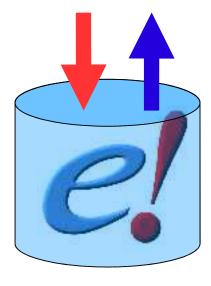


Ensembl and DAS



Eugene Kulesha 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

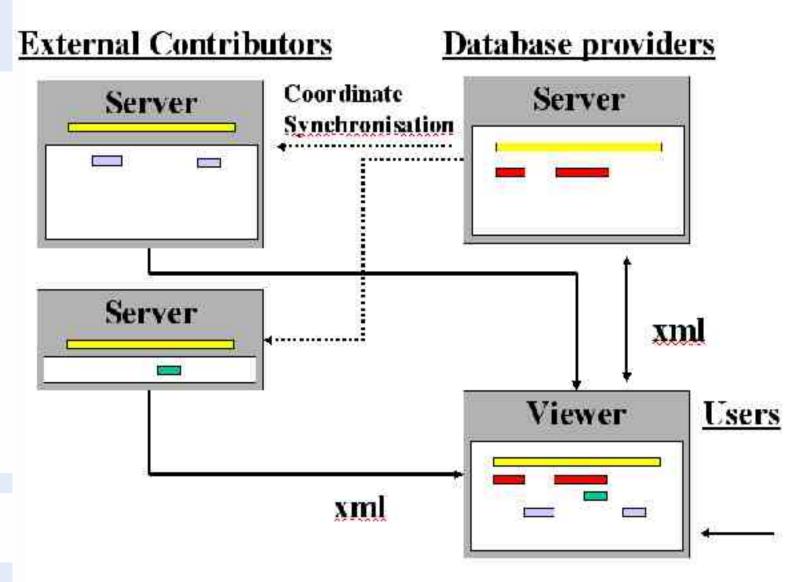
- Distributed Annotation System (DAS);
 - A server system for the sharing of Reference Sequences, and their annotations.
- DAS servers:
 - Reference server
 - Annotation server
- DAS requests:
 - dns
 - entry_points
 - dna
 - features
- Ensembl as DAS server:

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





Distributed Annotation System







DAS Essentials

`dsn` - Get the list of available sources

http://das.ensembl.org/das/dsn

```
Chini vergion-11.0" gtangaleng-"yeg"?>
c DOCTYPE DESIGNS SYPTEM THITT: //www.brus.es.cop/col/casd-ordidito
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 of 18th
    SSOLNOK od-Mong 34 potviOkarp*bong al afoviCkant4/SOUNCe>
    cMSPMARIER: tpu//d-a.e.semid.unij/e.semid1884c/WAPMARTR5>
    QUBBURLELDNYAITYmetyrim _OA_SNY_Array Mapping(/USS.M_PIDM>
  */TISH>
  C. 25203
    CSD BCH Ide"ens 35 - "Cytoka p"s-ns 35 -Cytokan c/SOBBSS>
    SPARFFABIERO : ttp://dig.orgemol.ocg/orgemel2635K/MAPAPSEKA>
    CORPORATE TO CART FOR FOLLOWING THE SME ALTHOU WAS INDUSTRIBLETIONS
  </LSN>
  * DSM's
    %SOLPCK Ld="end anoth dred : _'>end anoth dred : _%SOU+CE>
    CMSTVATTERS: I post//per wile president and other PORM/Idea/Accorded 1 of c/MAPHA9TERS
    QBeCRIFT 100 Fincorbi-matped Drocophila Conoc (/DesCRIFTION)
  * / FISH >
  <.../SID
    CSO RCR Tabellering char25 & energia const. 1 a 2 Egyment c/SOURCE's
    SPV_PASTERO titp://dirvitt.dinger.ac.uk:000/dad/dbriggere.00b4/NAPPM/8kx
    chesphitetroxoc. In hypna- (g-next pri-d of horac/beachtertoxo
  <7.115N >
```





DAS Essentials

`features` - Get the annotations

http://www.ebi.ac.uk/das-srv/asd/das/atd_human/features?segment=13:3770000,38100000

```
Comil persion-"..." at and sione-"yea"?
«!DOCTYPE TASGET SYSTEX "::tp://www.bicdas.org/dtd/dascof.cod")
< ASSITS
  /GET version=*1,01* href=*http://web59-todel.ebi.ac.uk:9100/cas/std_turat/festures*s
   %CEGMENT id="13" version="1.0" start="3770100" stor="D0100100"»
    «JEATURE 1d="5438:1.215740" label="6438:1.215740"5
      <TYPE ic-*excn* reference-"no" subparts-"no" superpents-"no">excn
      CSTART 326590L4 C/START>
      <DM5>32558215
      CORTENTATION S-6/CRIENCATIONS
      «LINB href-"http://www.sh..sc.us/asc grv/Atd.ogilret.od-TRANICRIPT/origin-AT:product-
      *GROUP 1d="5438" Label="MMSG000000133121 AT-1" />
    </PULTURES
    <!EATURE id="5438:1.315741" labat="6438:1.315741">
      <TYDE ic-*exon* reference-"no" subparts-'no" superpents-'no">exon(/TYPE)>
      CETARTABLESSESSIV/STARTA
      <END>323397E0</END>
      CORTENTATION N-4 (CERTATIONS
      <LDSK href-"http://www.eb..sc.us/ass_srv/Atd.ogiTret.od-TRANICRET.origit-AT;procust</p>
      "GROUP 1d="5438" _spe_="ENSG00010133121 AT-1"
   *VECATURE +
    *JEAT.RE 1d="5438:1.215742" label="6438:1.215742";
      <TYPE ic-*excn* reference-"no" subparts-"no" superpents-"no">exon
      <START>32637475
      «DNO»32537554
      CORTENTATION OF A / CRITICATION :
      CLINE href-"http://www.eb.vec.us/esc.grv/Atd.ogilret.od-TRAMCCRIPT.or.ugir-AT/product-
      *GROUP 1d="5438" Label="EMSC000001313131 AT-1" />
    </FUATURE>
```



</DSN>



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 NCB135. Contains 111 entry points of the highest assembly tier.
   </DSN>
- <DSN>
   <SOURCE id "Macaca mulatta" version "37 Ia">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>
 </r>
 <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.
```



- CDASEPS



Ensembl as DAS server

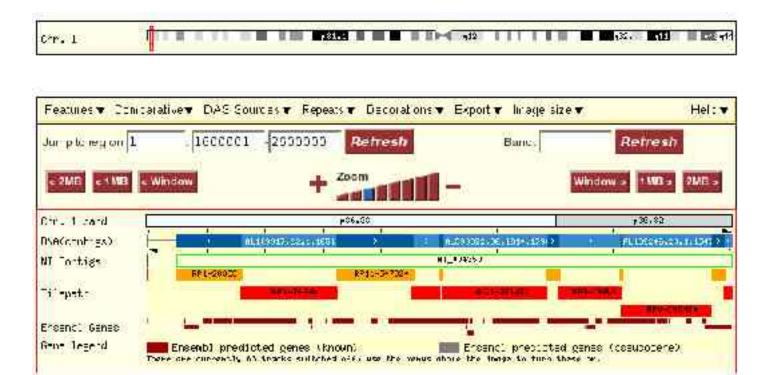
• list of entry points http://www.ensembl.org/das/Homo_sapiens.current.reference/entry_points http://www.ensembl.org/das/Homo_sapiens.NCBI36.reference/entry_points

```
-<ENTRY_POINTS href="http://www.ensembl.org/das" version='1.0">
    <SEGMENT id="1" start='1" stop="245522847" orientation='+'>1</SEGMENT>
   <8EGMENT id="10" start="1" stop="135413628" orientation="+">10</$EGMENT>
   <SEGMENT id..."10 NT 079544" start..."1" stop..."115275" orientation..."-">10 NT 079544</SEGMENT>
   <SEGMENT id="11" start="1" stop="134452384" orientation="+">11</SEGMENT>
    <SEGMENT id="12" start="1" stop="132449811" orientation="+">12</SEGMENT>
    <SEGMENT id="12_NT_091701" start="1" stop="466818" 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_N1_079546" start="1" stop="139250" orientation="=">15_NT_079545
    <SEGMENT id="15_NT_0795:17" start="1" stop="168820" orientation=" ">15_NT_0795:17</SEGMENT>
    <SEGMENT id="15_N1_079548" start="1" stop="119514" orientation="-">15_NT_079548</SEGMENT>
   <SEGMENT id="15_NT_079519" start="1" stop="111861" orientation=" ">15_NT_079519</SEGMENT>
    <SEGMENT id="15" NT 079553" start="1" stop="44888" orientation="=">15 NT 079553</SEGMENT>
   <SEGMENT id="16" start="1" stop="88827254" orientation="+">15</SEGMENT>
```





Exploring assembly







• Exploring assembly:

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

```
<DASGFE>
 <GFF>
 -- SEGMENT id "1" start 1" stop "1000000":>
    - CFEATURE id "I"b
       <START>I<START>
       <$TOP>100000000XTOP>
       <TYPE id="chromosome" category='component" reference="yes" superparts="no" subparts= yes">ciromesome</t YPE>
       <TARGET id= 1" start="1 stop="1000000 >1</TARGET>
      <FEATURE>
    - «FEATURE id "supercontig:NT_077912">
       CSTARTS 357583 d/NTARTS
       <$TOP>511231</$TOP>
       <"FYPY.id="supercontig" category="component" reference="yes" superparts="yes" subparts="yes" supercontig<"/TYPE>
       <TARGET id= NT 077912" start="1 stap="153649 > apercants NT 077912*71ARGET>
      </EEATURES
     <FEATLREId='supercontigeN1_077913'>
       <START>561232</START>
       <STOP>10000000</STOP>
       <TYPE id "supercontig" category "component reference "yes" superparts "yes" subparts. "yes" supercontage TYPE>.
       <TARGET id= NT_077913" start="1" stop="438769">superconty NT_077913</TARGET>
      CEEATURE>
     «FEATERE id="superconfig:NT_07/402">
        <START>I</START>
        <STOP>167280</STOP>
```





• Exploring assembly:

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

```
- «DASGUE»
      - «GFF»
                  <SEGMENT id-"NT_077912" start-"" stop- ">
                   - <FEATURE M-"NT 077912 >
                                 <51 AR 17>
                                 «STOP/»
                                <TYPE id="supercontig" category="component" reference="yes" superparts="yes" subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subparts="yes">subp
                                <TARGET Id= NT_077912" start="" stop="">NT_077912</TARGET>
                          STEATURES.
                     <PEATURE id="clone:AL732372.15">
                                <START>1</START>
                                <8TOP>153649</8TOP>
                                <I'YI'L Id="cienc category="component reference="yes" superparts="yes" subparts="yes >cions</1 YI'L>
                                <TARGET1d= A1.732372.15* start="1" stop="153649">close A1.732372.15
                          OFFATURE>
                - <FEATURE id "chromosome:1":-
                                <START>!</START>
                                 <STUP>15/649 & STOP>
                                <TYPF id "chromosome category "supercomponent reference "yes superparts "no subparts "yes />
                                <PARGET id= 1" start= 357583 stop='511231'/>
                         *FEATURES
                  SISEGMENT>
            <06tb>
```





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

```
- «DASGETS
 -<GPE>
    - <NEGMENT id "AL732372.15.1.153649" start "" stop "">
     -<FEATURE id="AL732372.15.1.153649">
          CSTARTA
         <STOP/>
         <TYPE id="contg" category=' component" reference= 'ye<sub>1</sub>" superpurts=' 'ye<sub>2</sub>" subparts="ne">contig</TYPE>
         <TARGET Id="AL732372.15.1.1536/19" start=" stop="">AL732372.15.1.153649</TARGET>
       </PEATURE>
      - <FEATURE id="clone: AL 732372.15">
         <START>I</START>
         <STOP>153649</STOP>
         <TYPE id="clone" category="supercomponent" reference="yes" superparts="yes" subparts="yes />
         <TARGET id=' AL732372.15" start="1" stop= '153649 '/>
        *STEATURE>
     SSEGMENT>
   </GFE>
 </DASGED>
```





• Exploring assembly:

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

```
- <SEGMENT Id="22" start="1" stop="49591432">
 - <FEATURE id='p|| 1'>
     <START>9607114</START>
    <STOP>11808744</STOP>
    <TYPE td='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/>
   C/FEATURE>
 - <FEATURE id='p12">
    <START>3002224</START>
    <STOP>6604890</STOP>
    <TYPE id='stalk'>stalk</TYPE>
    <METHOD id='ensembl'\>ensembl</METHOD>
    <ORIENTATION/>
   </FEATURE>
```

13 of 10





Adding DAS source to 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

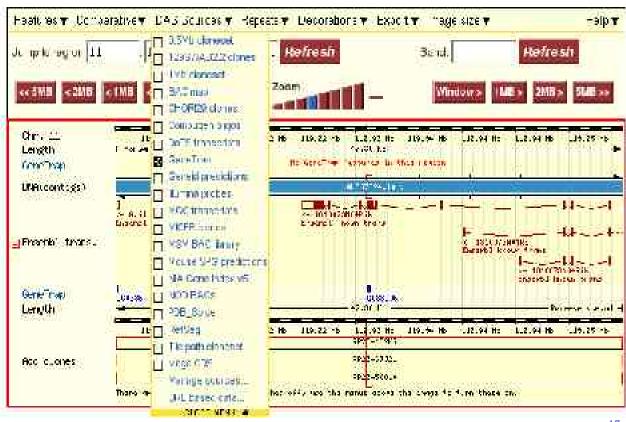
⊟ Gene DAS Rep	port
L DAS Bournes	Afficience (Afternative spice database) Afficience (Afternative francorpt Diversity Database) ArmyExpersit (Conc Express to Colonbox) GAD (Genetic Association Database) HONG (HUSO Gene Momenciature Committee) HUDO_Lest (PohMed test mining via HUCO synchol) Phenotypes (Associated directly or via orthologues or protein families) Frotonet (Slobal classification of proteins into theracciation (diasters) Resolution (Know holgs from all hiological processes) Un Prot (Protein knowledge base) **Asnage BCU (See





Switch on a pre-configured source in contigview and cytoview

E Detailed view







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







E-eV/ Jul	l.ac.uk/das-srw/uniprot/das/aristotic/
unizue iz	DS_109
nic 4nam ≡	unicrof
disclay n CA3 cli≑nts	Nation Eleternel Bookly
doscription	The UniPitt DAS Reference Server serves both sequence and feature data from UniPitt/Swiss-Prot and UniProt/ rt_MDL In addition to this, feature links to InterPro for all the proteins in UniProt are provided line uding basic information (position) and a brief description) and internet addresses to the relevant data gourse. The following kinds of protein ID / Accession number can be used. UniProt Accession numbers e.g. 036502 Swiss-Prot IDs e.g. A/_Human TrEMB_IDs e.g. Qr 2368 IPL Ds e.g. IPIC001817 UniParc IDs e.g. UP 0000125656 For a full description of the service, visit http://www.echaclick/uniprot-das/
adm nemail	unicrot-das_AT_eni ack
helderurl	http://www.chi.ac.uk/uniproticas/
DAS Capab libes:	sequence features entry points stylesheet
Test Docet	PEOPSE
Coordinate Systems.	UniProt, Protein Seguence
Registered at	20099.03/23
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	validate se ver
	edi. , is server, (das source admin only)
	remove this server, idas source admin on y)











DAS Wizard Step 1 of 3: Data location

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(for take r implometers to	ourens onter DSN here)	
	DAS Server DAS Registry	Tions .
(use the filter to na	DAB Registry http://das.ensemble.co.das http://das.sanger.ac.uk/das http://das.sanger.ac.uk/das	
T. 35-G-rum.	http://db.systemapiology.net B380/das tre 12-Genomics serve tp://peromics.micr.ces8080/das details about 60 General tp://ing.3d.gm.ores.fe0000/das tp://ing.ad.gm.ores.fe0000/das	
USIA - extended	http://www.ebiac.uk/dailftp://www.ebi.aningcr.ac.uk/8686/dais Entelyte Sto Anna Puttliftp://www.ebi.ani.uk/daisuk/end/dais dainthi daud CSA-water Tp://www.genescope.com/fr.gbin/ggl//8 eSiconom/com	por of
CSA- worker	Pargrowson whitem aid the high mode training rate are 2000 Albert Constitute At as, Manually curates so estion of catalytic are described in the ingrature, details about ISSA therature.	10
IMG Veren	http://imgtScligh.com/ir/9000/das/MGT Genes- Wrights do instruction of tills (IC) and The temperature (TB) gene removable in and one suither depails about 16°3T Genes	nant unan and malan, mad
V aFnuil	Migi*res provides a higher mit predicted genes (prote higher from the human and mouse go details about full sines.	enoines based on a.m.





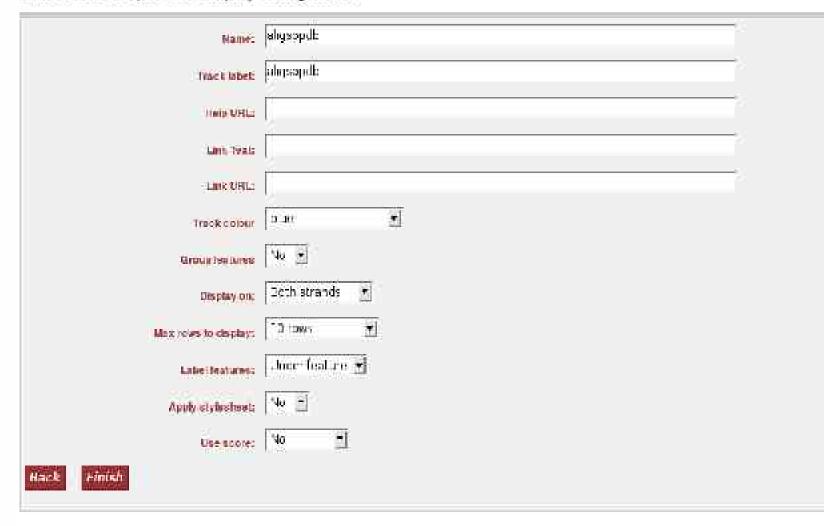
DAS Wizard Step 2 of 3: Data appearance

Coordinate System	F Ensemb Geor ID		
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	Transcript D		
	Entres Gene ID		
	THUGO ID		
	IPI Accession		
	FIR 6		
	UniprovOwiss Prot Name		
	UnipropSwiss-Proti/co		
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Enable on	framewess	Feedbyview	
	☐ cyloview	Fig. 19 (19 constant)	
Total Control			
k Next			





DAS Wizard Step 3 of 3: Display configuration







DAS sources

		Nume	DAS Server	Data Source	Coordinale System
	4	AllSylice	illu.//www.iroi.so.u-vidas-r/wasoither	avid_uw w	Ersemb Sana D
	回	Althor.	http://www.edu.ecu.idas-siwast/das	and gene	Emmemb Sene J
	輔	Д е ку€ процен	ilip ferson a iliana, Ohor - viga anti-Afrik	## TRIP; # DRES+	Uniper (Elektron For Acc)
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	团	H SNC	http://shys.gane.ue.se.uk/50000kcs	H6/3	Empt Cene ID
	[2]	HJGC_WA.	illy.//www.e-citata-citatwgg-reda-Alfas	tionn dig	HUSC ID
	1	l'henotype i	ntigr@www.eon.ec.tclies-crwgeneder.idea	phenotypes	Liraemb Gene D
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		i eastame	http://www.reactome.org/5.30.2/dat	GK_numan	Unip to swiss- 10: Acc
	個	L tiProi	http://www.noi.co.u.ktdcs.crw.un.orobe.os	e detaile.	Uniprostwips Process
F X	Til.	liya ueu _0000129*	iliu/kasemen blogdas	frydrau al_0000° 281	Er semb occator
JE		CTOUL-DAS	http://www.erol.ac.u.kdlasks/wpnde/digs	V1300	Unip to Ewiss: To Act
出来	31	An arimining	anticenter cato carter dan entre	town sing	Unipro:#wins = m: Anc.





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





Upload your data

DAS Wizard Step 1 of 3: Data location

Please READ THE UPLOAD INSTRU				hel-corner y
before uploads will work properly. The	instructions page 185 di	Hairec intormatic - about th	ne cara formate	
Please ead a a croenstand to <u>Erro</u>	mbilipo ey u rup boaded r	dulu		
Emall	ek3@sangenat.uk			100
Password	your onesi and passworn to	ensure that no cody else cent	modify your encomplion	# thet
Pasto your date				
orchoose a file to upload				
Upload Flia:	/.automourt/cbi1/re	ct/nl Browse		
Il you want to update an existing onn	otation en Ensembl DA	S Server enter its Data Se	ource Name and select	your action
Data source				
Action	← Overwrite	(= append		
Next				
			Fic as martice with	at tquicd





Upload your data

DAS Wizard Step 2 of 3: Data appearance

Successfully uploaded styles reet Successfully uploaded 10 entries Alastw DAS source has been challed	al billo //c as eosemol a ga	clas-hydranuf_10001300	
Coordinate System	Enternal Logation		
Enable on	L diprien L transven D detention	proty aw cont gy ew	
Hack Next			







View your data in geneview

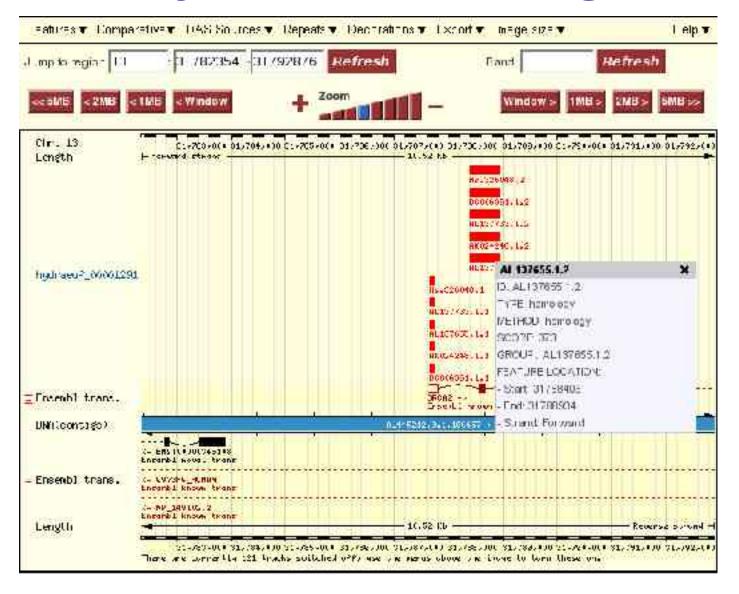
☐ Gene DAS Report

	homology, AK024248.1.1 for ology Feature contained by gene 373.00	
hydraeut_00001291	homology AK024248.1.2 homology Feature cents ned by gene 375,08	
	homology, ALI37855.1.1 homology Feature contained by gene 373.00	
	hamplegy AL107655.1.2 homology Faature cents ned by gone 372.00	
	homology, AL137733.1.1, homology, Feature contained by gene, 354,00	
	hamplegy AL137733.1.2 homology Feature cents ned by gene 354.00	
	homology 8C008361,1,1 hor oldgy Feature contained by gene 354,00	
	homology BCD06361.1.2 homology Feature centained by gene 384.00	
	homology Hs/326048.1 Hor oldey Feature contained by gene 375.00	
	homology Ha.325048.2 homology Heature centained by gone 37.5.00	
☐ DAS Sources Attorios (Alternative Spice database)		





View your data in contigview

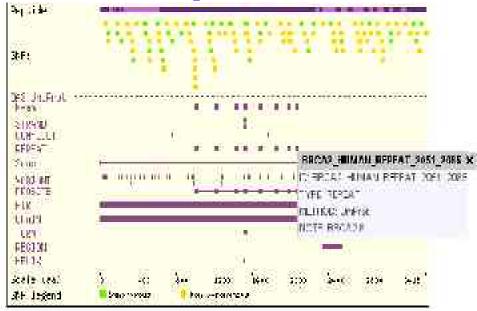






View your data in protview

Projeth Features



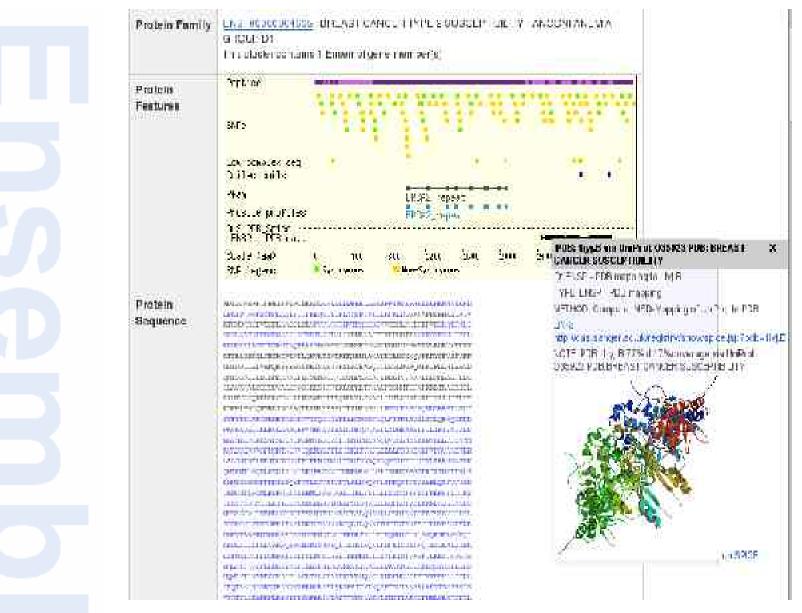
-I Protein DAS Report

UniProt		POTODOS	to Date stan FIS_FFS_Set Stants_Fase_States
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View your data in protview



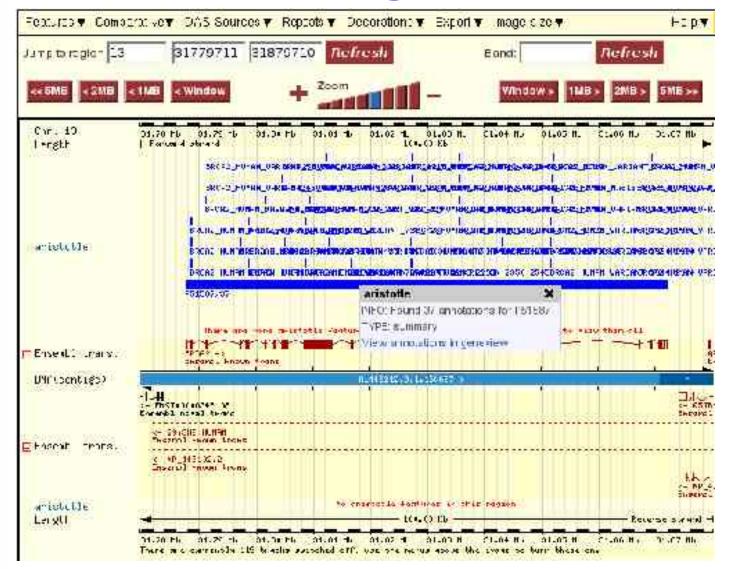








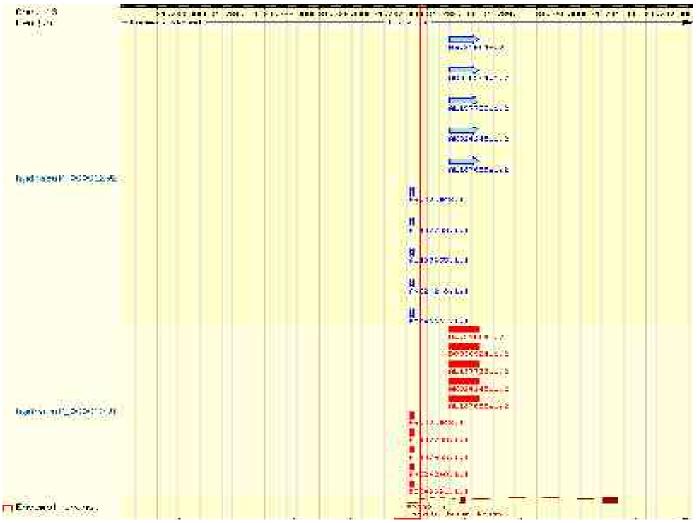
Gene-based annotations in contigview







Applying stylesheet

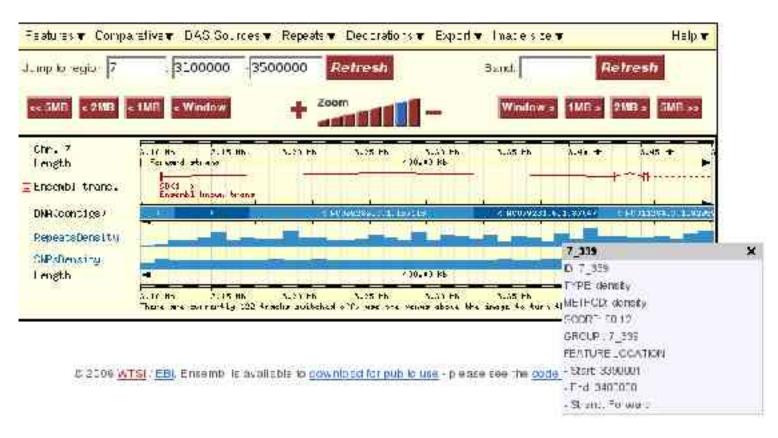


http://www.ensembl.org/info/data/external_data/das/CSS_support.pdf

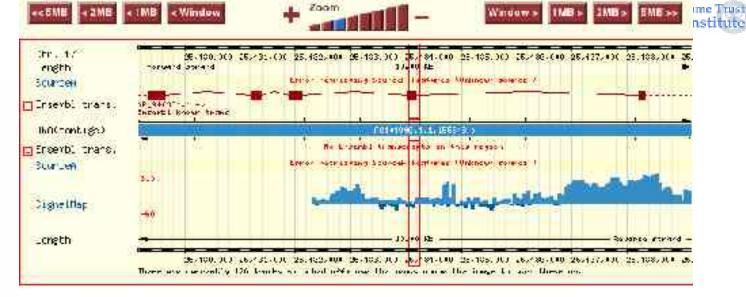




Using score data



e!









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)
```





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
        6503520 6641948 CTD-3084A17:AQ144413-AQ186293
19
                                                         1000
                                                                          6503520
6641948 0
                        462,512 0,137917
        6527567 6695619 RP11-357B22:AZ518790-AQ552859
19
                                                         1000
                                                                          6527567
6695619 0
                        470,525 0,167528
        6527640 6704480 RP11-134L9:AQ388324-AQ388334
                                                                          6527640
                                                         1000
6704480 0
                        307,557 0,176284
```

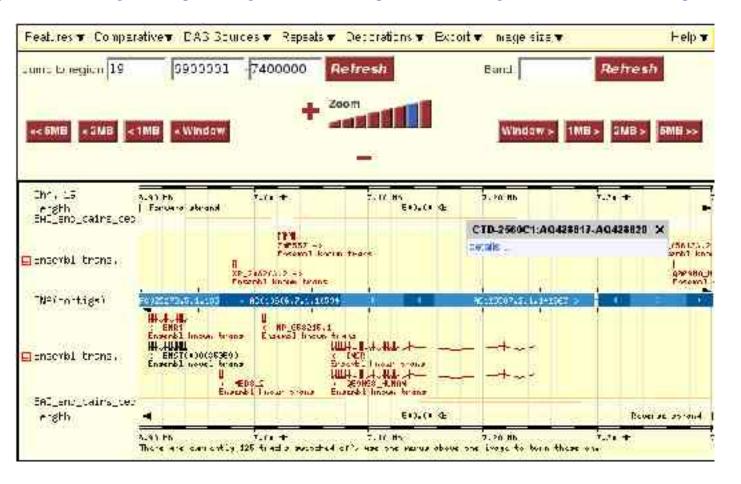
http://www.ensembl.org/info/data/external_data/examples/url_bed.txt http://www.ensembl.org/info/data/external_data/examples/url_pcl.txt http://www.ensembl.org/info/data/external_data/examples/url_gff.txt





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





Exercise I



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









- 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





```
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
```



≥ The Wellcome Trust > Sanger Institute

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 ]
```





[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

= y stylesheet = y

score = n

select = [contigview]

assembly = NCBIM34

fasta = [DNA_A_probes]





DAS setup **Data upload**

mysql> describe hydra_journal;

Filefild	−γре	NuTT	Key	Default	Extra
id ype	int(11) varchar(4)		FF.	KULL 1 Li	auto_increment
create date	date	YES.		NLLL	
access date	date	YES	MUL	NULL	
emat 2	varchar (64)	YES	PLL	NULL	
passw	varchar (337)	Y1 ::		MULT	
CSS	text	YES		NULL	
2				Tanananaa.	

7 rows in set [6.63 sec]

mysql> select * from hydra journal limit 1;

±d.	-туре	create_date	access_date	email.	passw	css
4.4.44					4-4-4-4-4-4-4	4-41-0-14-4
1	ELF	2005-02-24	2005-02-24	ek3@sanger.ac.uk		NLLL
	얼마는 얼마는 아는 아들이다.	들어 걸 하는 바람이 하는 아이들이 없는 아이들이 얼마나 아니다.	그렇게 시민과 얼마난 시민사 얼마난 시민이 날리고요.	얼마나 얼마는 아이라 얼마는 아이라 얼마는 아이는 얼마는 아이는 얼마는	지수는 아일하는 아는 아일다	그 성장이 얼마난 시장이 다







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 ?



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