



CMTV

Comparative Map and Trait Viewer

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OUTLINE

- Introduction to CMTV and some of its functionality
- Integration of CMTV with the GCP Platform
 - ISYS-Eclipse

CMTV

- The Comparative Map and Trait Viewer (CMTV) provides visual integration of genomic data from disparate sources and allows rich client side interactivity and manipulation

CMTV - Development

- Development of CMTV has been headed by NCGR, in association with four CGIAR centers (CIAT, CIMMYT, CIP and IRRI)
- Originally developed as part of ISYS

ISYS

- ISYS (Integrated Systems) is a dynamic, flexible platform for the integration of bioinformatics tools, databases, and web-based resources
 - Component based architecture, allowing plugging-and-playing tools of interest
 - “DynamicDiscovery™ ” technology creates an exploratory environment where the user can navigate freely amongst registered components
 - The plug-in components, in synchronicity, tell you what can be done with a given set of data
- Components include CMTV, Blast, Entrez, maxdView and many others

CMTV – Main Features

- The ability to visualize QTL data in “heat strips” or histogram plots, or as regions of significance above a threshold

NCGR/CGIAR Comparative Map and Trait Viewer

File Edit View Filter Map comparison Help

Map	Mapp...	Refer...
Ch1:...	24	<input type="checkbox"/>
Ch1:...	24	<input type="checkbox"/>
Ch1:...	20	<input type="checkbox"/>
Ch1:...	26	<input type="checkbox"/>
Ch1:...	18	<input type="checkbox"/>
Ch2:...	21	<input type="checkbox"/>
Ch2:...	15	<input type="checkbox"/>
Ch2:...	20	<input type="checkbox"/>
Ch2:...	15	<input type="checkbox"/>

Select maps and...

View separately

View together

Save to CMTV XML

Delete

Map comparisons

Select comparisons and..

View graphically

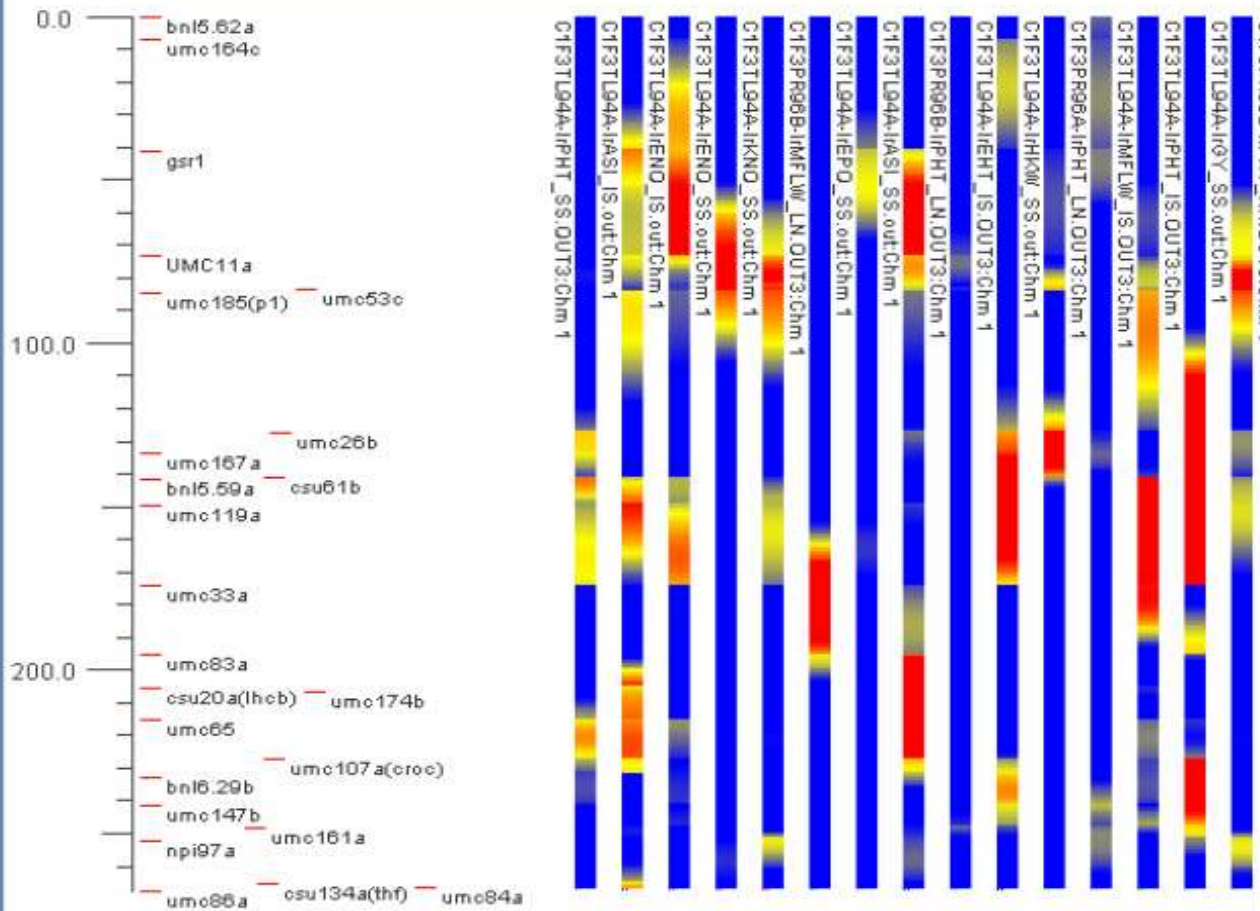
View tabular

Save

Delete

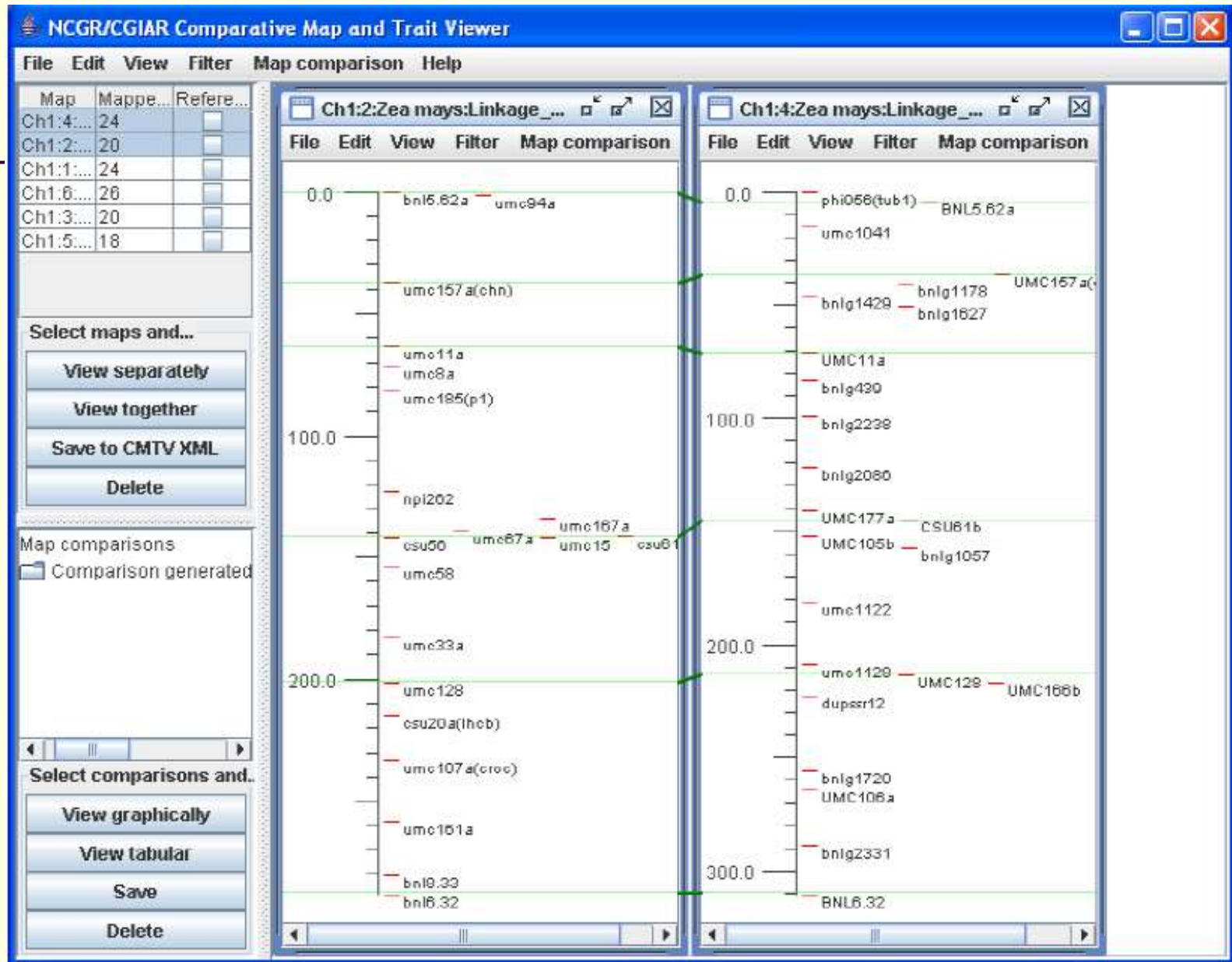
Ch1:1:Zea mays:Linkage_Map:C1.map.txt:Ch1

File Edit View Filter Map comparison



CMTV – Main Features

- Construction and visualization of comparisons of sets of maps based on analysis of corresponding loci



CMTV – Main Features

- Construction of consensus maps using corresponding well-ordered loci to anchor the interpolation of the data from multiple experiments

Map	Mappe...	Refere...
Ch1:4:	24	<input type="checkbox"/>
Ch1:2:	20	<input type="checkbox"/>
Ch1:1:	24	<input type="checkbox"/>
Ch1:6:	26	<input type="checkbox"/>
Ch1:3:	20	<input type="checkbox"/>
Ch1:5:	18	<input type="checkbox"/>
conse...	38	<input type="checkbox"/>

Select maps and...

-
-
-
-

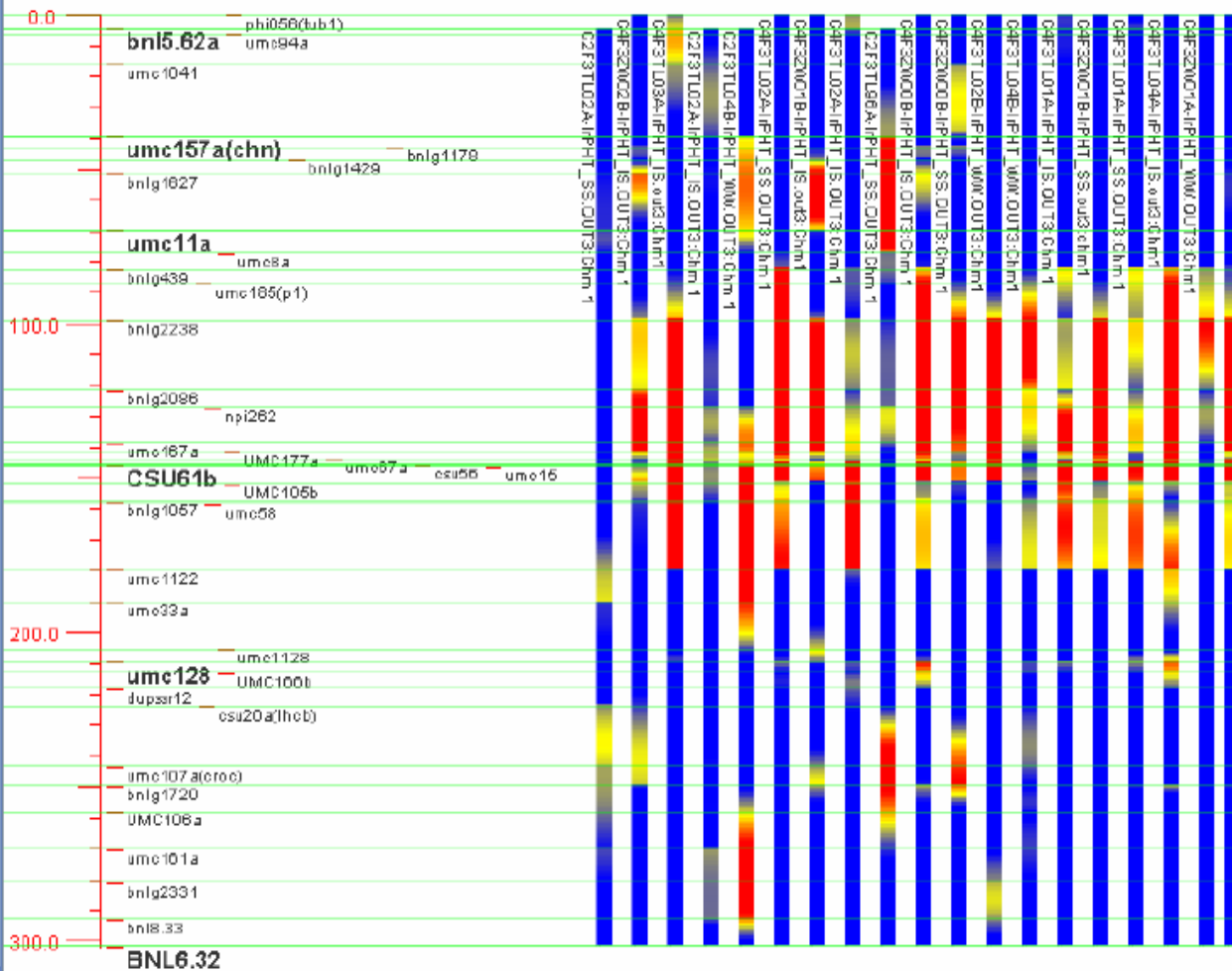
Map comparisons

- Comparison generated
- Ch1:4:Zea mays Lir
- Ch1:2:Zea mays Lir
- Map Comparisons for C

Select comparisons and...

-
-
-
-

consensus map (Ch1:4:Zea mays:Linkage_Map:C4.map.txt:Ch1, Ch1:2:Zea mays:Linkage_Map:C2.map.txt:Ch1)



CMTV, part of ISYS

- CMTV uses ISYS to connect to data sources and other tools
- CMTV can interact with ISYS components via user driven events such as feature selection or filtering
- CMTV's structural/comparative perspective on data may be simultaneously viewed in relation to functional classification systems such as GO or biochemical interaction networks such as PathDB

NCBI/NCBI Comparative Map and Trait Viewer

File Edit View Filter Map comparison Help

Map	Mapp	Flags
Droso	371	<input type="checkbox"/>
Droso	43	<input type="checkbox"/>
Droso	40	<input type="checkbox"/>
Droso	42	<input type="checkbox"/>
Droso	110	<input type="checkbox"/>
Droso	81	<input type="checkbox"/>

Select maps and...

View separately
View together
Save to CMTV XML
Delete

Map comparisons

Map comparisons base...
Map comparisons base...
Map comparisons base...
Map comparisons base...
Map comparisons base...

Select comparisons and...

View graphically
View tabular
Save
Delete

Drosophila virilis Drosophila... α^+ α^+

File Edit View Filter Map comparison

Similarity Search Browser: B62898/drosoph.nt

File View Tools

H	Description	Score	Expect
10726765	Drosophila melanogaster genomic scaff...	188.0	2.0E-45
10727554	Drosophila melanogaster genomic scaff...	81.8	2.0E-14
7290000	Drosophila melanogaster genomic scaff...	71.9	6.0E-12
10726460	Drosophila melanogaster genomic scaff...	71.0	6.0E-12
1298303	Drosophila melanogaster genomic scaff...	71.9	2.0E-11

ggl10726765:gblAE003644.2|AE003644 Drosophila melanogaster genomic scaffold 142000011306015 section 37 of 43, complete sequence
Length = 264851

Score = 188 bits (95), Expect = 2e-045
Identities = 245/295 (83%)
Strand = Plus / Plus

Query: 2142 cctagaccttggtagaccttgcrcgtatccagaccodgacttattgcccagctgacgg 220
|||||
Subject: 143747 cctagaccttggtagaccttgcrcgtatccagaccodgacttattgcccagctgacgg 145

Query: 2203 caaccacccacagggtagagctacatittatccctatcgtgtacactgaccodgacgg 226
|||||
Subject: 145807 caaccacccacagggtagagctacatittatccctatcgtgtacactgaccodgacgg 145

CMTV, used at CIMMYT

- At CIMMYT, CMTV has been used to successfully construct drought tolerance consensus maps for Maize
 - By taking the QTL data produced for different drought tolerant traits assayed under different conditions, the consensus maps were then used as a common framework for viewing the QTL data

Integration of CMTV with GCP Platform

- What is the Generation Challenge Programme (GCP) Platform?
 - An attempt to model all types of germplasm, genotyping, phenotyping, genomics and GIS data
 - Ultimately, creating standard data formats for storage, interchange, analysis and visualization of this data can be developed
 - This will allow one tool, for example, to use output from another tool and establish and construct conceptual linkages between data

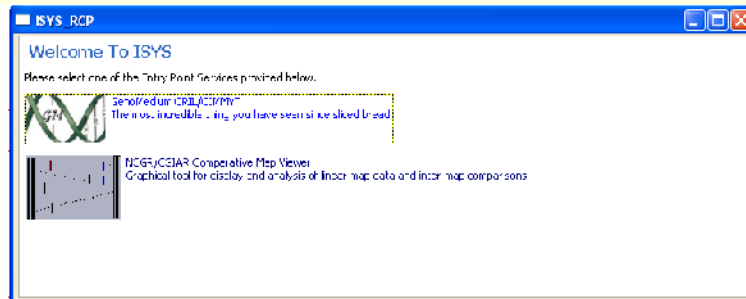
Integration of CMTV with GCP Platform

- To carry out this integration:
 - Created a PostgreSQL database, amalgamating CIMMYT and ISYS Map and QTL data (Previously scattered across data files and an Access Database)
 - Map the database onto the GCP Platform's domain model using Hibernate
 - Map the required objects in the domain model into ISYS objects (*For CMTV to visualize data from the domain model, they need to be wrapped as ISYS objects*)

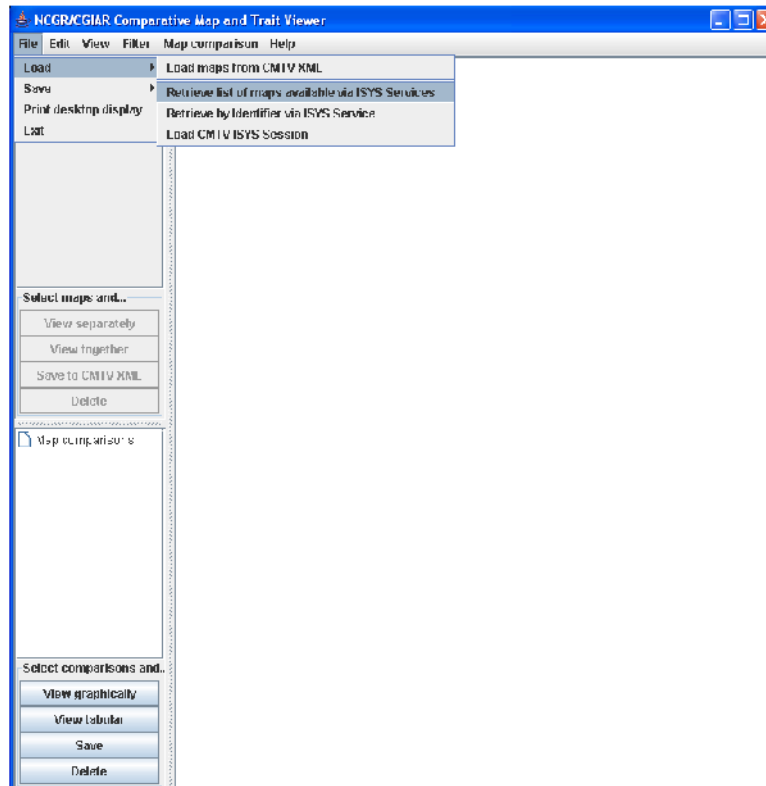
ISYS-Eclipse

- Standalone RCP carrying out integration
- CMTV, data sources and other ISYS tools are distributed as plug-ins
- Uses Eclipse update manager
- Result: Fully customizable and extendible application in terms of a list of services and data sources available

ISYS-Eclipse



ISYS-Eclipse (within CMTV) ...Retrieving Maps from ISYS



ISYS-Eclipse (within CMTV) ...Table View of ISYS Maps

The screenshot shows the 'Listing of available maps' dialog box within the NCGR/CGIAR Comparative Map and Trait Viewer. The dialog box has a menu bar with 'File', 'View', and 'Options'. Below the menu bar is a section titled 'Select maps for full retrieval' containing a table with the following columns: ID, Identifier, Annotations, nearObject, and linkageGroupName. The table contains 26 rows of data. At the bottom of the dialog box are 'OK' and 'Cancel' buttons, and a status bar that reads '50 rows (0 filtered), sort ascending on ID'.

ID	Identifier	Annotations	nearObject	linkageGroupName
14	2 objects, 48.3]			C13*4
23C	9 objects, 27.0]			C8.C*1C
34F	7 objects, 43.0]			C8.C*6
7-E	10 objects, 13.8]			C2.C*6
54F	7 objects, 44.0]			C8.C*3
6-E	2 objects, 41.1]			C2.C*8
731	20 objects, 68.7]			C8.C*1
0-L	4 objects, 40.2]			C2.C*0
9-7	1 objects, 20.8]			C1.C*7
10-0	7 objects, 26.0]			C4.C*0
11-6	2 objects, 33.8]			C1.C*6
124C	2 objects, 47.7]			C9.C*6
1331	24 objects, 33.2]			C1.C*1
14-5	3 objects, 33.9]			C1.C*5
15-2	6 objects, 45.2]			C2.C*2
16-2F	3 objects, 30.5]			C8.C*6
17-8	7 objects, 43.6]			C1.C*8
184E	6 objects, 36.7]			C6.C*8
1924	22 objects, 43.8]			C8.C*4
20-7	24 objects, 42.7]			C1.C*1
214E	3 objects, 32.7]			C6.C*9
2232	24 objects, 25.1]			C4.C*2
234E	4 objects, 36.3]			C6.C*2
243E	6 objects, 39.8]			C4.C*3
25-L	11 objects, 29.5]			C1.C*1L

ISYS-Eclipse (within CMTV)

...4 Maps retrieved

