries
 A new DAS source has been created at http://www.ensembl.org/das/hydra/uf_00001000

Coordinate System genomic location

Enable on

<input checked="" type="checkbox"/> geneview	<input type="checkbox"/> protein
<input type="checkbox"/> transview	<input type="checkbox"/> contigview
<input type="checkbox"/> cytview	

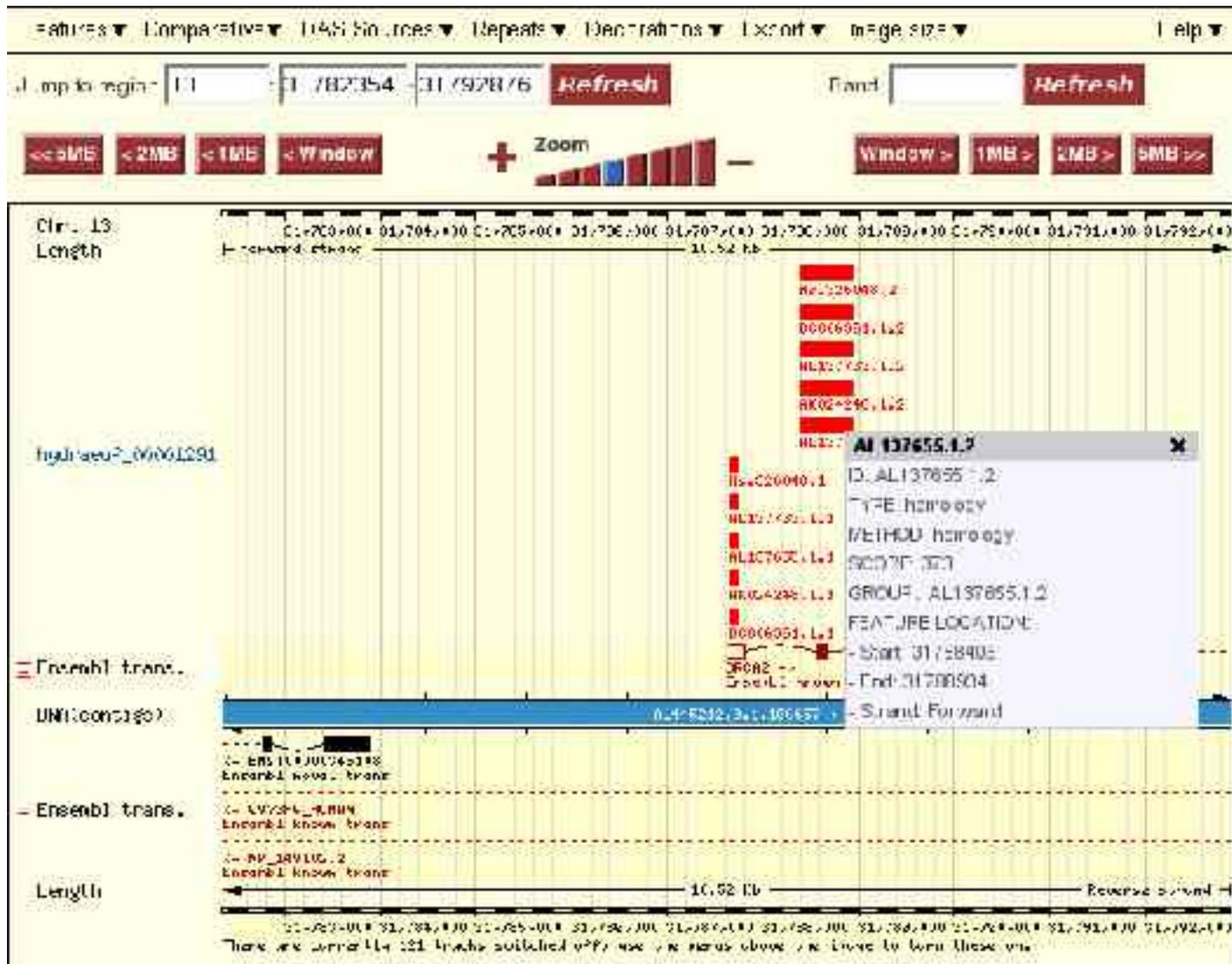
Back **Next**

View your data in geneview

Gene DAS Report

hydraeuf_00001291	homology AK024248.1.1	homology	Feature contained by gene	373.00
	homology AK024248.1.2	homology	Feature contained by gene	373.00
	homology AL137855.1.1	homology	Feature contained by gene	373.00
	homology AL137855.1.2	homology	Feature contained by gene	373.00
	homology AL137733.1.1	homology	Feature contained by gene	354.00
	homology AL137733.1.2	homology	Feature contained by gene	354.00
	homology BC006361.1.1	homology	Feature contained by gene	354.00
	homology BC006361.1.2	homology	Feature contained by gene	354.00
	homology Hs.326048.1	homology	Feature contained by gene	373.00
	homology Hs.326048.2	homology	Feature contained by gene	373.00
DAS Sources	<input type="checkbox"/>	AltSplice	(Alternative spliced database)	
	<input type="checkbox"/>	AltTrans	(Alternative Transcript Diversity Database)	
	<input type="checkbox"/>	ArrayExpress	(Gene Expression Database)	
	<input type="checkbox"/>	GAD	(Genetic Association Database)	
	<input type="checkbox"/>	HGNC	(HUGO Gene Nomenclature Committee)	
	<input type="checkbox"/>	HUGO_text	(PubMed text-mining via HUGO symbol)	
	<input type="checkbox"/>	PRIDE-DAS		
	<input type="checkbox"/>	Phenotypes	(Associated directly or via orthologues or protein families)	
	<input type="checkbox"/>	Protonet	(Global classification of proteins into hierarchical clusters)	
	<input type="checkbox"/>	Reactome	(Knowledgebase of biological processes)	
	<input type="checkbox"/>	UniProt	(Protein knowledgebase)	
	<input checked="" type="checkbox"/>	hydraeuf_00001291		
	<input type="button" value="Manage Sources"/>			

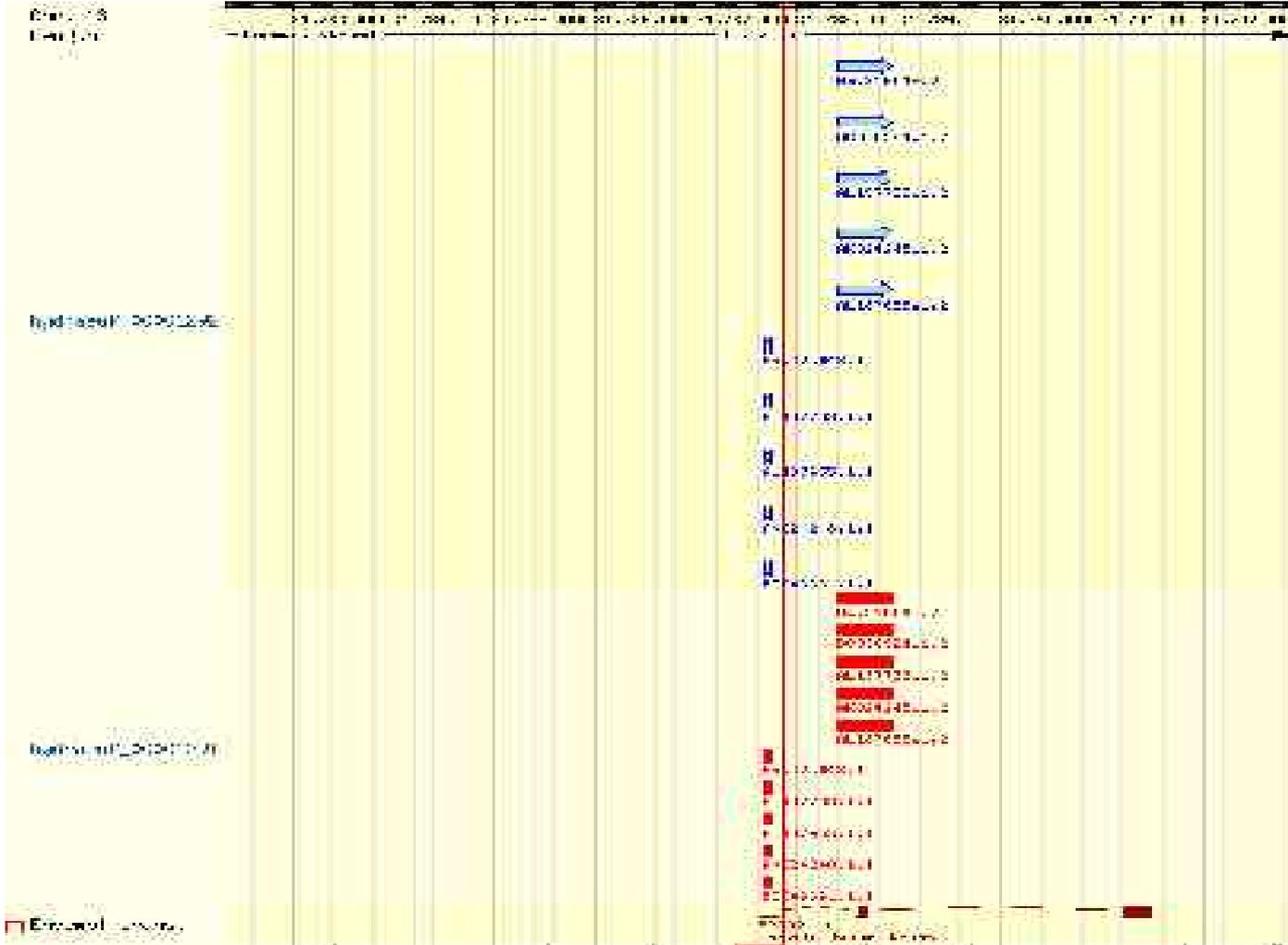
View your data in contigview



Ensembl

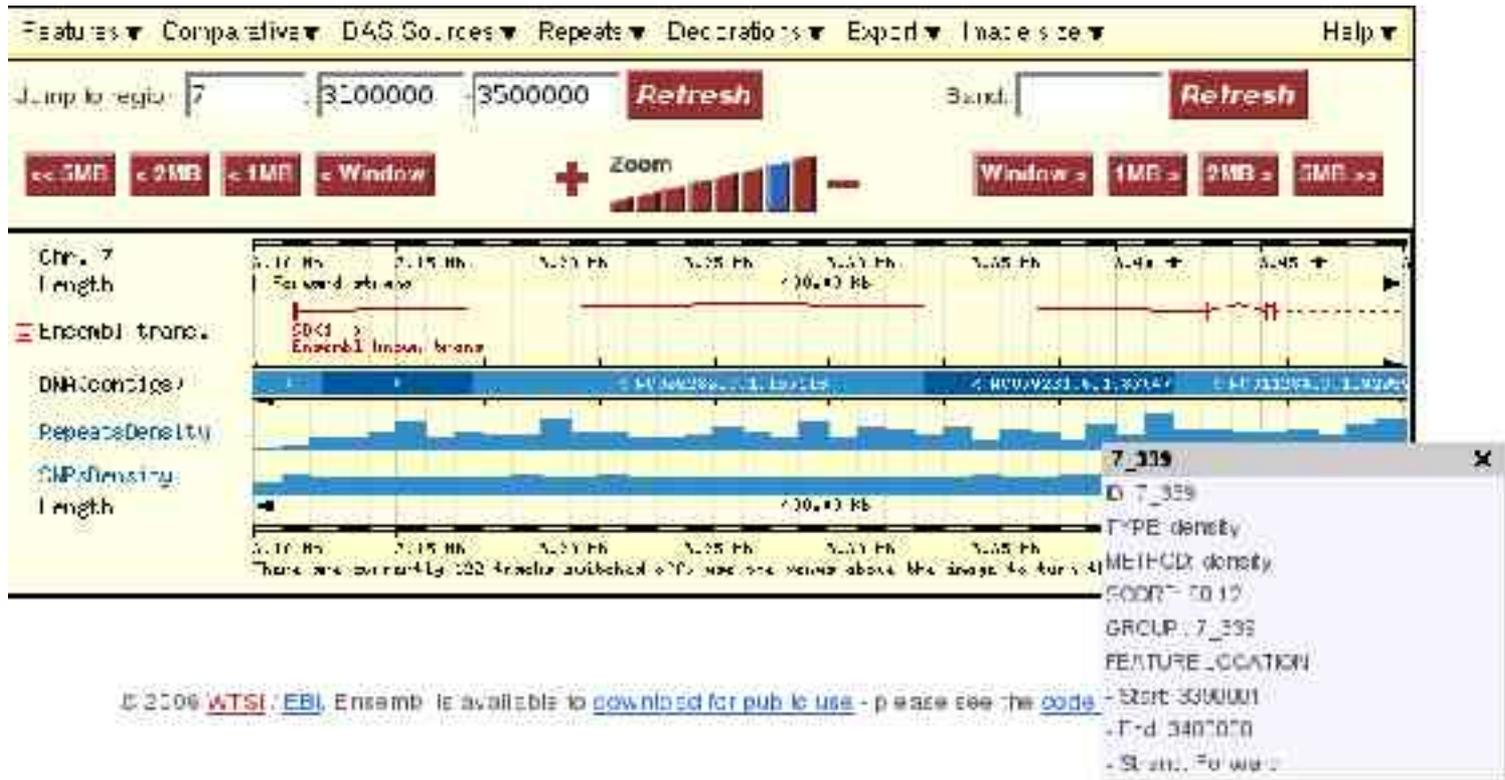


Applying stylesheet



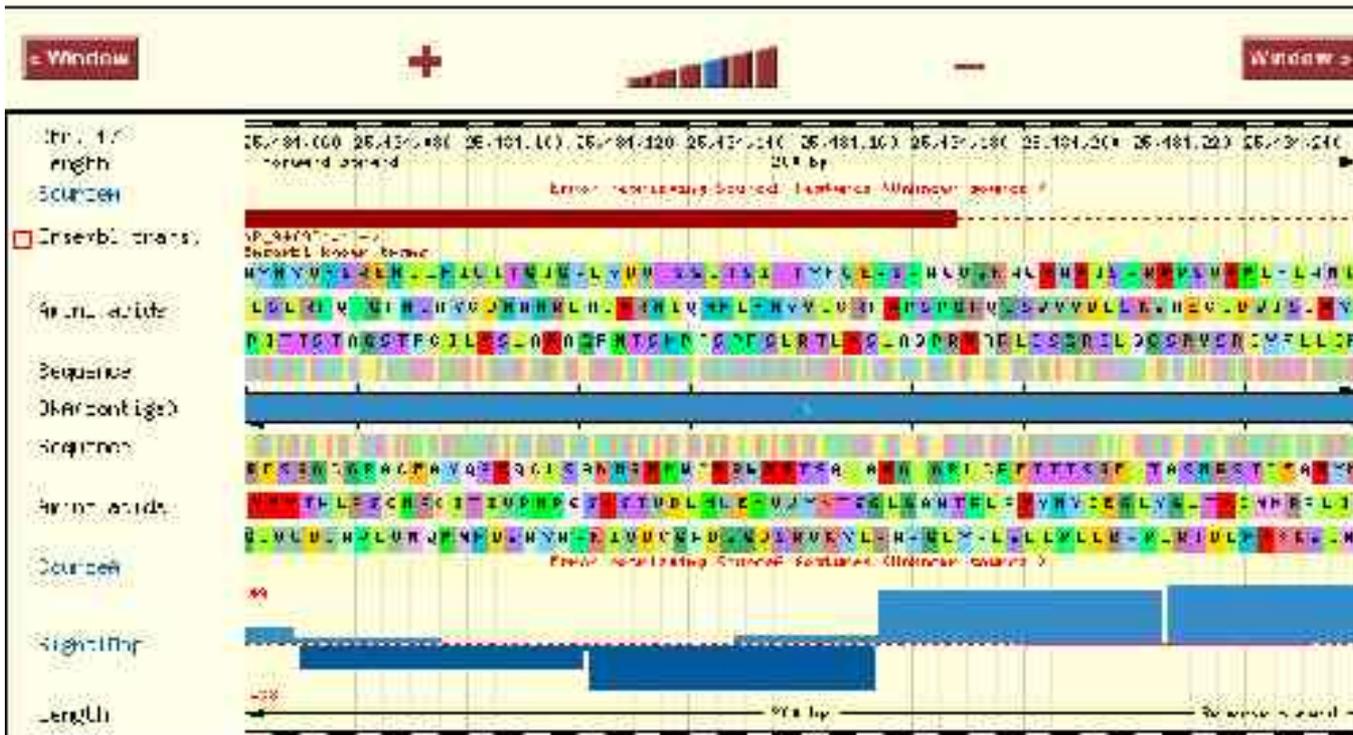
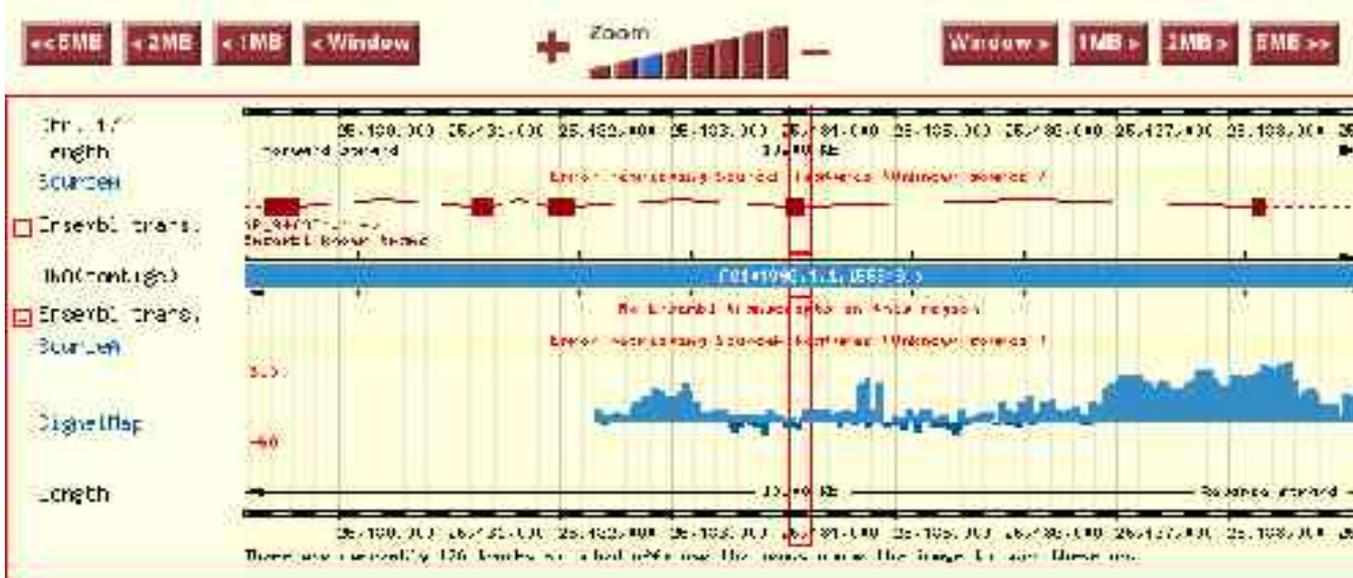
http://www.ensembl.org/info/data/external_data/das/CSS_support.pdf

Using score data



e!

Ensembl



Send the source

http://www.ensembl.org/Homo_sapines/contigview?

[conf_script=contigview;c=13:31829752.5:1;w=500000;h=;](#)

[add_das_source= \(name=hydraeuf_00001291+](#)

[url=http://das.ensembl.org/das+dsn=hydraeuf_00001291+](#)

[type=ensembl_location+color=red+strand=b+labelflag=u+stylesheet=n](#)

[+group=n+depth=10+score=n+active=1\)](#)



Ensembl

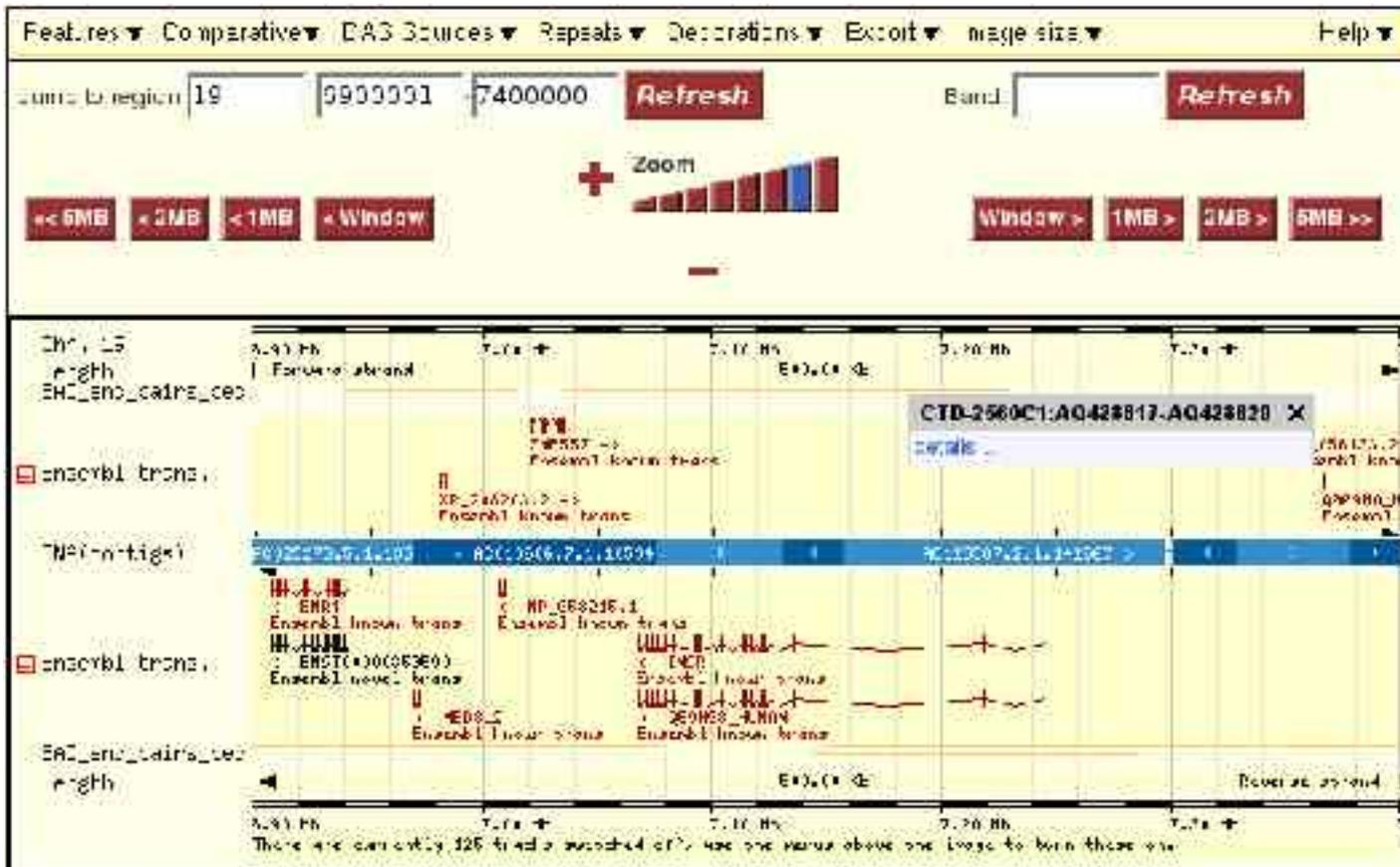
Web-based source

```
browser position chr19:6900001-7400000
track name=BAC_end_pairs_bed description="BAC end pairs (BED)" useScore=1
color=ffcc66 url=http://www.ensembl.org/human/fastaview?faid=DNA_bacend_1533&id=$$
height=0.1
19      6503520 6641948 CTD-3084A17:AQ144413-AQ186293    1000    -      6503520
6641948 0        2        462,512 0,137917
19      6527567 6695619 RP11-357B22:AZ518790-AQ552859    1000    -      6527567
6695619 0        2        470,525 0,167528
19      6527640 6704480 RP11-134L9:AQ388324-AQ388334    1000    -      6527640
6704480 0        2        307,557 0,176284
```

http://www.ensembl.org/info/data/external_data/examples/url_bed.txt
http://www.ensembl.org/info/data/external_data/examples/url_pcl.txt
http://www.ensembl.org/info/data/external_data/examples/url_gff.txt

Display of web-based source

http://www.ensembl.org/Homo_sapiens/contigview?data_URL=http://www.ensembl.org/info/data/external_data/examples/url_bed.txt



Ensembl



Exercise 1

Create a file for upload :

- two features should belong to the group 'Probe A' and
- three features should belong to the group 'Probe B'
- stylesheet section that renders Probe A features in red and Probe B features in green

Upload the file and view the track in contigview

Attach the same source via auto-attach URL, but with stylesheet switched off and features grouped

- File format:

<http://www.sanger.ac.uk/Software/formats/GFF/>

http://www.ensembl.org/info/data/external_data/das/CSS_support.pdf

- Examples:

http://www.ensembl.org/info/data/external_data/das/das_upload_v1.euf

Ensembl

DAS setup



DAS setup

- Resources
 - DasLite: <http://search.cpan.org/~rpettett/Bio-DasLite-0.14>
 - BioDas: <http://www.biodas.org/download/Bio::Das>
 - SOAP : <http://soaplite.com>
- Ini-files
 - DEFAULTS.ini
 - Preconfigure a source
- Data Upload
 - data journal
 - ProServer configuration

Ensembl



DAS setup

DEFAULT.ini

;

; Web services (Used for DAS etc)

;

ENSEMBL_WWW_PROXY =

DAS_REGISTRY_URL = <http://das.sanger.ac.uk/registry>

ENSEMBL_DAS_SERVERS = [das.ensembl.org]

ENSEMBL_DAS_UPLOAD_SERVER = das.mydomain.org

ENSEMBL_DAS_UPLOAD_DB_HOST = das.mydomain.org

ENSEMBL_DAS_UPLOAD_DB_PORT = 3306

ENSEMBL_DAS_UPLOAD_DB_NAME = ens_upload

ENSEMBL_DAS_UPLOAD_DB_USER = root

ENSEMBL_DAS_UPLOAD_DB_PASS =

ENSEMBL



DAS setup

Preconfigure a source

```
Homo_sapiens.ini
MULTI.ini
;
; DAS Config
;
[ENSEMBL_INTERNAL_DAS_SOURCES]
SourceA = 1
SourceB = 1
SourceC = 1

[SourceA]
dsn      = projectA
url      = http://das.ensembl.org/das
on       = [ contigview cytoview geneview ]
```

DAS setup

```
[SourceA]
dsn                = projectA
url                = http://das.ensembl.org/das
on                 = [ contigview cytoview geneview ]
type               = ensembl_location
label              = Source A probes
caption            = Source A probes
col                = black
labelflag          = U
homepage           = http://das.ensembl.org/das/projectA
helplink           = http://das.ensembl.org/das/projectA
strand             = r
depth              = 9999
group              = 0
stylesheet         = y
score              = n
select             = [ contigview ]
assembly           = NCBIM34
fasta              = [ DNA_A_probes ]
```

DAS setup

Data upload

```
mysql> describe hydra_journal;
```

Field	Type	Null	Key	Default	Extra
id	int(11)		PRY	NULL	auto_increment
filetype	varchar(4)			''	
create_date	date	YES		NULL	
access_date	date	YES	PRY	NULL	
email	varchar(64)	YES	PRY	NULL	
passwd	varchar(32)	YES		NULL	
css	text	YES		NULL	

```
7 rows in set (0.03 sec)
```

```
mysql> select * from hydra_journal limit 1;
```

id	filetype	create_date	access_date	email	passwd	css
1	ELF	2005-02-24	2005-02-24	ek3@sanger.ac.uk		NULL

DAS setup

Data upload

Configure ProServer (eg/proserver.ini)

```
[hydraeuf]
state          = on
adaptor        = upload_euf
hydra          = dbi
transport      = dbi
basename      = euf
dbname         = ens_upload
host           = das.mydomain.org
port           = 3306
username       = rw_user
password       =
```

Future development



Future development

- User logins
 - preserving Ensembl DAS configuration
- Ensembl as DAS server
 - serving Ensembl data as DAS sources
- DAS for Functional genomics
 - combining features and real value data
- Ensembl Upload Format, version 2
 - uploading gene and protein based data
- `meta` request
 - configure Ensembl display at the source
- Cross-assembly mapping
 - display sources based on old assemblies on the current Ensembl
- DAS2 ?

Ensembl

http://www.ensembl.org/info/data/external_data/das/index.html

http://www.ensembl.org/info/data/external_data/das/DASTalk.ppt

http://www.ensembl.org/info/data/external_data/das/DASTalk.pdf