BIOINFORMÁTICA

Vicente Arnau Llombart

http://www.uv.es/~varnau/bioinformatica.pdf

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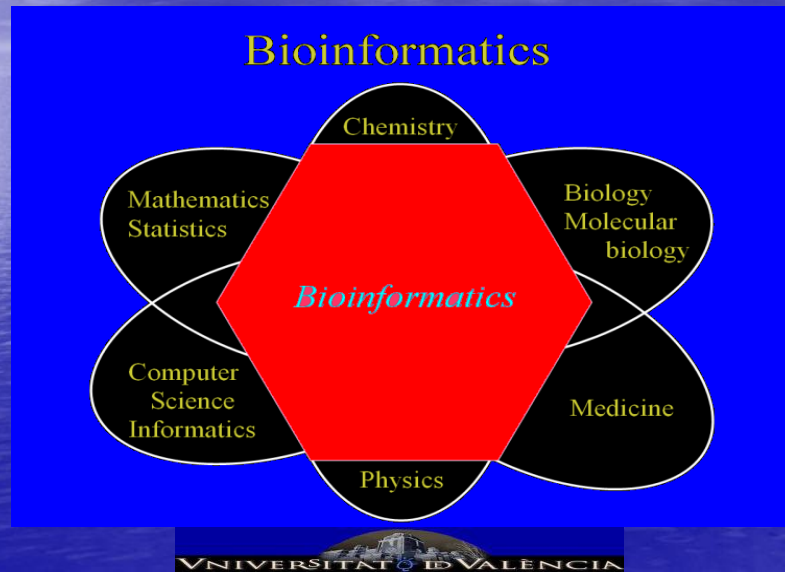
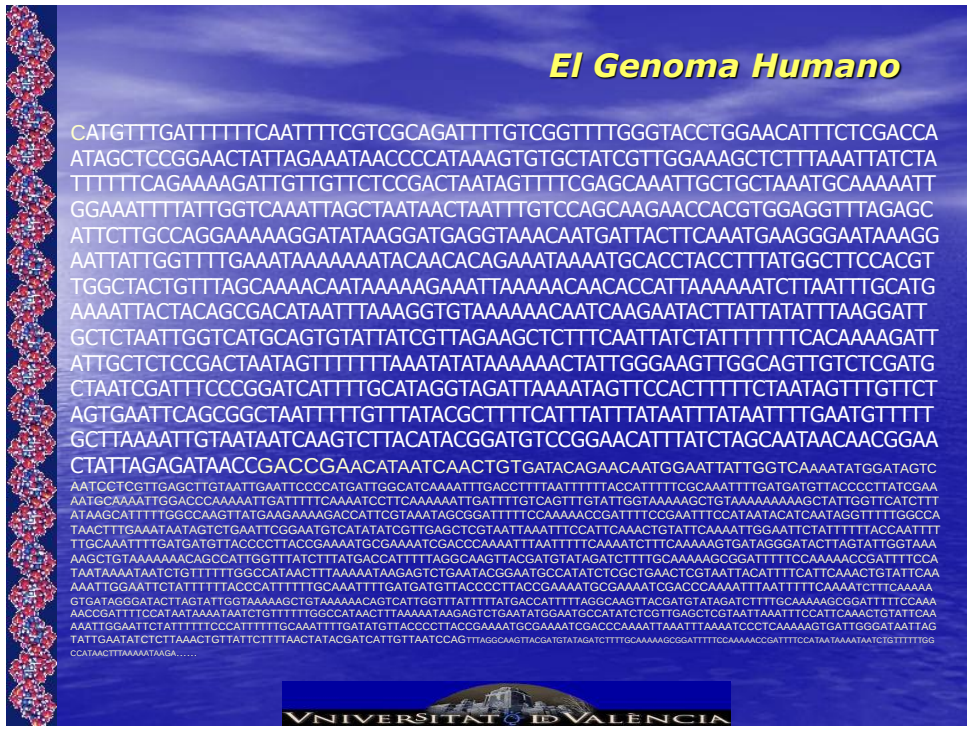
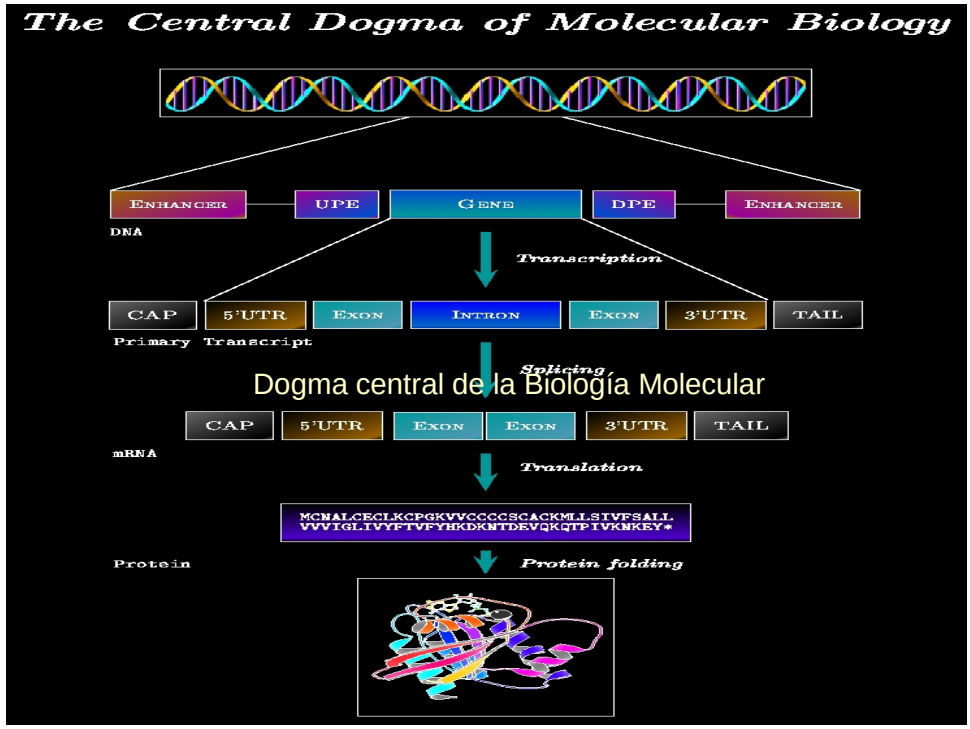
¿Que es la BIOINFORMÁTICA?

BIOLOGIA MOLECULAR ↔ INFORMÁTICA







Dogma central de la Biología Molecular

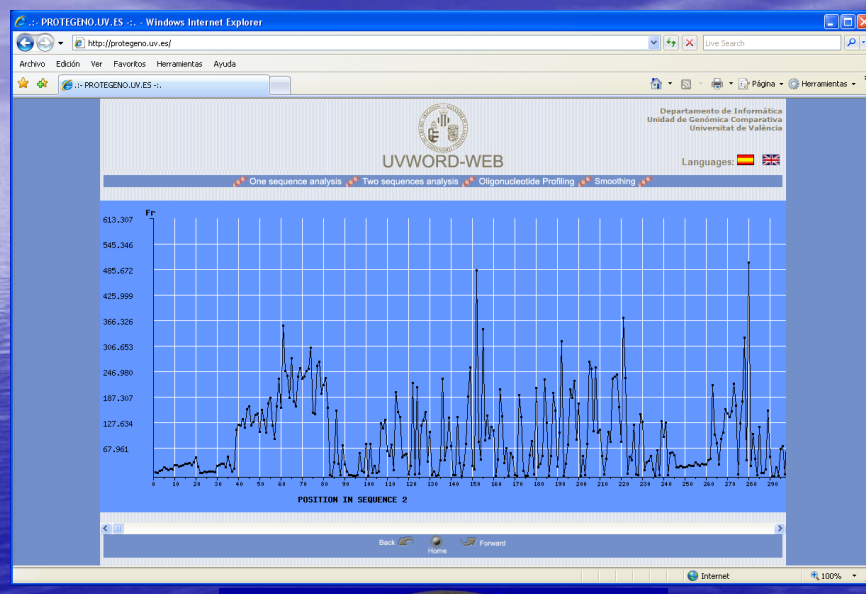
El Genoma Humano

PREGUNTA:
¿Cómo podemos saber que regiones de un gen o de un genoma son regiones codificantes y cuales no?.

RESPUESTA:

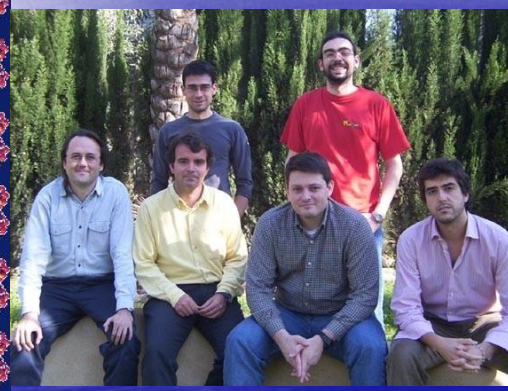
```
>Adh
TCACGTACTGTGGTCGTCCCTTGTTTATGGGCAGGCATCCCTCGTGCGTTGGACTGCTCG
TACATGTGGGCGAGGTTCCGTAAACGTCGGCATGTTGTCCACTGAGACAAACTTGTAAA
CCCGTTCCCGAACCAGCTGTATCAGAGATCCGTATTGTGTGGCCGTGGGGAGACCCTTCT
CGCTTAGCATCGAAAGTAACCTGCGGGAAAAGAAAAATACAAATGTTAAAATTGTCC
TTGTATCTTATGTTGTATGCGTATCTCTTCTATTAAAGTGGGTTCATCTAACCATTATAC
ATTTCATAAATAAATAGATTACAATTGGGTCAAAATAAATGTTCAGTGAAGCTTCCCTT
CTCAAGGTCATAAAAGCATTTAAAAAAAATAGCACAATCAATAATTAAAAACTAATTTT
GAAATCTCTTTGAACAAGACAGATATTTTGGTTCAGTCGCTGAACAAATCTGTTTACTGT
CTAAAATCTGAAAACCATTTTTCCGACAGCTGACAGCTTCGAACAGAATATAGTACACAA
TTTGCAGTCCAAAAATGAGTACAAAAAACAAAACAAATAATGACGACGCGACTGGGCAT
CTCTTAGTATTGAGATATATGTATTTAATTTTCTTAAAATAAAAGCATTTTTTGTCAATT
AAATGCAAAACCGACAAGTTTGATTGGAGGGTTTGTAAAAAATAAAATTCGAATGTAAAA
AGAGTTTCAGTTAGCGCAGGTGGATTTTACAGAAAAAAATGCAATGCAATTAAACATTAC
ATGTATCGATGAGTCCATTAATCATTTCATTTGGTTCAATTCGCGCCACTGAGCTTAAAT
TATAATGATACAATAAAAAAAATTGATGATAAAGAGAGACTA ...
```

El Genoma Humano



El Genoma Humano

GRUPO DE GENÓMICA DE LA UNIVERSIDAD DE VALENCIA



VNIVERSITAT DE VALÈNCIA

Departamento de Genética

Análisis de Patrones Globales de Evolución Genómica

TESIS DOCTORAL

Miguel Gallach Caballero

Valencia,2008

VNIVERSITAT DE VALÈNCIA

El Genoma Humano

Departamento de Informática
Unidad de Genómica Comparativa
Universitat de València
Instituto de Biomedicina (CSIC)

UVWORD-WEB

Languages:

Oligonucleotide Profiling | Oligo Smoothing | Oligo Counting | Singular Oligo Search

UVWORD-WEB is a web tool devised for fast screening of the oligonucleotides composing DNA sequences. The fast analysis of relative abundances of DNA-words (oligonucleotides) is very useful to detect specific oligonucleotides among discrete DNA sequences, chromosomes or even genomes.

UVWORD-WEB implements four kind of analysis based on the exhaustive computing of the oligonucleotides from 1 to 14 nucleotides-length present in any DNA sequence.

Oligonucleotide profiling tool computes for all oligonucleotide frequencies in a DNA sequence (Source). Later, oligos from a second DNA sequence (Target) are scanned to count their frequencies in Source. An additional parameter, window size, must be defined. Window size is the number of consecutive oligonucleotides the user wants to add together to obtain average counts. For window size = 1, no averages are calculated and only the frequencies for every one of the oligonucleotides are computed. For window size > 1, a third column with the average associated variances is added in the table.

In **Smoothing** option, unlike to the previous option, averages are calculated for sliding windows.

One sequence analysis counts all different oligonucleotides of a given length present in a DNA sequence. The user may choose the option "all" or "between" two defined frequencies (L_INF and L_SUP). The former returns a table in text format with all the oligonucleotides found in the sequence and their respective frequencies. The later returns a table with those oligos which frequencies are equal or higher than L_INF but also equal or lower than L_SUP.

In **Two sequences analysis** all different oligonucleotides are computed, and the analysis returns a table with all the oligos (and their respective frequencies) that are less or as frequent than a number F_INF in the first sequence and at the same time more or equally frequent than F_SUP in the second sequence.

For any question or suggestions contact with: **Vicente.Arnau@uv.es**.

http://protegeno.uv.es/

Back | Home | Forward

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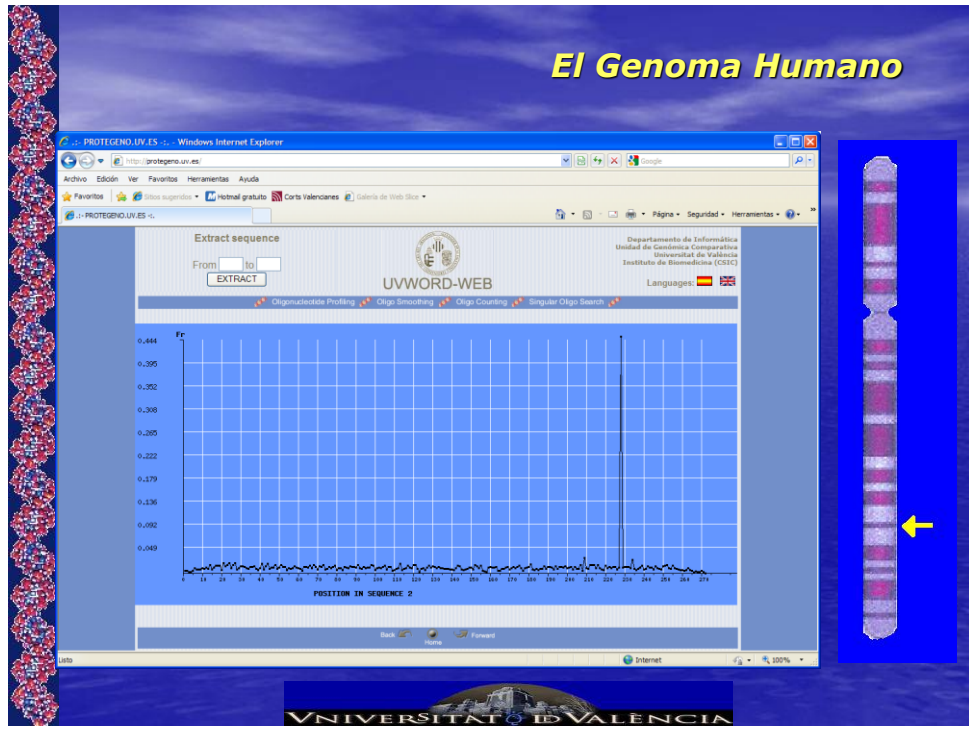
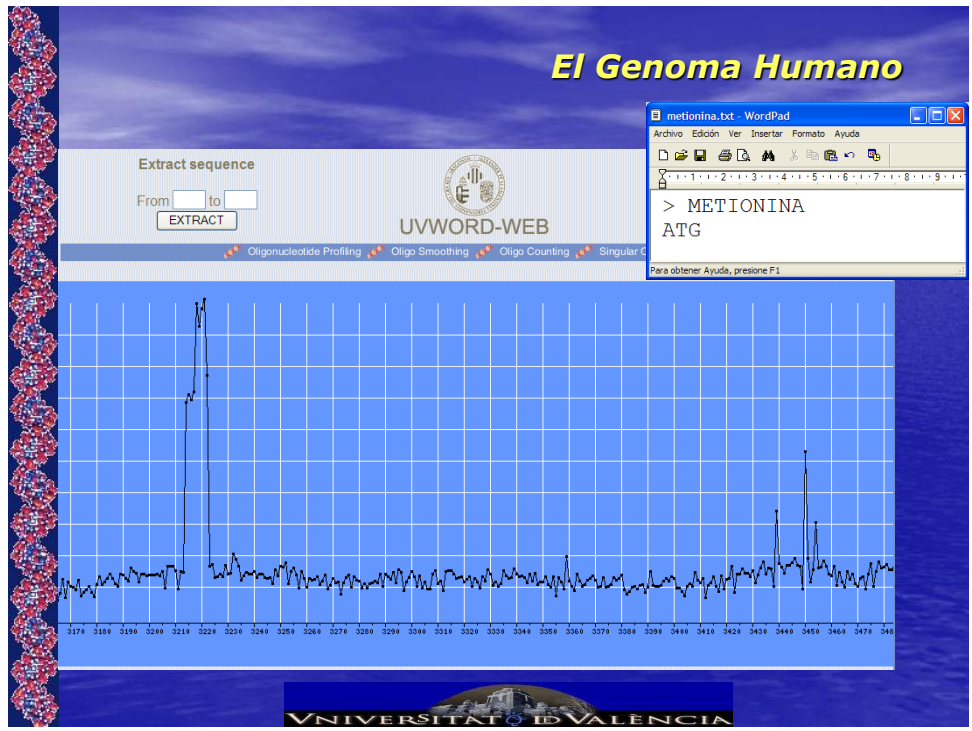
El Genoma Humano

El Genoma Humano

```
=====================================================
=                U  V  W  O  R  D                   =
=====================================================
= V. Arnau; F. Ferri; I. Marin.   11 - V - 2005     =
=====================================================

 35058378 WORDS of 12 nucleotides in File human_chr22
 35449345 WORDS of 12 nucleotides in File human_chr21

 FINF = 2    FSUP = 60

=====================================================
   WORD          Frec_1          Frec_2
-----------------------------------------------------

AAATGTCCACTT          1              98
AACTCTGTGAGT          2              62
AATGGATTGGAA          2              61
AATGTCCACTTG          1              82
ATATCCACTTGC          1              72
ATGGAATGCAAT          2             151
ATGGACTGGAAT          2              82
ATGTCCACTTGC          1              80
CAAATGTCCACT          1              79
CAATGGAATGGA          2             190
CATTGTTTTGGG          2              75
CCCATTGTTTTG          2              60
CTTGAATGGAAT          2              70
GAAGCGCATTCA          0              62
GAATGGAATGTA          2              76
GAATGGACTGGA          1              85
GATTGGAATGGA          2              74
GCAATGGAATGG          2             144
GGAATGGACTCG          0             261
GGAATGGACTGG          1              71
GTCCACTTGCAG          2              81
GTGGAATGGAAT          2             300
GTGGAATGGAGT          1             114
GTGGAGTGGAAT          1             163
TCTGAGAAACTT          2              65
TGAGTGGTGAGT          2             142
TGAGTTGAATGC          1              60
TGCAATGGAATG          2             155
```


El Genoma Humano
PROTEGENO.UV.ES - Windows Internet Explorer
Extract sequence
From to
EXTRACT
UVWORD-WEB
Oligonucleotide Profiling
Oligo Smoothing
Oligo Counting
Singular Oligo Search
POSITION IN SEQUENCE 2
VNIVERSITAT DE VALÈNCIA


El Genoma Humano
metionina.txt - WordPad
Archivo Edición Ver Insertar Formato Ayuda
> METIONINA
ATG
Para obtener Ayuda, presione F1
Extract sequence
From to
EXTRACT
UVWORD-WEB
Oligonucleotide Profiling
Oligo Smoothing
Oligo Counting
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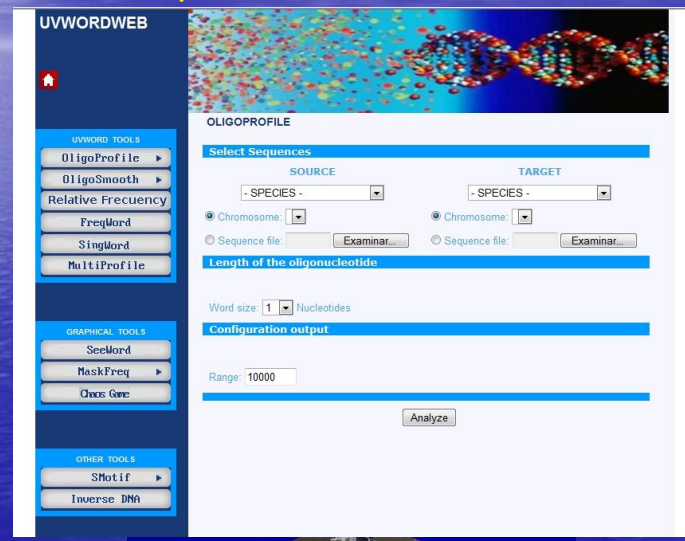
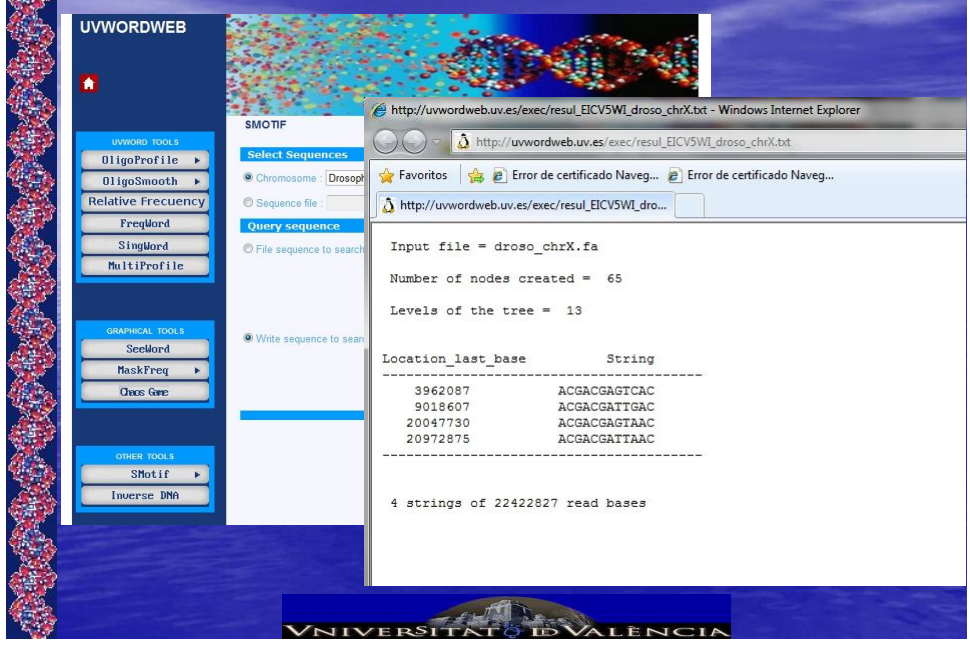
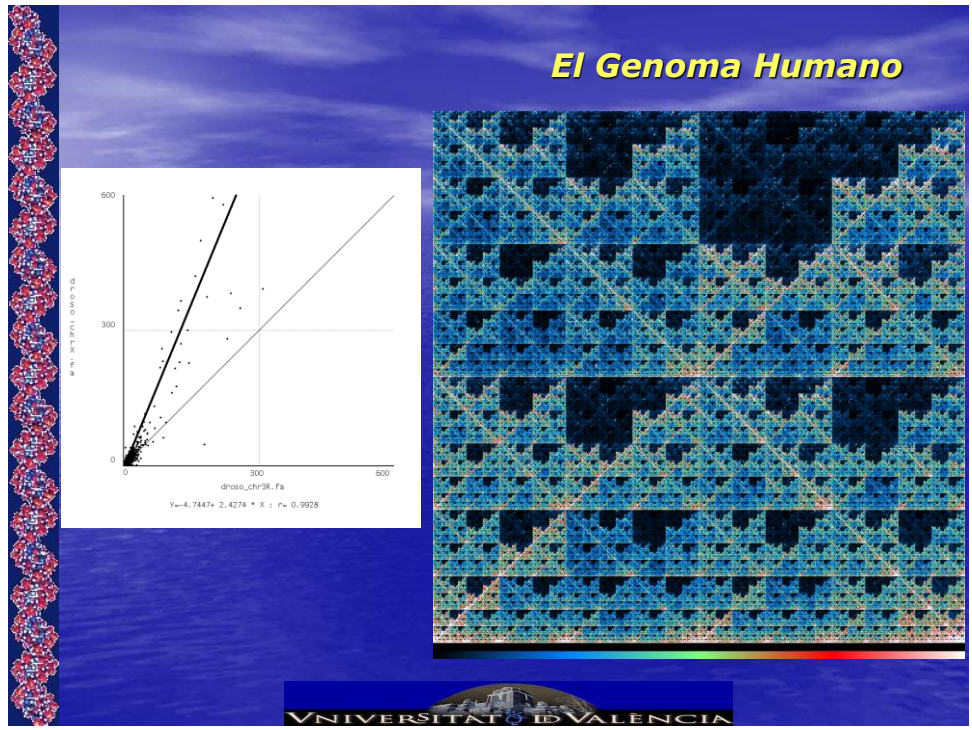
El Genoma Humano

http://uvwordweb.uv.es/



El Genoma Humano




El Genoma Humano
600
300
0
0
300
600
droso_chr3R.fa
Y=-4.7447+ 2.4274 * X ; r= 0.9928
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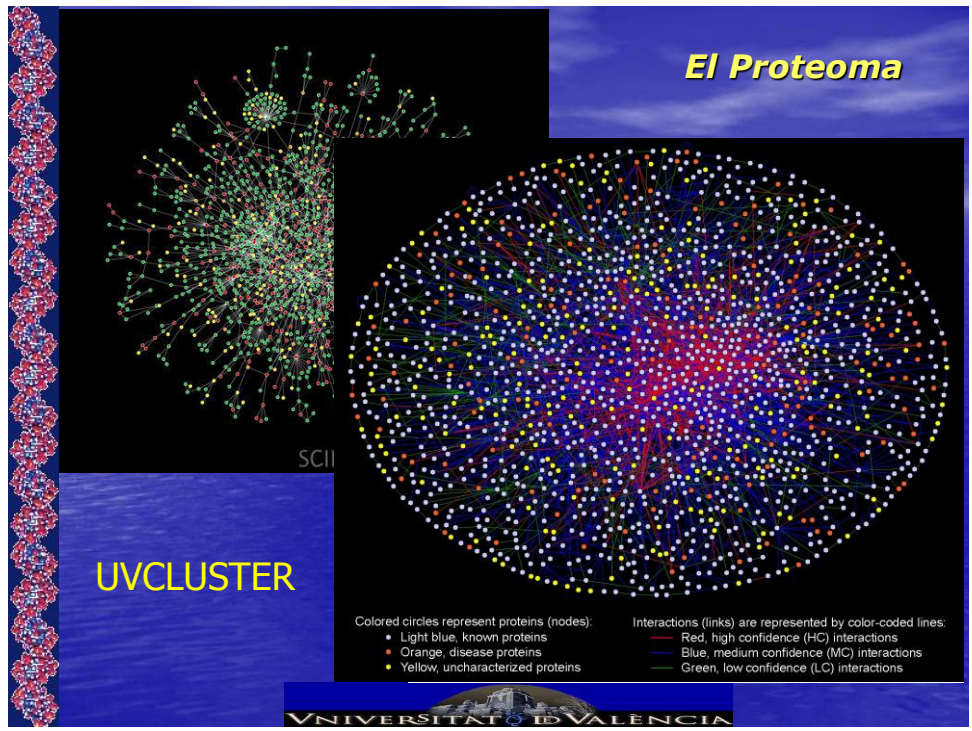
El Proteoma
UVCLUSTER
Colored circles represent proteins (nodes):
Light blue, known proteins
Orange, disease proteins
Yellow, uncharacterized proteins
Interactions (links) are represented by color-coded lines:
Red, high confidence (HC) interactions
Blue, medium confidence (MC) interactions
Green, low confidence (LC) interactions
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El Proteoma

GRAFO DE INTERACCIONES

- Leemos de la base de datos un conjunto de interacciones directas entre proteínas y creamos el grafo.

Bni1 ↔ Act1

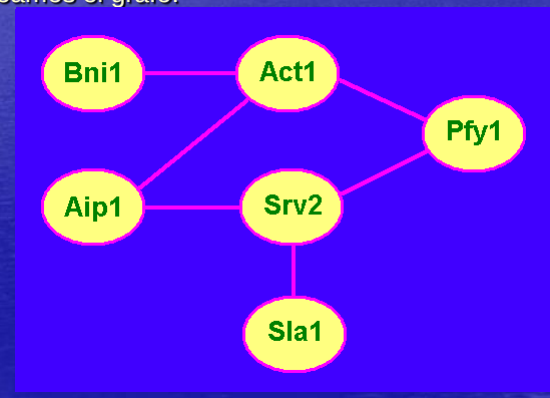
Aip1 ↔ Srv2

Aip1 ↔ Act1

Pfy1 ↔ Act1

Pfy1 ↔ Srv2

Srv2 ↔ Sla1



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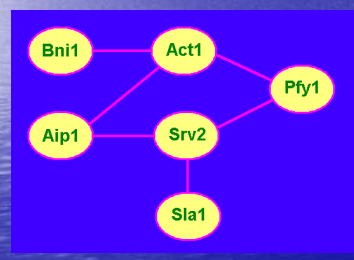
El Proteoma

UVCLUSTER: ANÁLISIS DE INTERACCIONES ENTRE PROTEÍNAS

Convertimos Grafo de Interacciones en Tabla de Distancias entre proteínas.



	Bni1	Act1	Aip1	Srv2	Pfy1	Sla1
Bni1	0	1	2	3	2	4
Act1	1	0	1	2	1	3
Aip1	2	1	0	1	2	2
Srv2	3	2	1	0	1	1
Pfy1	2	1	2	1	0	2
Sla1	4	3	2	1	2	0

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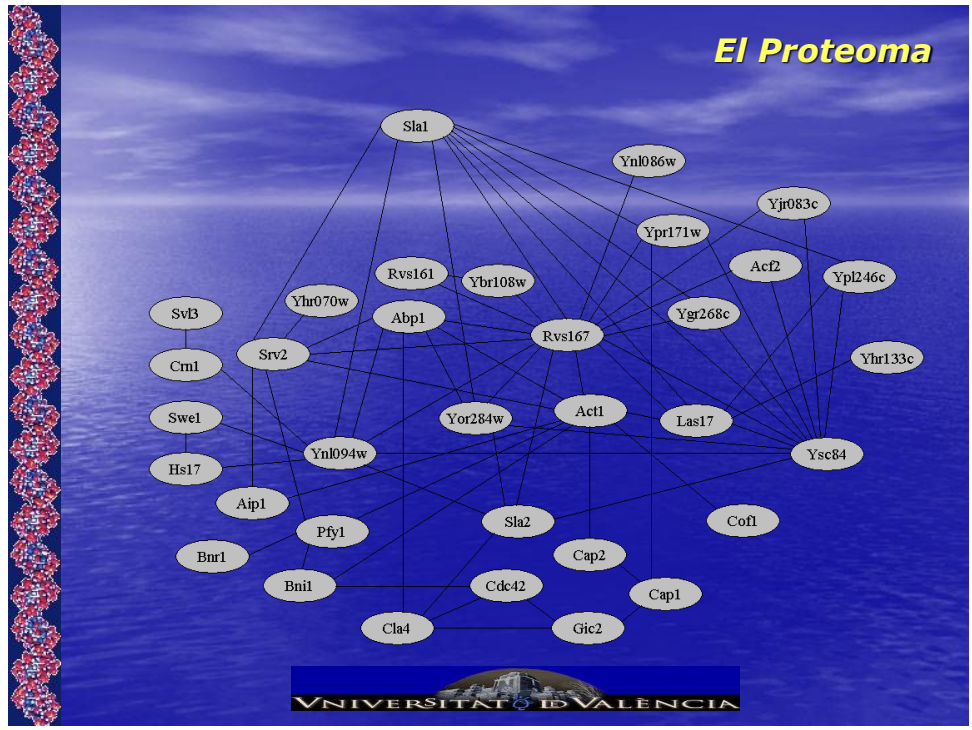
El Proteoma
Sla1
Ynl086w
Yjr083c
Ypr171w
Acf2
Ypl246c
Rvs161
Ybr108w
Yhr070w
Abp1
Ygr268c
Svl3
Rvs167
Srv2
Yhr133c
Crn1
Swe1
Yor284w
Act1
Las17
Ynl094w
Ysc84
Hs17
Aip1
Sla2
Cof1
Pfy1
Bnr1
Cap2
Bni1
Cdc42
Cap1
Cla4
Gic2
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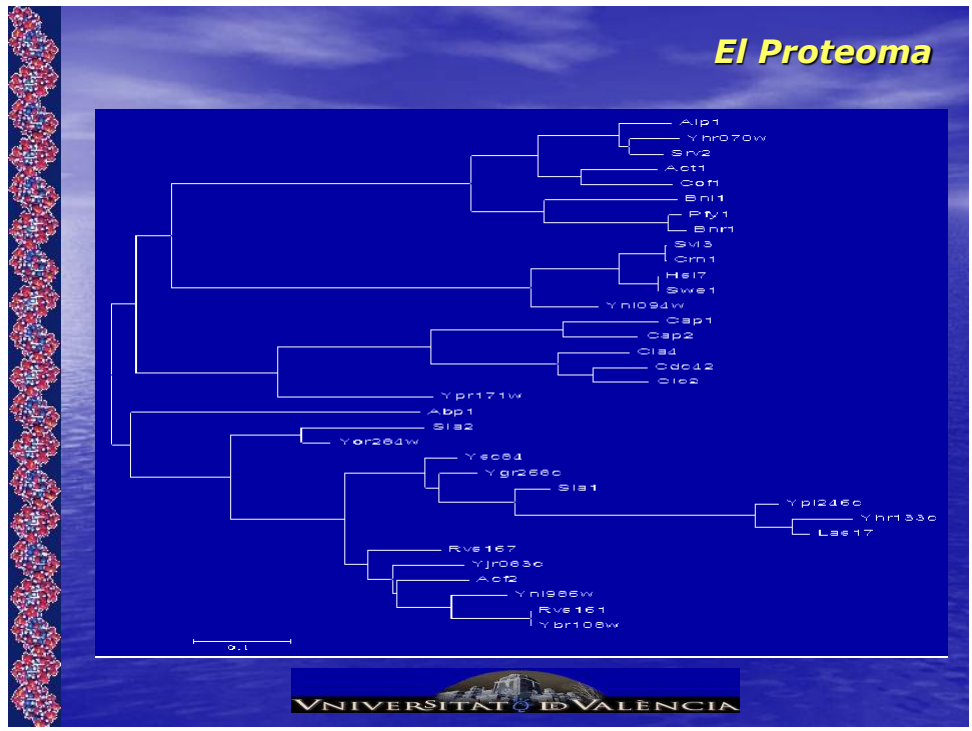
El Proteoma
Aip1
Yhr070w
Srv2
Act1
Cof1
Bni1
Pfy1
Bnr1
Svl3
Crn1
Hsl7
Swe1
Ynl094w
Cap1
Cap2
Cla4
Cdc42
Gic2
Ypr171w
Abp1
Sla2
Yor284w
Yec61
Ygr266c
Sla1
Ypl246c
Yhr133c
Las17
Rvs167
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Acf2
Ynl086w
Rvs161
Ybr108w
0.1
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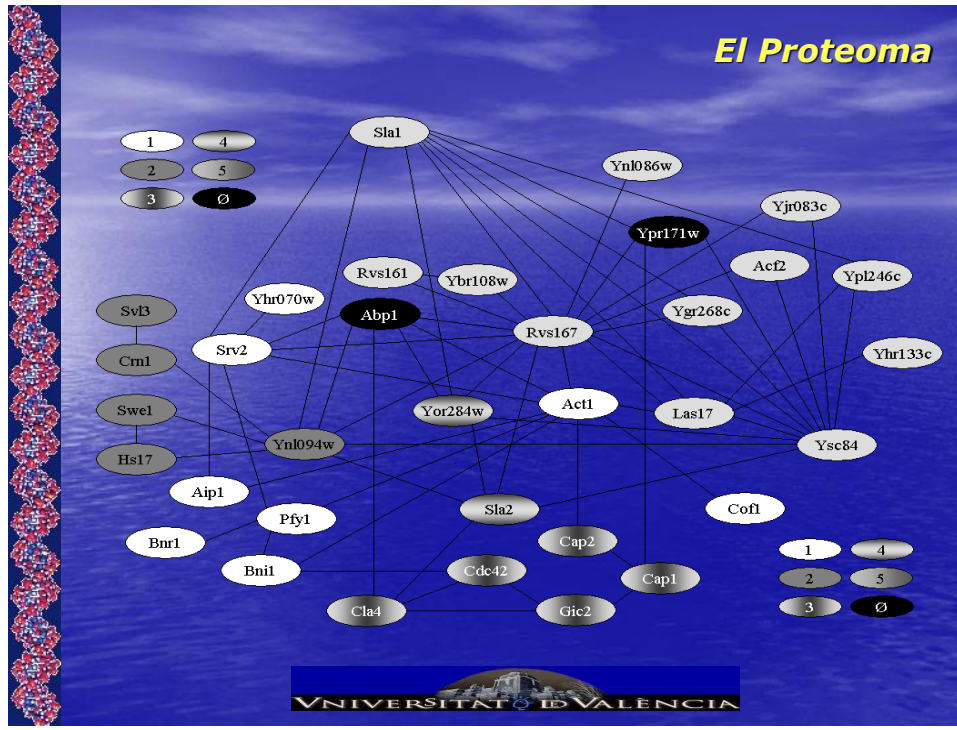
El Proteoma
1
4
2
5
3
Ø
Sla1
Ynl086w
Yjr083c
Ypr171w
Acf2
Ypl246c
Rvs161
Ybr108w
Yhr070w
Abp1
Ygr268c
Svl3
Rvs167
Srv2
Yhr133c
Crn1
Swe1
Yor284w
Act1
Las17
Ynl094w
Ysc84
Hs17
Aip1
Sla2
Cof1
Pfy1
Cap2
Bnr1
Bni1
Cdc42
Cap1
Cla4
Gic2
1
4
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El Genoma Humano
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Unidad de Enzimopatología Estructural
Unidad de Proteinómica Estructural
Unidad de Genética Molecular
Unidad de Genética y Medicina Molecular
U. de Cristalografía de Macromoléculas
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Unidad de Regeneración Neural
Unidad de Patología Metabólica Experimental
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Correo (IBV)
Ubicación
Curso de Genética Humana
24-26 Enero de 2008
Cofinanciado FEDER
Próximo Seminario
Apoptosis, inflamación y diferenciación celular, ¿tres en uno?
Enrique Pérez Payá
miércoles, 30 de enero de 2008
12:30
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Consejo Superior de Investigaciones Científicas
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BIOINFORMÁTICA

José Enrique Pérez

Joaquín Moreno

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BIOINFORMÁTICA

JOAQUIN DOPAZO: Secuenciación masiva de ADN

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El Genoma Humano

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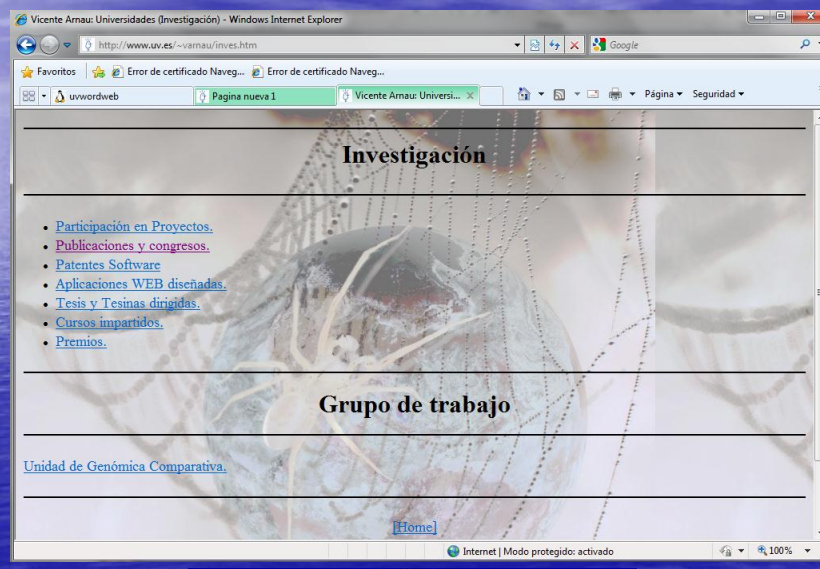

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BIOINFORMÁTICA
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E-mail: Vicente.Arnau@uv.es