



Universidade de São Paulo
Instituto de Química



Comparação de sequências

aula 4

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2022

Alinhamento múltiplo de sequências longas

- O programa MAUVE
- Darling AC, Mau B, Blattner FR, Perna NT. Mauve: multiple alignment of conserved genomic sequence with rearrangements. Genome Res. 2004 Jul;14(7):1394-403.

How MAUVE works

- Seed-and-extend hashing
- Seeds/anchors: Maximal Multiple Unique Matches of minimum length k
- Result: **Local Collinear Blocks** (LCBs)
- $O(G^2n + Gn \log Gn)$, $G = \#$ genomes, $n =$ average genome length

Alignment algorithm

1. Find Multi-MUMs
2. Use the multi-MUMs to calculate a phylogenetic guide tree
3. Find LCBs (subset of multi-MUMs; filter out spurious matches; requires *minimum weight*)
4. Recursive anchoring to identify additional anchors (extension of LCBs)
5. Progressive alignment (CLUSTALW) using guide tree

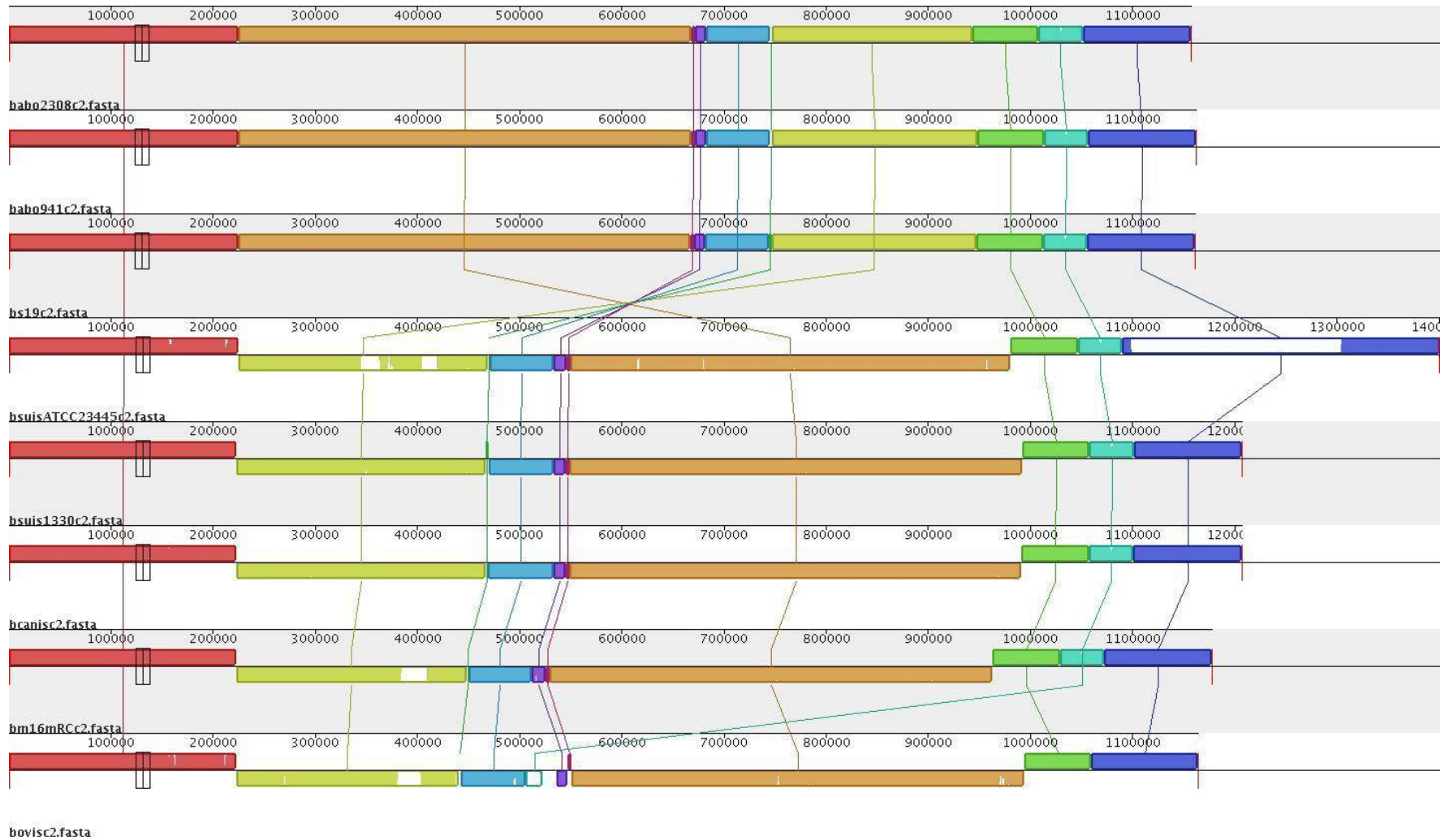
Exemplos de alinhamentos obtidos com MAUVE

- As cores indicam os LCBs encontrados

Brucella: Main chromosome alignment

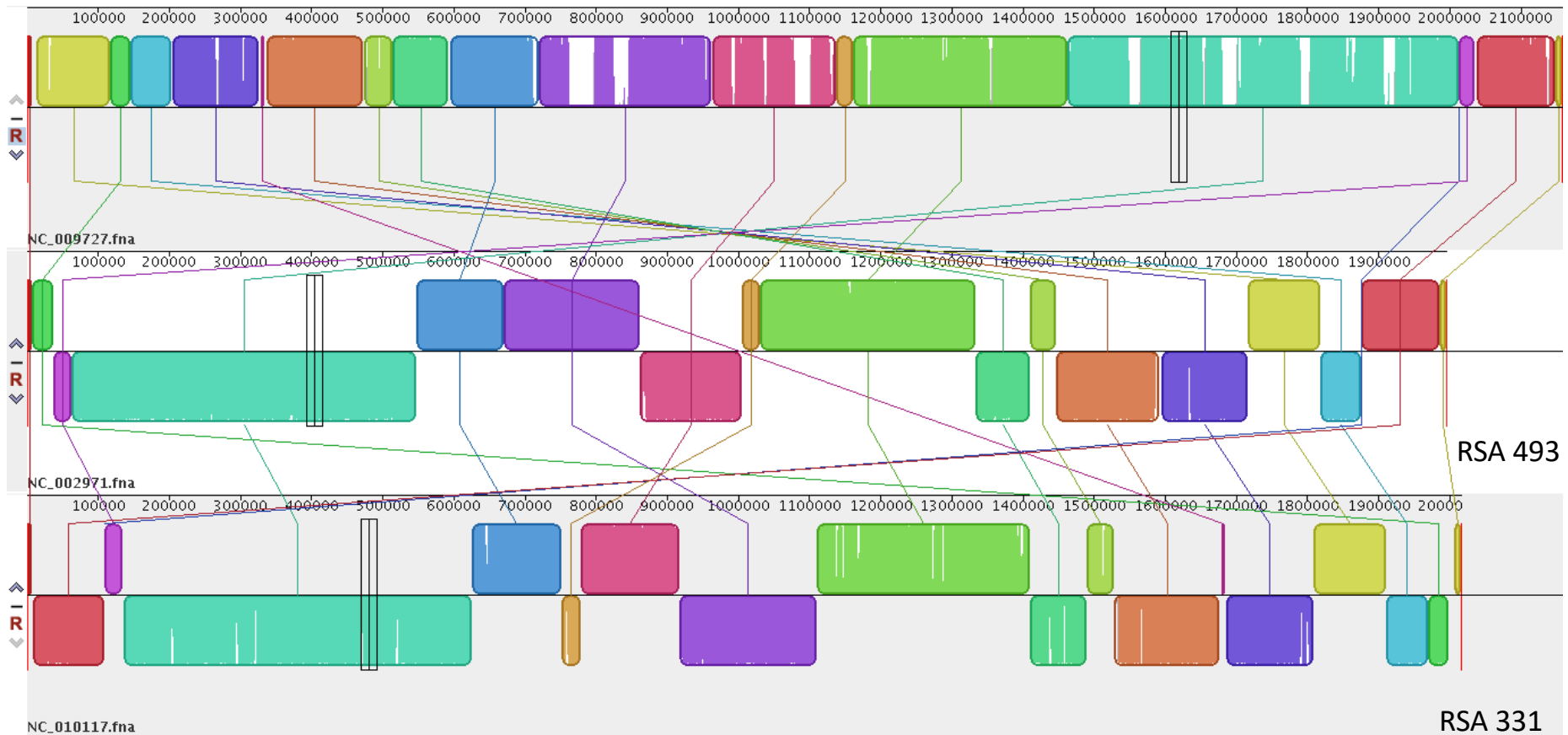


Brucella: Chromosome 2 alignment

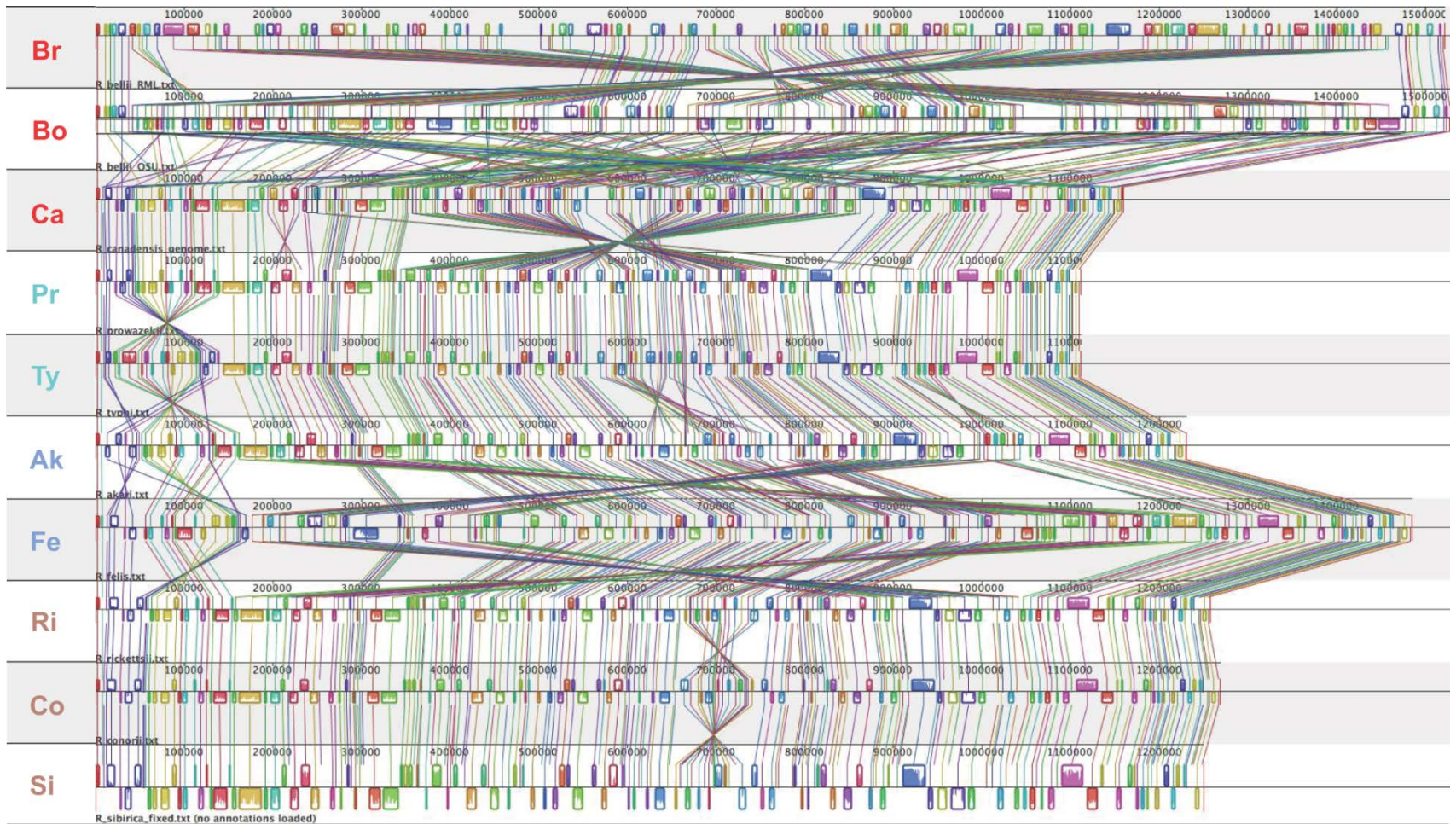


Coxiella: Chromosome alignment

Dugway



Rickettsia



Exercício

- Usando o serviço de alinhamento de genomas da plataforma PATRIC, compare 2 ou mais cromossomos de bactérias
- https://docs.patricbrc.org/user_guides/services/genome_alignment_service.html
- Esse serviço roda MAUVE

Sumário de comparação de sequências

	Sequências curtas	Sequências longas
2-a-2	Prog. Dinâmica	Mummer
2-a-2 muitas vezes	BLAST, usearch, diamond	Mummer
múltiplo	Muscle, MAFFT	Mauve, MUGSY

Distância genômica

- Ao comparar genomas, muitas vezes é útil poder expressar essa comparação por meio de **um único número**
 - Quando se comparam **pares** de replicons
 - Que podem ser “replicons” concatenados
- Distância pode ser entendida como o **inverso da similaridade**

Distância e similaridade

- São conceitos muito parecidos
- Em particular *distância de edição*
- Como transformar sequência s em sequência t
- Operações
 - **Substituição** do caracter a por b (custo = 1)
 - **Inserção** ou **Remoção** de um caracter (custo = 2)
- O algoritmo de PD já visto resolve esse problema (com pequenas modificações)

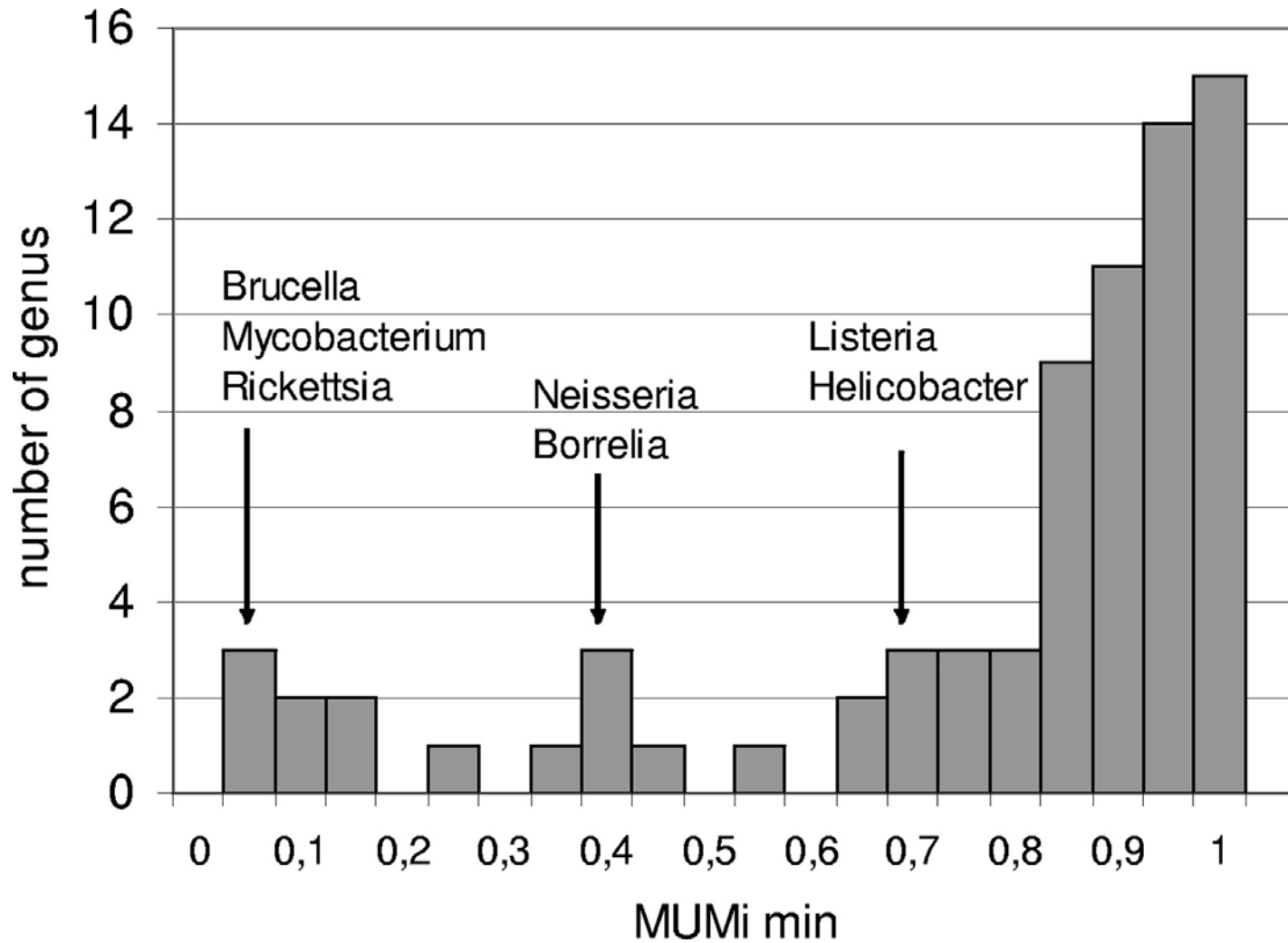
Uma fórmula de distância genômica

- MUMi = MUM index
- Baseado em MUMmer
- **Deloger et al. 2009**
- $MUMi = 1 - L_{mum}/L_{av}$
- L_{mum} = soma dos comprimentos de todos os MUMs que não tem sobreposição
- L_{av} = comprimento médio dos 2 genomas sendo comparados
- Para obter MUMi, basta rodar MUMmer com um script perl desses autores

O que significa o índice MUMi

- Identical sequences: **zero**
- Totally different sequences: **1**
- The boundary between **genus** and **species** is around **0.8**

Distribution of all minimal MUMi values per genus.



Marc Deloger et al. J. Bacteriol. 2009;191:91-99

Journal of Bacteriology

Conclusão

- Não dá para comparar distâncias MUMi entre diferentes gêneros; apenas entre diferentes espécies do mesmo gênero
- ou entre diferentes cepas da mesma espécie

Uma matriz de distâncias genômicas em *Brucella*

Strain	MUMi value ^b					
	83-13	BO2	NF 2653	BO1	<i>B. suis</i>	<i>B. microti</i>
<i>B. neotomae</i> 5K33	0.145	0.168	0.146	0.168	0.017	0.022
<i>Brucella</i> sp. strain 83-13		0.172	0.009	0.175	0.147	0.150
<i>Brucella</i> sp. strain BO2			0.168	0.107	0.169	0.169
<i>Brucella</i> sp. strain NF 2653				0.172	0.147	0.146
<i>B. inopinata</i> BO1					0.169	0.167
<i>B. suis</i> biovar 3 686						0.020

↵a Only the sequence of *B. microti* was complete, and its two chromosome sequences were concatenated. Concatenation was done by inserting a string with 100 nucleotides between contigs.

↵b The minimum MUMi value is 0, and the maximum MUMi value is 1.

Valores MUMi em Xanthomonas

XacA628	0.4017	0.0176	0.0172	0.0090	0.0193		0.0084	0.0083	0.0069	0.0606	0.0523	0.0558	0.0536	0.0536	0.0535	0.0536	0.0482	0.0538	0.0169	0.0169	0.0149	0.0150
XacA636	0.4030	0.0177	0.0182	0.0088	0.0238	0.0084		0.0085	0.0116	0.0624	0.0550	0.0584	0.0560	0.0560	0.0560	0.0560	0.0511	0.0561	0.0179	0.0180	0.0169	0.0169
XacA654	0.4033	0.0131	0.0136	0.0036	0.0251	0.0083	0.0085		0.0119	0.0625	0.0557	0.0592	0.0568	0.0568	0.0568	0.0568	0.0512	0.0569	0.0133	0.0133	0.0180	0.0180
XacA828	0.4040	0.0208	0.0211	0.0123	0.0178	0.0069	0.0116	0.0119		0.0646	0.0558	0.0598	0.0565	0.0565	0.0565	0.0565	0.0518	0.0566	0.0210	0.0210	0.0181	0.0181
XacAS270	0.4073	0.0656	0.0655	0.0629	0.0707	0.0606	0.0624	0.0625	0.0646		0.0131	0.0067	0.0603	0.0600	0.0603	0.0600	0.0352	0.0601	0.0654	0.0654	0.0639	0.0639
XacAS8	0.4031	0.0590	0.0588	0.0558	0.0633	0.0523	0.0550	0.0557	0.0558	0.0131		0.0085	0.0541	0.0538	0.0541	0.0538	0.0291	0.0539	0.0588	0.0588	0.0561	0.0561
XacAS9	0.4045	0.0621	0.0619	0.0593	0.0661	0.0558	0.0584	0.0592	0.0598	0.0067	0.0085		0.0558	0.0555	0.0558	0.0555	0.0304	0.0556	0.0619	0.0619	0.0578	0.0578
XacAW13	0.4074	0.0584	0.0581	0.0567	0.0637	0.0536	0.0560	0.0568	0.0565	0.0603	0.0541	0.0558		0.0001	0.0001	0.0001	0.0611	0.0004	0.0578	0.0578	0.0554	0.0554
XacAW14	0.4074	0.0581	0.0578	0.0568	0.0633	0.0536	0.0560	0.0568	0.0565	0.0600	0.0538	0.0555	0.0001		0.0001	0.0001	0.0611	0.0004	0.0575	0.0575	0.0551	0.0551
XacAW15	0.4074	0.0584	0.0581	0.0567	0.0637	0.0535	0.0560	0.0568	0.0565	0.0603	0.0541	0.0558	0.0001	0.0001		0.0001	0.0610	0.0004	0.0578	0.0578	0.0554	0.0554
XacAW16	0.4074	0.0581	0.0578	0.0568	0.0633	0.0536	0.0560	0.0568	0.0565	0.0600	0.0538	0.0555	0.0001	0.0001	0.0001		0.0611	0.0004	0.0575	0.0575	0.0551	0.0551
XacAs1682	0.4007	0.0599	0.0597	0.0518	0.0643	0.0482	0.0511	0.0512	0.0518	0.0352	0.0291	0.0304	0.0611	0.0611	0.0610	0.0611		0.0613	0.0594	0.0594	0.0574	0.0574
XacAw12879	0.4074	0.0583	0.0579	0.0568	0.0636	0.0538	0.0561	0.0569	0.0566	0.0601	0.0539	0.0556	0.0004	0.0004	0.0004	0.0004	0.0613		0.0576	0.0577	0.0553	0.0553
XacBL18	0.4094	0.0007	0.0003	0.0125	0.0222	0.0169	0.0179	0.0133	0.0210	0.0654	0.0588	0.0619	0.0578	0.0575	0.0578	0.0575	0.0594	0.0576		0.0000	0.0063	0.0063
XacFB19	0.4094	0.0007	0.0003	0.0125	0.0222	0.0169	0.0180	0.0133	0.0210	0.0654	0.0588	0.0619	0.0578	0.0575	0.0578	0.0575	0.0594	0.0577	0.0000		0.0063	0.0063
XacGD2	0.4077	0.0057	0.0063	0.0171	0.0194	0.0149	0.0169	0.0180	0.0181	0.0639	0.0561	0.0578	0.0554	0.0551	0.0554	0.0551	0.0574	0.0553	0.0063	0.0063		0.0000
XacGD3	0.4077	0.0058	0.0063	0.0171	0.0194	0.0150	0.0169	0.0181	0.0182	0.0639	0.0561	0.0579	0.0557	0.0553	0.0557	0.0553	0.0575	0.0555	0.0064	0.0064	0.0005	
XacJX4	0.4077	0.0065	0.0070	0.0168	0.0196	0.0146	0.0173	0.0177	0.0178	0.0641	0.0563	0.0579	0.0557	0.0554	0.0557	0.0554	0.0572	0.0556	0.0068	0.0071	0.0024	0.0024
XacJX5	0.4077	0.0065	0.0070	0.0167	0.0196	0.0146	0.0172	0.0177	0.0179	0.0640	0.0561	0.0578	0.0556	0.0553	0.0556	0.0553	0.0571	0.0555	0.0071	0.0071	0.0024	0.0024
XacLMG941	0.4125	0.1430	0.1429	0.1354	0.1467	0.1324	0.1345	0.1348	0.1348	0.1380	0.1364	0.1365	0.1535	0.1535	0.1535	0.1535	0.1309	0.1537	0.1427	0.1427	0.1388	0.1388
XacMF20	0.4094	0.0007	0.0003	0.0125	0.0222	0.0170	0.0180	0.0133	0.0210	0.0652	0.0587	0.0617	0.0578	0.0575	0.0578	0.0575	0.0595	0.0577	0.0000	0.0000	0.0063	0.0063
XacMN10	0.4076	0.0056	0.0062	0.0168	0.0195	0.0144	0.0171	0.0176	0.0177	0.0638	0.0560	0.0576	0.0556	0.0553	0.0556	0.0553	0.0570	0.0555	0.0062	0.0062	0.0024	0.0024
XacMN11	0.4075	0.0052	0.0058	0.0169	0.0186	0.0146	0.0172	0.0177	0.0182	0.0639	0.0559	0.0577	0.0560	0.0557	0.0560	0.0557	0.0569	0.0559	0.0059	0.0058	0.0026	0.0026
XacMN12	0.4076	0.0054	0.0060	0.0166	0.0186	0.0144	0.0169	0.0175	0.0177	0.0638	0.0560	0.0577	0.0556	0.0553	0.0556	0.0553	0.0569	0.0555	0.0060	0.0061	0.0023	0.0023
XacNT17	0.4095	0.0005	0.0001	0.0125	0.0221	0.0171	0.0180	0.0135	0.0209	0.0656	0.0589	0.0621	0.0580	0.0577	0.0580	0.0577	0.0596	0.0578	0.0002	0.0002	0.0062	0.0062
XacUI6	0.4077	0.0059	0.0065	0.0171	0.0190	0.0149	0.0177	0.0181	0.0182	0.0644	0.0566	0.0583	0.0558	0.0555	0.0558	0.0555	0.0572	0.0557	0.0063	0.0065	0.0025	0.0025
XacUI7	0.4076	0.0055	0.0060	0.0173	0.0190	0.0150	0.0177	0.0182	0.0183	0.0644	0.0567	0.0583	0.0557	0.0554	0.0557	0.0554	0.0571	0.0556	0.0061	0.0061	0.0014	0.0014
XacX18	0.3933	0.1462	0.1461	0.1379	0.1488	0.1348	0.1368	0.1378	0.1364	0.1522	0.1446	0.1455	0.1543	0.1543	0.1543	0.1543	0.1399	0.1544	0.1459	0.1459	0.1422	0.1422
XacX20	0.4086	0.1559	0.1559	0.1476	0.1590	0.1447	0.1469	0.1476	0.1462	0.1417	0.1337	0.1351	0.1471	0.1471	0.1471	0.1471	0.1367	0.1472	0.1557	0.1557	0.1519	0.1519
XagCFBP7119	0.4154	0.1611	0.1608	0.1537	0.1650	0.1507	0.1531	0.1535	0.1521	0.1552	0.1469	0.1488	0.1544	0.1544	0.1544	0.1544	0.1453	0.1545	0.1606	0.1606	0.1574	0.1574
XalfacFBP3836	0.1448	0.3896	0.3893	0.3831	0.3930	0.3808	0.3822	0.3826	0.3832	0.3924	0.3882	0.3888	0.3951	0.3952	0.3952	0.3951	0.3839	0.3952	0.3892	0.3893	0.3867	0.3867
Xalfaf1	0.1413	0.3926	0.3923	0.3876	0.3965	0.3852	0.3866	0.3870	0.3868	0.3951	0.3905	0.3916	0.3980	0.3980	0.3980	0.3980	0.3871	0.3980	0.3921	0.3921	0.3900	0.3900
Xalfacm1510	0.1390	0.3895	0.3892	0.3829	0.3935	0.3807	0.3810	0.3824	0.3822	0.3910	0.3864	0.3875	0.3942	0.3942	0.3942	0.3942	0.3822	0.3943	0.3891	0.3891	0.3871	0.3871
Xalfacm1637	0.1398	0.3903	0.3901	0.3832	0.3932	0.3814	0.3810	0.3831	0.3823	0.3938	0.3888	0.3901	0.3960	0.3960	0.3960	0.3960	0.3853	0.3961	0.3899	0.3899	0.3874	0.3874
Xaub11122	0.4191	0.2843	0.2842	0.2767	0.2833	0.2726	0.2749	0.2762	0.2709	0.2837	0.2811	0.2829	0.2919	0.2919	0.2919	0.2919	0.2792	0.2919	0.2841	0.2841	0.2808	0.2808
Xaub1561	0.4264	0.2948	0.2946	0.2872	0.2984	0.2854	0.2857	0.2874	0.2867	0.2949	0.2925	0.2941	0.3021	0.3021	0.3021	0.3021	0.2902	0.3022	0.2945	0.2945	0.2914	0.2914
Xauc10535	0.4164	0.2877	0.2876	0.2800	0.2912	0.2777	0.2784	0.2798	0.2798	0.2912	0.2853	0.2876	0.2962	0.2962	0.2962	0.2962	0.2823	0.2962	0.2874	0.2874	0.2842	0.2842
Xauc1559	0.4412	0.3166	0.3166	0.3101	0.3201	0.3085	0.3079	0.3104	0.3100	0.3216	0.3156	0.3178	0.3255	0.3255	0.3255	0.3255	0.3126	0.3256	0.3164	0.3164	0.3135	0.3135
Xauc1609	0.4354	0.3036	0.3034	0.2974	0.3070	0.2951	0.2959	0.2972	0.2969	0.3081	0.3021	0.3039	0.3130	0.3130	0.3130	0.3129	0.2991	0.3130	0.3033	0.3033	0.3004	0.3004
Xauc535	0.4241	0.2953	0.2953	0.2875	0.2989	0.2854	0.2861	0.2872	0.2871	0.2984	0.2919	0.2941	0.3041	0.3041	0.3041	0.3041	0.2890	0.3041	0.2951	0.2951	0.2921	0.2921
Xauc763	0.4409	0.2807	0.2806	0.2729	0.2843	0.2702	0.2740	0.2722	0.2724	0.2844	0.2783	0.2805	0.2804	0.2804	0.2804	0.2804	0.2750	0.2805	0.2804	0.2804	0.2772	0.2772

XacMN12	0.4076	0.0054	0.0060	0.0166	0.0186	0.0144	0.0169	0.0175	0.0177	0.063
XacNT17	0.4095	0.0005	0.0001	0.0125	0.0221	0.0171	0.0180	0.0135	0.0209	0.065
XacUI6	0.4077	0.0059	0.0065	0.0171	0.0190	0.0149	0.0177	0.0181	0.0182	0.064
XacUI7	0.4076	0.0055	0.0060	0.0173	0.0190	0.0150	0.0177	0.0182	0.0183	0.064
XacX18	0.3933	0.1462	0.1461	0.1379	0.1488	0.1348	0.1368	0.1378	0.1364	0.152
XacX20	0.4086	0.1559	0.1559	0.1476	0.1590	0.1447	0.1469	0.1476	0.1462	0.141
XagCFBP7119	0.4154	0.1611	0.1608	0.1537	0.1650	0.1507	0.1531	0.1535	0.1521	0.155
XalfaCFBP3836	0.1448	0.3896	0.3893	0.3831	0.3930	0.3808	0.3822	0.3826	0.3832	0.392
XalfaF1	0.1413	0.3926	0.3923	0.3876	0.3965	0.3852	0.3866	0.3870	0.3868	0.395
Xalfacm1510	0.1390	0.3895	0.3892	0.3829	0.3935	0.3807	0.3810	0.3824	0.3822	0.391
Xalfacm1637	0.1398	0.3903	0.3901	0.3832	0.3932	0.3814	0.3810	0.3831	0.3823	0.393
XauB11122	0.4191	0.2843	0.2842	0.2767	0.2833	0.2726	0.2749	0.2762	0.2709	0.283
XauB1561	0.4264	0.2948	0.2946	0.2872	0.2984	0.2854	0.2857	0.2874	0.2867	0.294
XauC10535	0.4164	0.2877	0.2876	0.2800	0.2912	0.2777	0.2784	0.2798	0.2798	0.291
XauC1559	0.4412	0.3166	0.3166	0.3101	0.3201	0.3085	0.3079	0.3104	0.3100	0.321
XauC1609	0.4354	0.3036	0.3034	0.2974	0.3070	0.2951	0.2959	0.2972	0.2969	0.308
XauC535	0.4241	0.2953	0.2953	0.2875	0.2989	0.2854	0.2861	0.2872	0.2871	0.298
XauC762	0.4100	0.2907	0.2906	0.2790	0.2910	0.2790	0.2740	0.2790	0.2791	0.294

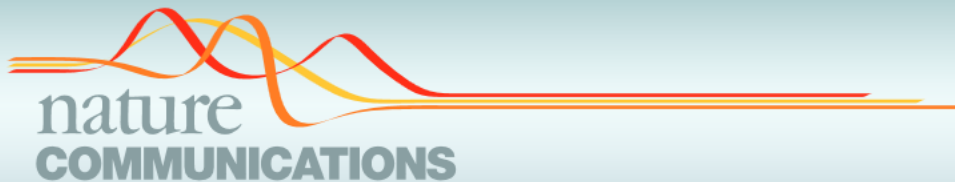
Largest distance: **0.4506** (*X. perforans* 91-118 and *X. fuscans aurantifolii* C 1559)

For comparison: distance between *Stenotrophomonas maltophilia* and Xac 306: **0.912**

ANI

- **Average Nucleotide Identity** [Goris et al. 2007]
- Baseado em BLAST
- one-way ANI (best hits)
- two-way ANI (reciprocal best hits)
- Typically, 2 species will have **ANI $\geq$ 95%**
- **< 75%** : not to be trusted
- <http://enve-omics.ce.gatech.edu/ani/>

FastANI



ARTICLE

DOI: 10.1038/s41467-018-07641-9

OPEN

High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries

Chirag Jain^{1,2}, Luis M. Rodriguez-R^{3,4} , Adam M. Phillippy², Konstantinos T. Konstantinidis^{3,4} & Srinivas Aluru^{1,5}

FastANI can be downloaded at <https://github.com/ParBLiSS/FastANI/releases>.

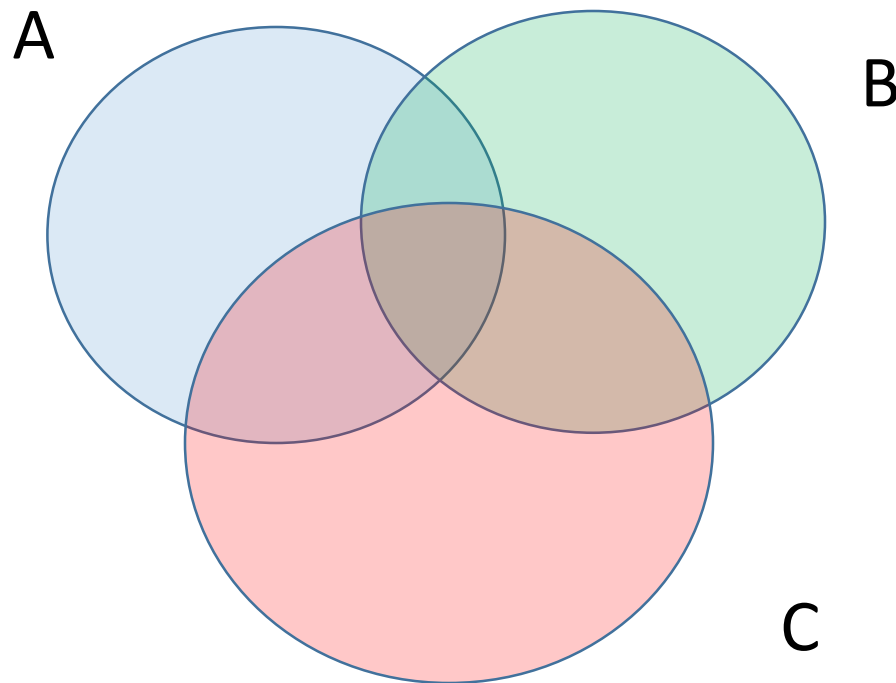
GGDC

- Genome-to-genome distance calculator
- rigorous *in silico* replacement for DNA-DNA hybridization wet-lab experiments
- <http://ggdc.dsmz.de>
- Meier-Kolthoff, J.P., et al., *Genome sequence-based species delimitation with confidence intervals and improved distance functions*. BMC Bioinformatics, 2013. 14: p. 60

Comparação de conjuntos de genes

- Given a set of genomes, represented by their 'proteomes' or sets of protein sequences
- Given homologous relationships (as given for example by orthoMCL, veja adiante)
 - Which genes are shared by genomes X and Y ?
 - Which genes are unique to genome Z ?
 - Venn or extended Venn diagrams

3-way genome comparison



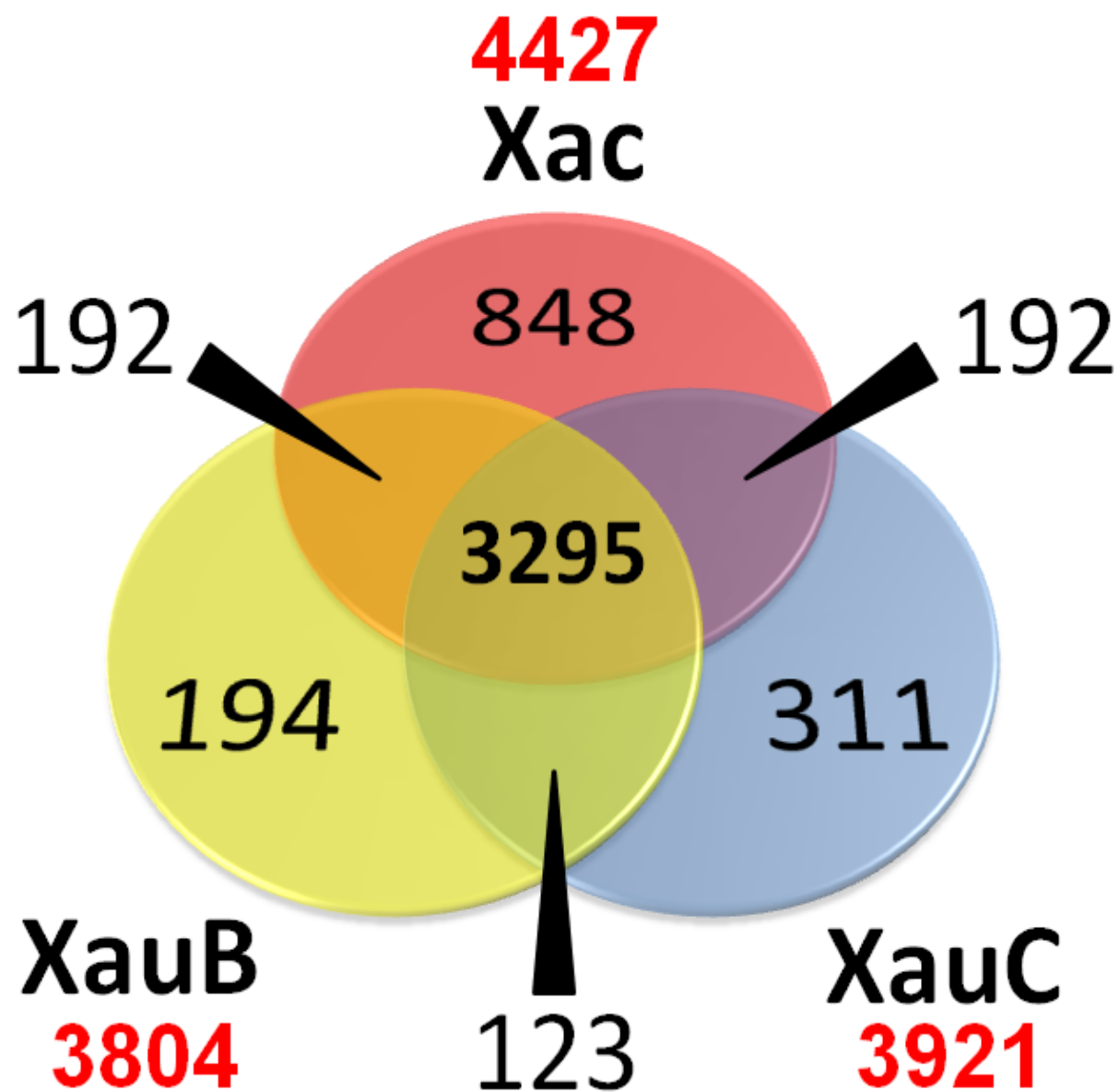
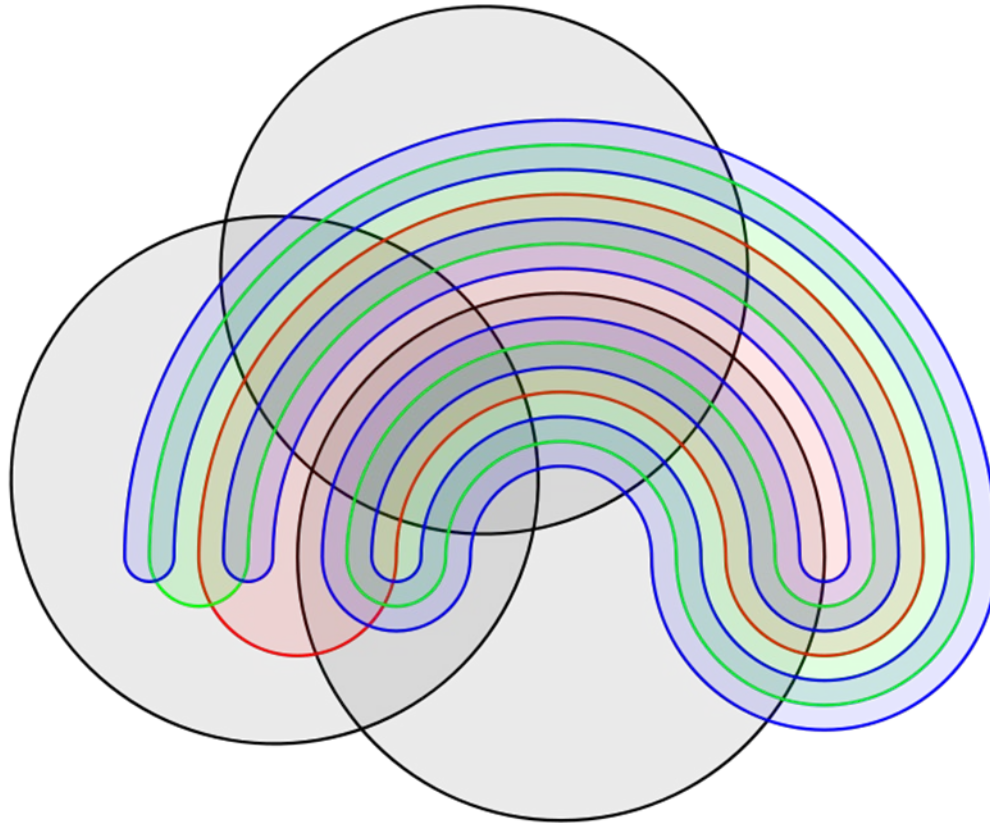


Diagrama de Venn para $n = 6$



Número de comparações é quadrático em n
Número de regiões num diagrama de Venn = 2^n

Source: wikipedia

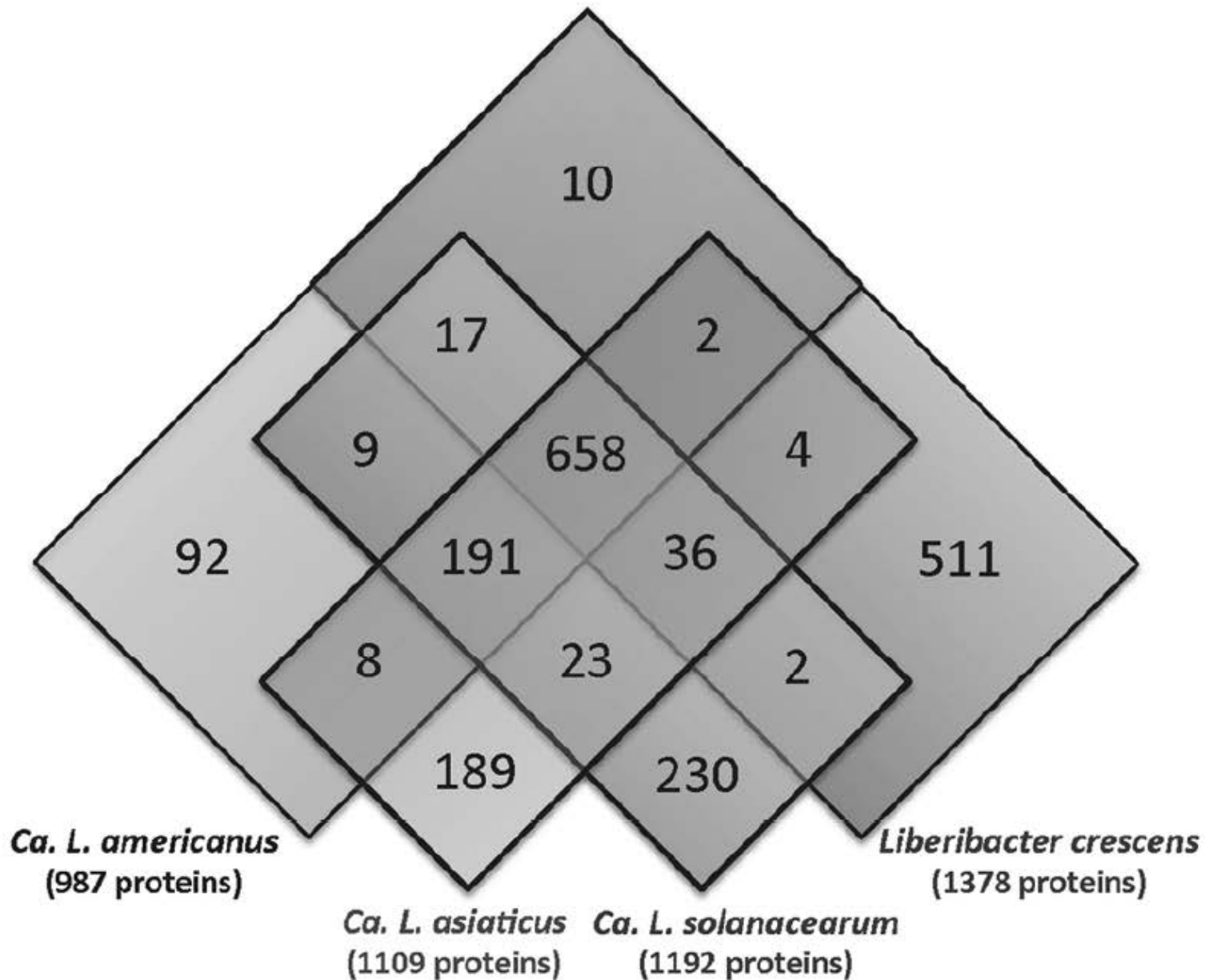
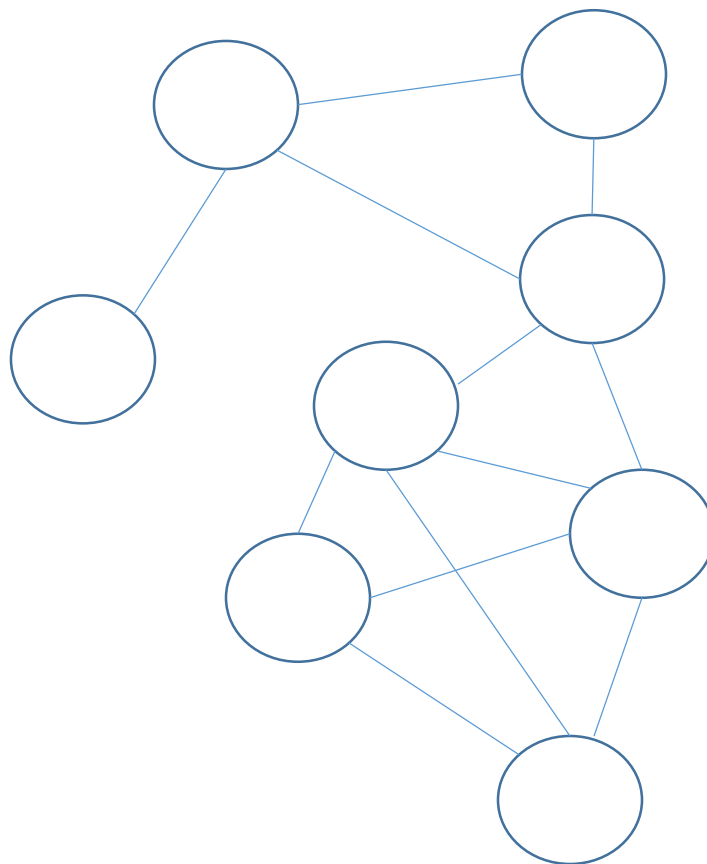
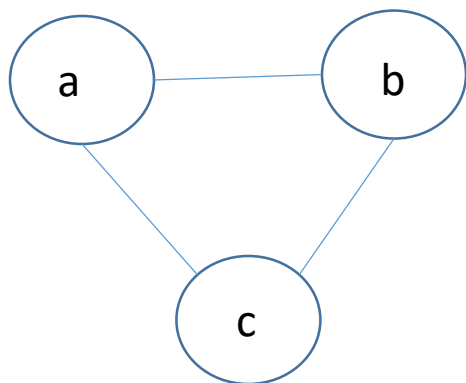


Fig. 2. Venn diagram showing protein-coding gene sharing among the four *Liberibacter* genomes. Numbers below each species are the total number of predicted protein-coding genes for that genome.

Cômputo de famílias de proteínas

1. Verificar as similaridades entre as sequências
 - a) Usando (por exemplo) BLAST + critérios
2. Representar as similaridades num **grafo**
3. Aplicar um **algoritmo de clusterização** sobre o grafo

Clusterização é necessária porque o grafo pode ser complexo



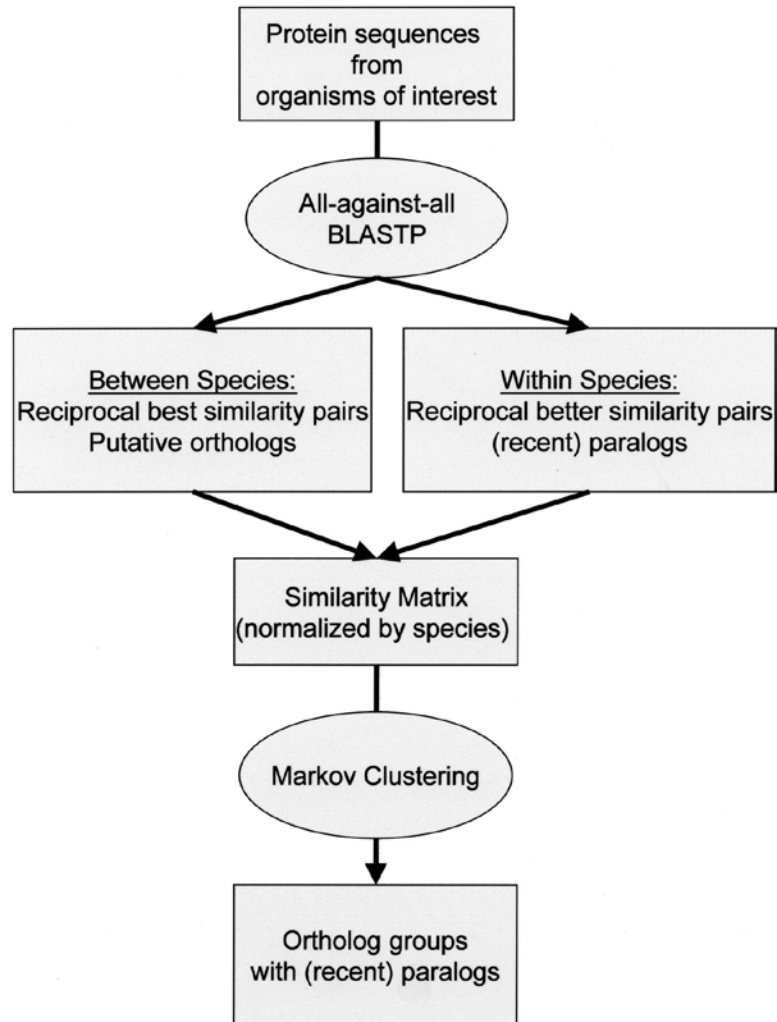
Resultado da clusterização

- Matriz com genes nas colunas (g_j), genomas nas linhas (O_i)
- Cada coluna representa uma **família de genes homólogos**

	g1	g2	g3	g4	...
O1	✓		✓	✓	
O2		✓	✓		
O3	✓		✓		
O4			✓	✓	✓
O5	✓		✓		✓
O6			✓		
...			✓		

Foi este tipo de processamento que permitiu obter dados para construir a árvore da vida vista na primeira aula do tema “comparação de sequências”

orthoMCL pipeline



Li Li et al. *Genome Res.* 2003; 13: 2178-2189

OrthoMCL DB

Ortholog Groups of Protein Sequences

■ [Home](#)

■ [About OrthoMCL](#) ▾

■ [Data](#) ▾

■ [Search](#) ▾

■ [Tools](#) ▾

NEWS

Mar 31, 2011

OrthoMCL-DB Version 5 is released. We have included 150 genomes in this release.

May 31, 2010

OrthoMCL-DB Version 4 is released. There are 138 genomes included in version 4.

Oct 9, 2009

OrthoMCL-DB Version 3 is released. The new dataset includes 128 genomes. New web site features include: (1) a tool to assign your proteins to OrthoMCL groups (see the new tools menu); (2) a mapping from Version 3 groups to Version 2 and 1 is available for searching, allowing you to track changes across versions; (3) the phyletic pattern in the groups result page is configurable, so you can tailor it to the clades you are interested in.

Sep 22, 2009

OrthoMCL-DB pipeline re-engineered. We have completely overhauled how we produce the database, encoding the entire process in a pipeline system. This should dramatically improve our ability to deliver new versions of the database.

Feb 28, 2008

OrthoMCL-DB Version 2 is released. The

Welcome to OrthoMCL DB

Ortholog Groups of Protein Sequences from Multiple Genomes!

Current Release:

Version: 5

Number of Genomes: 150

Number of Protein Sequences: 1398546

Number of Ortholog Groups: 124740

Search for Groups

- [by IDs, Keyword, or PFam domain](#)
- [by Phyletic Pattern](#)
- [by Phyletic Pattern - Advanced](#)
- [by Group Properties](#)
- [Query History - Groups](#)

Search for Sequences

- [by IDs, Keyword, Taxonomy or PFam domain](#)
- [by BLAST Search](#)
- [Query History - Sequences](#)

Tools

- [Assign your proteins to OrthoMCL groups](#)

OrthoMCL Software

Database Download



Xanthomonas fuscans str. *aurantifolii* Genome Project



Choose genomes to see OrthoMCL families containing genes from them

Include	Exclude	I don't care	
☐	☐	☒	<i>Xanthomonas fuscans</i> subsp. <i>aurantifolii</i> str. 11122 (B)
☐	☐	☒	<i>Xanthomonas fuscans</i> subsp. <i>aurantifolii</i> str. 10535 (C)
☐	☐	☒	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. 8004
☐	☐	☒	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str. ATCC 3391
☐	☐	☒	<i>Xanthomonas campestris</i> pv. <i>campestris</i> B100
☐	☐	☒	<i>Xanthomonas campestris</i> pv. <i>vesicatoria</i> str. 85-10
☐	☐	☒	<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306
☐	☐	☒	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> KACC10331
☐	☐	☒	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> MAFF 311018
☐	☐	☒	<i>Xanthomonas oryzae</i> pv. <i>oryzae</i> PXO99A
☐	☐	☒	<i>Xanthomonas albilineans</i> GPE PC73
☐	☐	☒	<i>Xylella fastidiosa</i> 9a5c
☐	☐	☒	<i>Xylella fastidiosa</i> M12
☐	☐	☒	<i>Xylella fastidiosa</i> M23 plasmid pXFAS01
☐	☐	☒	<i>Xylella fastidiosa</i> Temecula1

☐ check all ☐ check all ☐ check all(see all families)

Submit Query

Reset

```

=====
>Family 5286 -- Gblocks 331/384 (86%)
21243924 nr alkanesulfonate transporter substrate-binding subunit [Xanthomonas axonopodis pv. citri str. 306]
9810940 nr - nitrate transport protein [Xanthomonas fuscans subsp. aurantifolii str. 11122 (B)]
9929350 nr - nitrate transport protein [Xanthomonas fuscans subsp. aurantifolii str. 10535 (C)]

count_ = 3
=====
>Family 5287 -- Gblocks 346/346 (100%)
21243925 nr oxidoreductase [Xanthomonas axonopodis pv. citri str. 306]
9810930 nr - oxidoreductase [Xanthomonas fuscans subsp. aurantifolii str. 11122 (B)]
9929360 nr - oxidoreductase [Xanthomonas fuscans subsp. aurantifolii str. 10535 (C)]

count_ = 3
=====
>Family 5288 -- Gblocks 442/442 (100%)
21243926 nr nitrilotriacetate monooxygenase component A [Xanthomonas axonopodis pv. citri str. 306]
9810920 nr - nitrilotriacetate monooxygenase component A [Xanthomonas fuscans subsp. aurantifolii str. 11122 (B)]
9929370 nr - nitrilotriacetate monooxygenase component A [Xanthomonas fuscans subsp. aurantifolii str. 10535 (C)]

count_ = 3
=====
>Family 5289 -- Gblocks 356/356 (100%)
21243950 nr avirulence protein [Xanthomonas axonopodis pv. citri str. 306]
9814680 nr - type III secretion system hopX1-like protein [Xanthomonas fuscans subsp. aurantifolii str. 11122 (B)]
9900040 nr - type III secretion system hopX1-like protein [Xanthomonas fuscans subsp. aurantifolii str. 10535 (C)]

count_ = 3
=====
>Family 5290 -- Gblocks 291/297 (97%)
21243956 nr hypothetical protein XAC3230 [Xanthomonas axonopodis pv. citri str. 306]
9826830 nr - conserved hypothetical protein [Xanthomonas fuscans subsp. aurantifolii str. 11122 (B)]
9923780 nr - conserved hypothetical protein [Xanthomonas fuscans subsp. aurantifolii str. 10535 (C)]

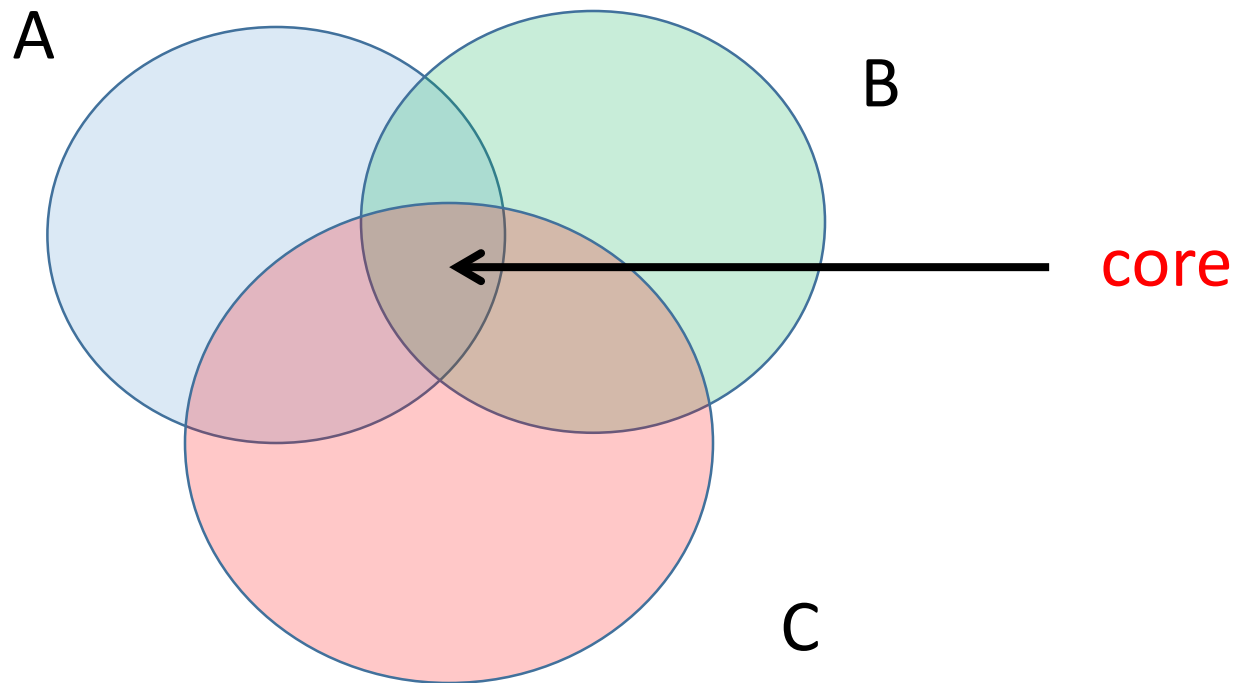
count_ = 3
=====
>Family 5291 -- Gblocks 203/373 (54%)
21243959 nr transposase [Xanthomonas axonopodis pv. citri str. 306]
9803570 nr - transposase [Xanthomonas fuscans subsp. aurantifolii str. 11122 (B)]
9900450 nr - transposase [Xanthomonas fuscans subsp. aurantifolii str. 10535 (C)]

count_ = 3
=====
>Family 5292 -- Gblocks 163/171 (95%)
21243960 nr hypothetical protein XAC3234 [Xanthomonas axonopodis pv. citri str. 306]
9820110 nr - conserved hypothetical protein [Xanthomonas fuscans subsp. aurantifolii str. 11122 (B)]

```



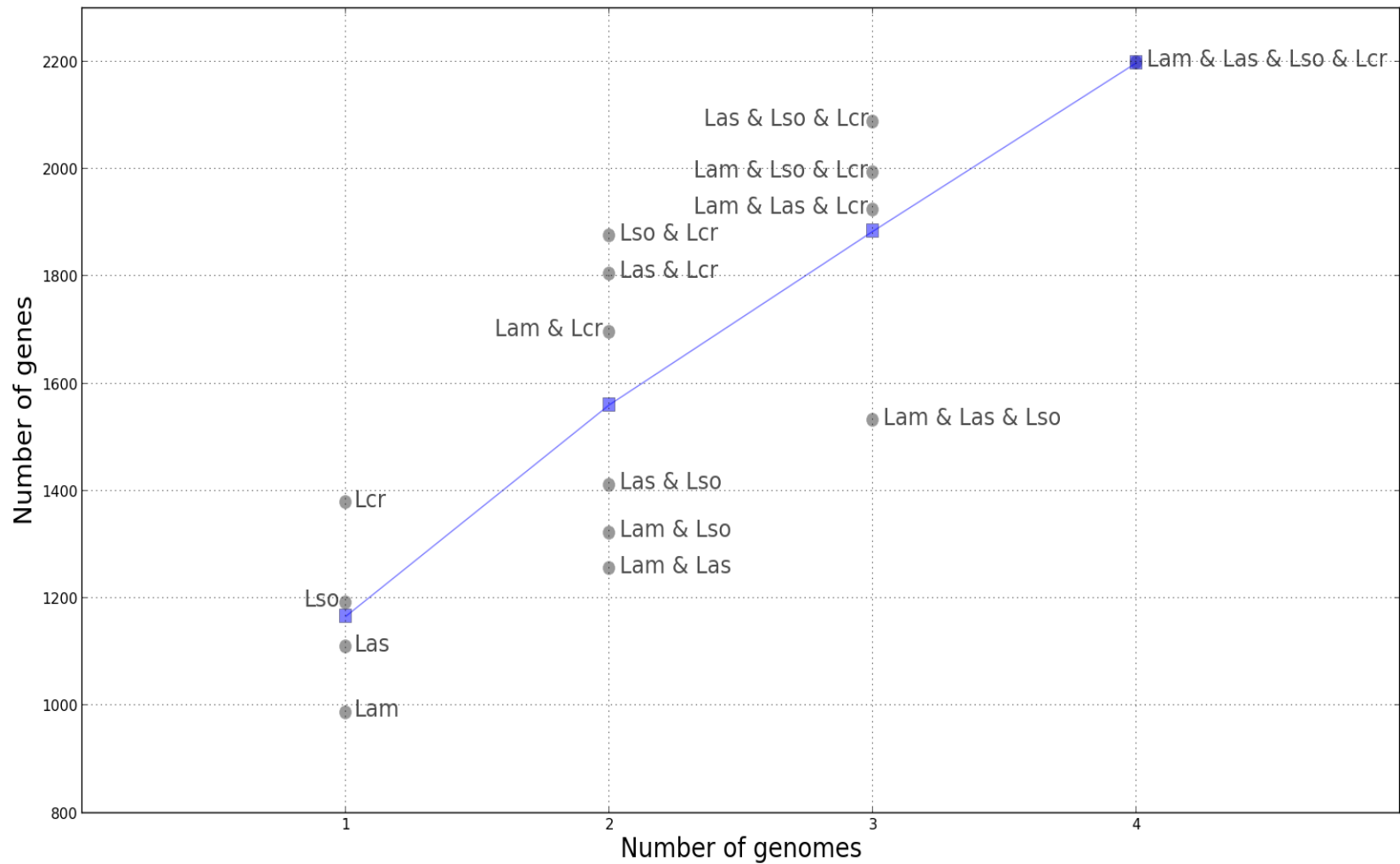
Pan genoma; genoma core e genoma acessório



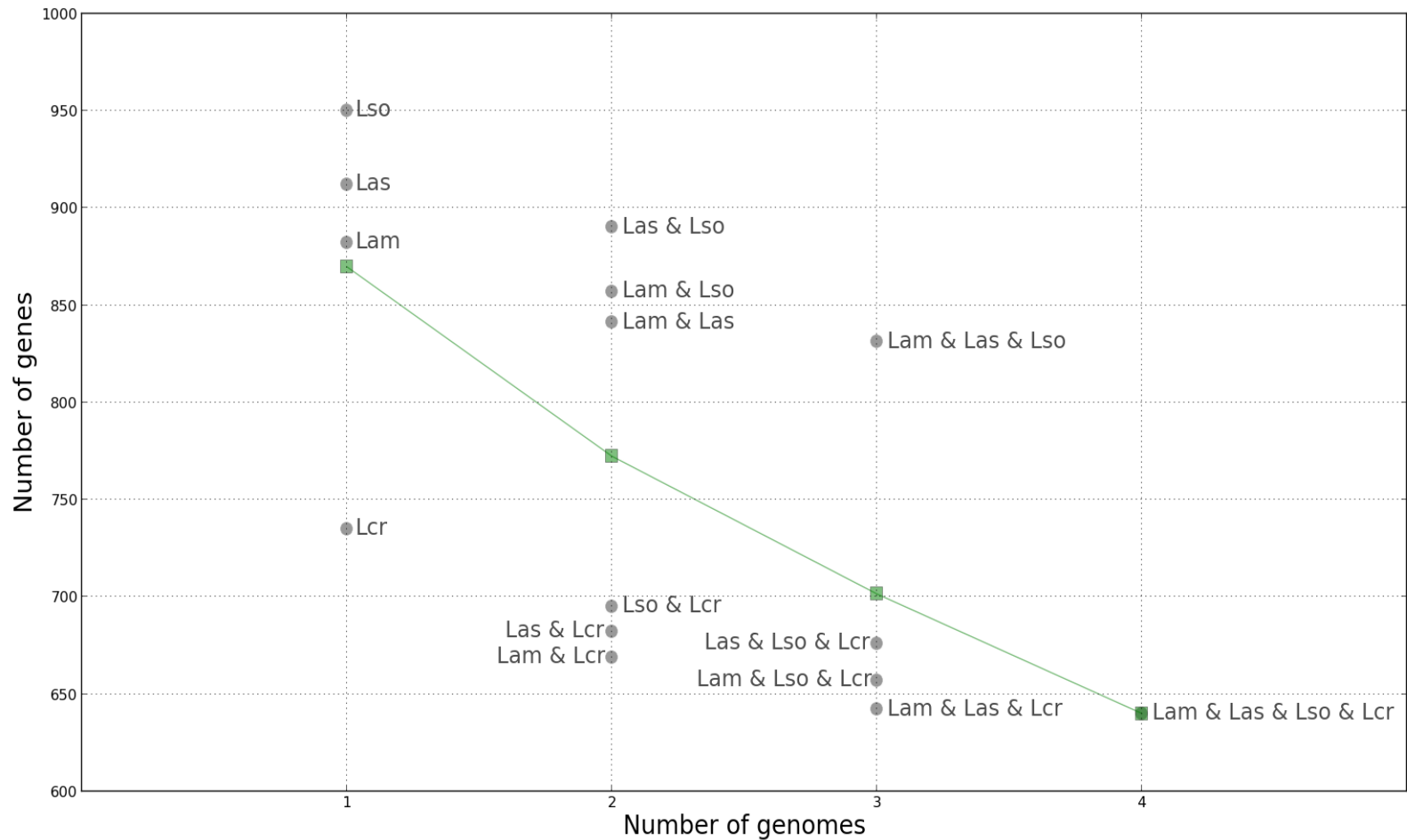
pan: $A \cup B \cup C$

acessório: pan menos core

Curva de pan-genoma (n = 4)



Curva de core genoma (n = 4)



O número de genes para x=1 não é o mesmo do gráfico anterior pois os singletons são descartados

Genomas fechados e abertos

- Fechado

- O número de genes/famílias do pan-genoma atinge um platô

- Aberto

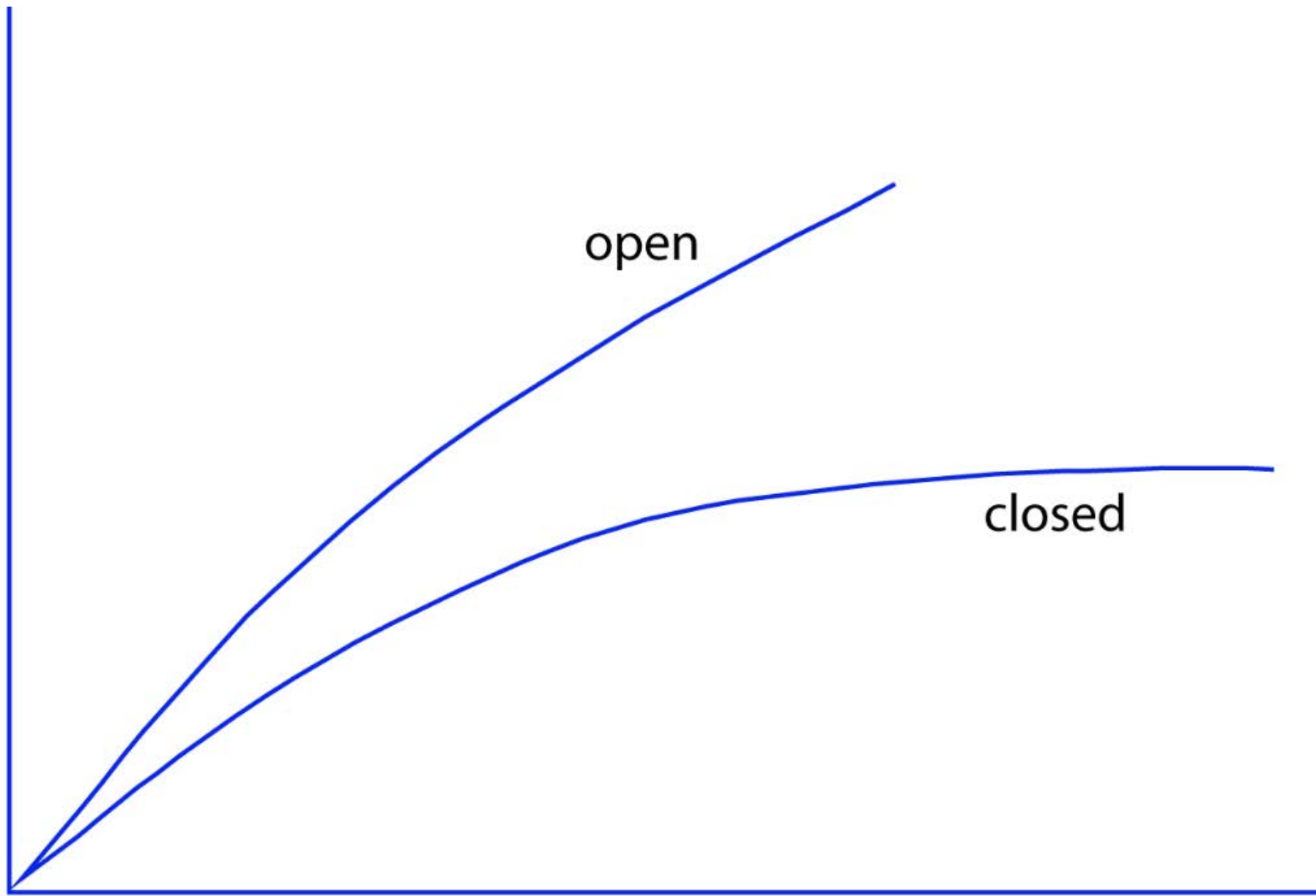
- O número de genes/famílias não atinge um platô; cresce sempre que se acrescentam novos genomas

genes

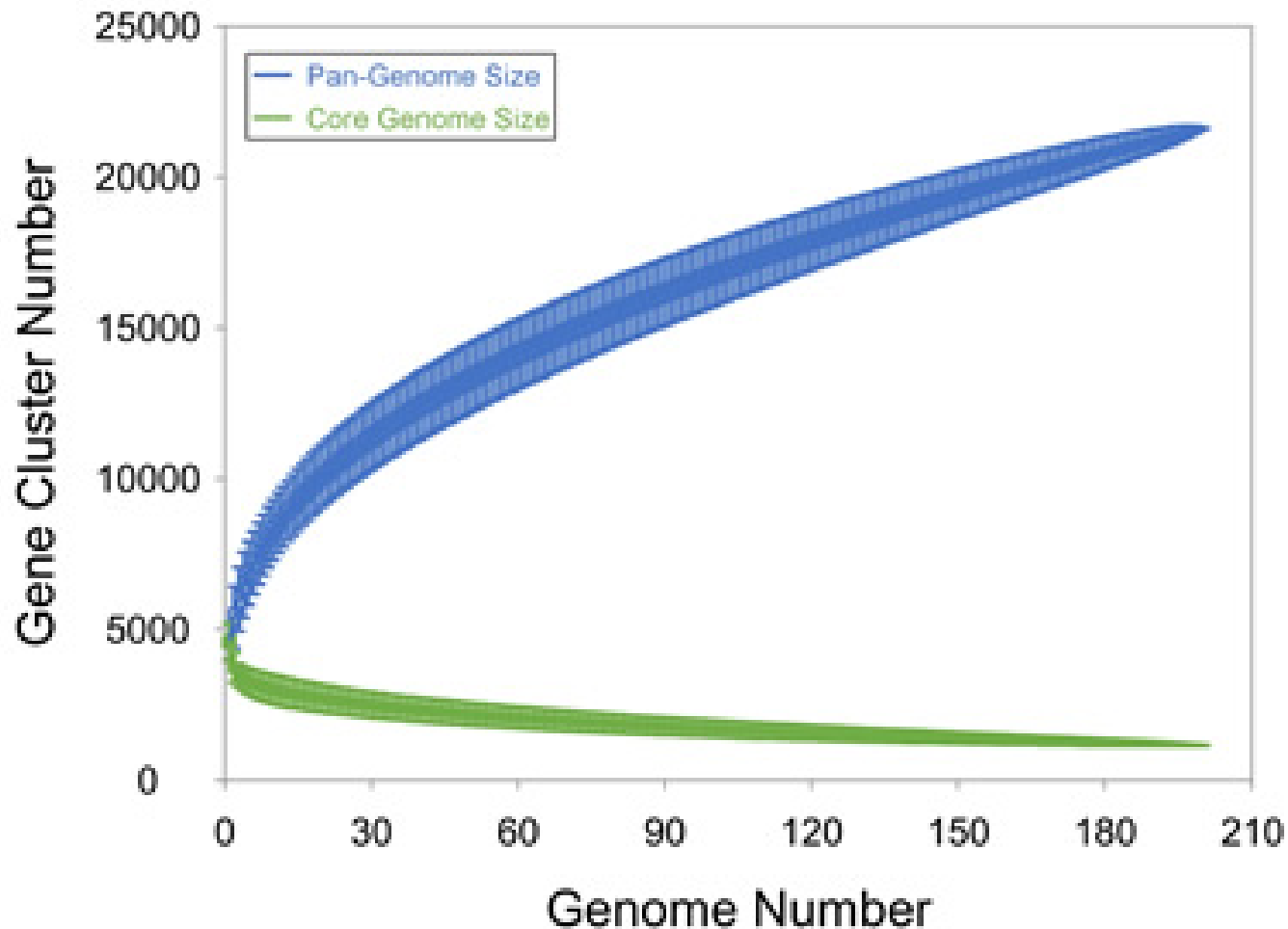
open

closed

genomes



O genoma de *E. coli* é aberto



Bacillus anthracis

- Genoma fechado
- Cerca de 3.000 genes

Ferramentas para análise pan/core

- Get_Homologues
 - Contreras-Moreira, B. and P. Vinuesa, *GET_HOMOLOGUES, a versatile software package for scalable and robust microbial pangenome analysis.* Appl Environ Microbiol, 2013. 79(24): p. 7696-701
- Panaroo
 - Tonkin-Hill, G., MacAlasdair, N., Ruis, C. et al. Producing polished prokaryotic pangenomes with the Panaroo pipeline. Genome Biol 21, 180 (2020). <https://doi.org/10.1186/s13059-020-02090-4>

Conjuntos + contexto

- Como genes compartilhados aparecem em seus respectivos genomas?
- **Filogenômica**
- Busca de **sintenia** = preservação de ordem
- Basta fazer um alinhamento
 - Os “caracteres” a serem alinhados são os genes
 - *alinhamento de ortólogos*

Alinhamento de ortólogos obtido no IMG/JGI

é a “vizinhança ortóloga” do gene vermelho

Xanthomonas axonopodis pv. *citri* str. 306: NC_003919



Xanthomonas fuscans subsp. *aurantifolii* str. ICPB 11122 xaub_ctg679_0: NZ_ACPX01000220



Xanthomonas axonopodis pv. *malvacearum* GSPB1386 : AHIB01000037



Xanthomonas axonopodis pv. *malvacearum* GSPB2388 : AHIC01000016

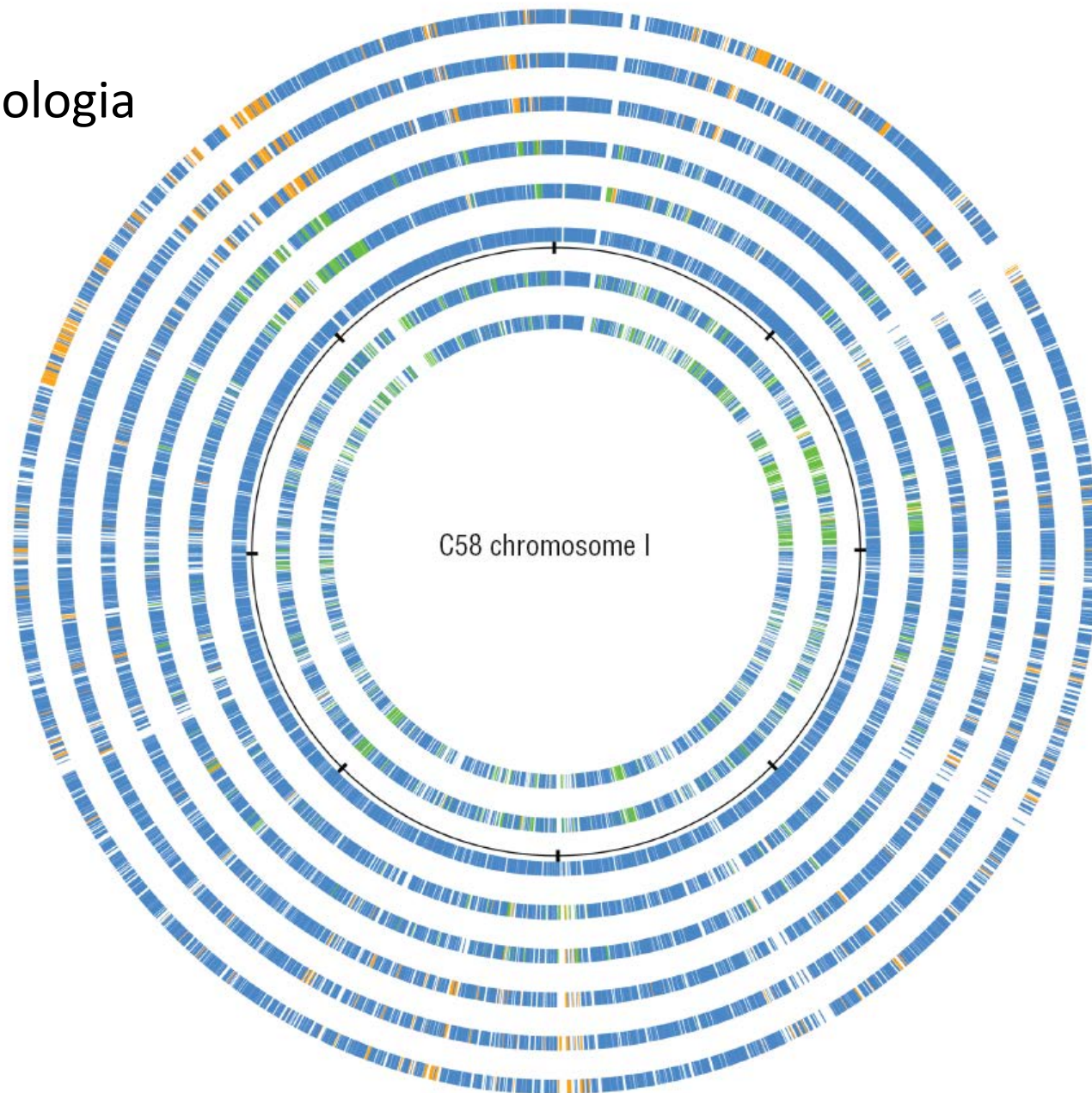


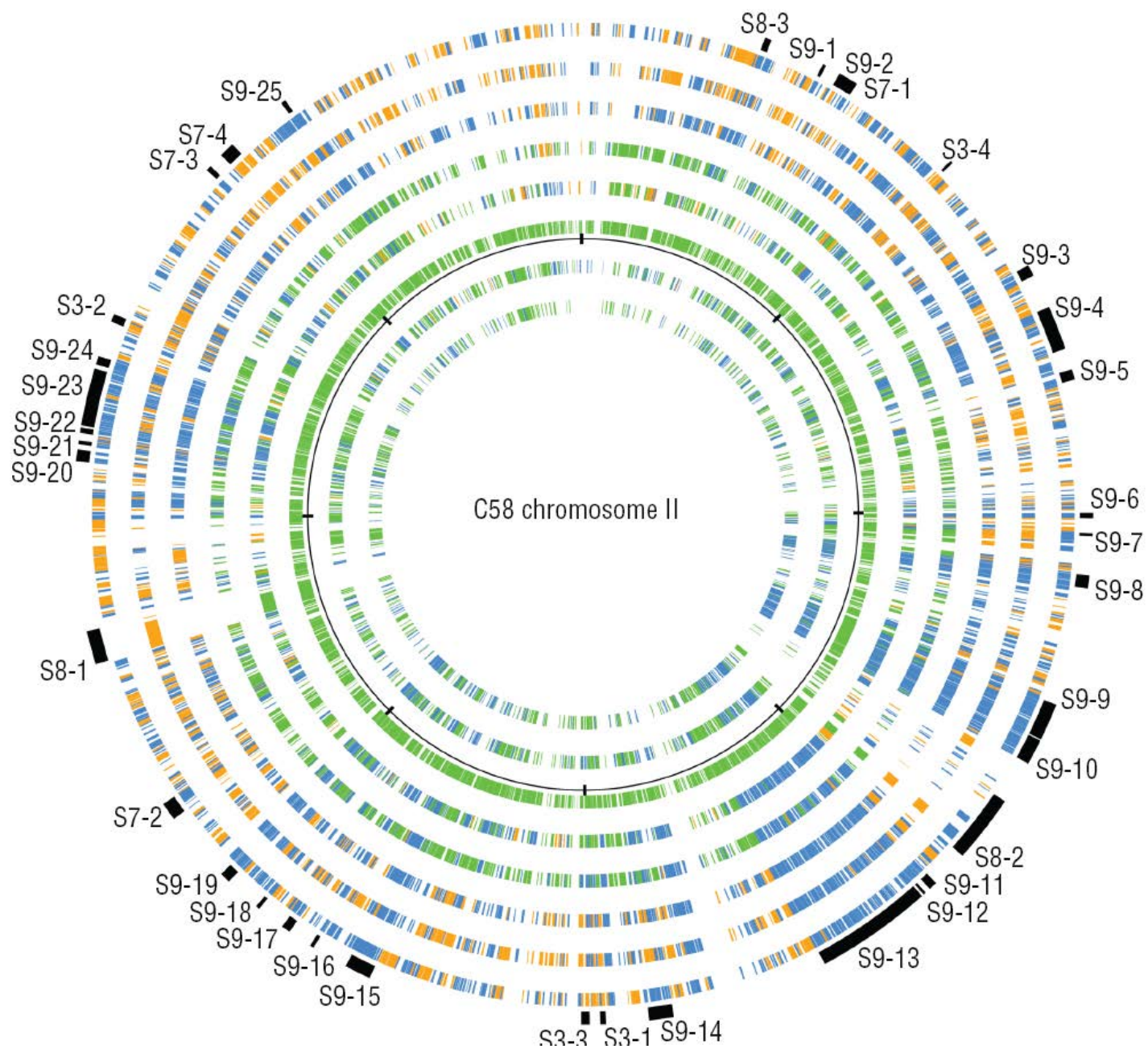
Xanthomonas axonopodis pv. *punicae* LMG 859 : CAGJ01000020



genes de mesmas cores são ortólogos

Roda da ortologia





Protein family resources



Clusters of orthologous groups (COG, KOG, eggNOG)

KEGG orthologs

Pfam 26.0 (November 2011, 13672 families)

The Pfam database is a large collection of protein families, each represented by **multiple sequence alignments** and **hidden Markov models (HMMs)**. [More...](#)



QUICK LINKS

[SEQUENCE SEARCH](#)

[VIEW A PFAM FAMILY](#)

[VIEW A CLAN](#)

[VIEW A SEQUENCE](#)

[VIEW A STRUCTURE](#)

[KEYWORD SEARCH](#)

[JUMP TO](#)

YOU CAN FIND DATA IN PFAM IN VARIOUS WAYS...

Analyze your protein sequence for Pfam matches

View Pfam family annotation and alignments

See groups of related families

Look at the domain organisation of a protein sequence

Find the domains on a PDB structure

Query Pfam by keywords

[Go](#)

[Example](#)

Enter any type of accession or ID to jump to the page for a Pfam family or clan, UniProt sequence, PDB structure, etc.

Or view the [help](#) pages for more information

Recent Pfam [blog](#) posts

[Hide the](#)

[Does my family of interest have a determined 3D protein structure?](#) (posted 9 May 2012)

Two related questions that we are often asked via the Pfam helpdesk is 'Which families have a known three-dimensional structure?' and 'Why is a particular a PDB structure not found in Pfam'. You may think that there are obvious answers to these questions – but as with many things in life the answer is not [...]

[TreeFam is back with a new release!](#) (posted 27 March 2012)

Query by accession

Protein: *PDK1_HUMAN* (Q15118)

 1 architecture

 1 sequence

 0 interactions

 1 species

 3 structures

Summary

Features

Sequence

Interactions

Structures

TreeFam

Jump to...

[Go](#)

Summary

PDK1_HUMAN

This is the summary of UniProt entry [PDK1_HUMAN](#) ([Q15118](#)).

Description:	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 1, mitochondrial EC=2.7.11.2
Source organism:	Homo sapiens (Human) (NCBI taxonomy ID 9606) View Pfam proteome data.
Length:	436 amino acids

Please note: when we start each new Pfam data release, we take a copy of the UniProt sequence database. This snapshot of UniProt forms the basis of the overview that you see here. It is important to note that, although some UniProt entries may be removed *after* a Pfam release, these entries will not be removed from Pfam until the *next* Pfam data release.

Pfam domains

This image shows the arrangement of the Pfam domains that we found on this sequence. Clicking on a domain will take you to the page describing that Pfam entry. The table below gives the domain boundaries for each of the domains.



Source	Domain	Start	End
sig_p	n/a	1	21
low_complexity	n/a	2	41
Pfam A	BCDHK_Adom3	55	221
Pfam A	HATPase_c	268	392

KEYWORD SEARCH

SEQUENCE SEARCH

Enter a protein sequence: ?

Sequence query limits: Protein - 50kb

The PANTHER (Protein **AN**alysis **TH**rough Evolutionary Relationships) Classification System is a unique resource that **classifies genes by their functions**, using published scientific experimental evidence and evolutionary relationships to predict function even in the absence of direct experimental evidence. Proteins are **classified by expert biologists** according to:

- ✧ [Gene families and subfamilies](#), including annotated phylogenetic trees
- ✧ [Gene Ontology classes](#): molecular function, biological process, cellular component
- ✧ [PANTHER Protein Classes](#)
- ✧ [Pathways, including diagrams](#)

PANTHER is part of the [Gene Ontology Reference Genome Project](#).

PANTHER is supported by a research grant from the National Institute of General Medical Sciences [grant [GM081084](#)] and maintained by the [Thomas lab at the University of Southern California](#).

Quick links

[Whole genome function views](#)[Gene expression tools](#)[cSNP tools](#)[Upload multiple gene IDs](#)[Community Curation](#)[My Workspace](#)[HMM scoring](#)[Downloads](#)[Genome statistics](#)[Site map](#)

Newsletter subscription

Enter your Email:

What can I do on the PANTHER site?

[Guide to getting started](#)

News

(March 16, 2012)

PANTHER 7.2 is released.

[Click](#) for additional info.

Publications

[How to cite PANTHER](#)

"PANTHER version 7: improved phylogenetic trees, orthologs and collaboration with the Gene Ontology Consortium." [Mi, et al.](#)

"Applications for protein sequence-function evolution data: mRNA/protein expression analysis and coding SNP scoring tools." [Thomas, et al.](#)

"PANTHER: a library of protein families and subfamilies indexed by function." [Thomas, et al.](#)

Search

PANTHER families

Go

Quick links

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[Gene expression tools](#)

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PANTHER HMM SEQUENCE SCORING RESULTS ?

The top scoring HMM is reported, along with the E-value (the number of expected false-positive hits expected). If the E-value is less than 1e-3, no hits are reported.

PANTHER Hit: [PROLINE SYNTHETASE CO-TRANSCRIBED BACTERIAL HOMOLOG PROTEIN](#) (PTHR10146)

HMM E-value score: 2.2e-113 ●●● ?

Sequence	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
sequence	1/1	1	234	11	253	387.5	2.2e-113

Alignments of top-scoring domains:

sequence: domain 1 of 1, from 1 to 234: score 387.5, E = 2.2e-113

```
*->lgvaanLakVlerikaaaakagRdppavrLvAVSKTkPaelileayd
++va+nL++V+++++a+ak+ R + +LvAVSKTkP+e+++eay+
sequence 1 MAVAKNLLAVRAKVAEAVAKSARQ-QQCTLVAVSKTKPVEDLQEAYE 46

aGqRhFGENYvQEElleKap1LpdlcpdikWHFIGhLQsNKvkk11.gvpn
a qRhFGENY+QE1++Kap1Lp d+kWH+IGh+QsNK+k+l+++vpn
sequence 47 ADQRHFGENYIQELVQKAPLLPK---DVKWHYIGHVQSNKAKPLVrDVPN 93

ldmvhsvDslklAdklknaaaaklkg1gkplkv1vQVNtsGEesKsGvppe
l++v++vDs+k+A++lnka ++ ++++l+v+vQVNts Ee+KsG++ +
sequence 94 LFVVETVDSIKIANALNKASGEF--RSEKLNVMVQVNTSEEEQKSGIDAD 141

Elpellkhv1kkcpnLellGLMTIGpfdgdlekgnpdpdFalLaklrkevc
+el++h+++ c++L+l GLMTIG++++ ++ F +L+++rk+v+
sequence 142 GSVELAQHIVSSCEHLNLTGLMTIGRYGDTTSE----CFDRLVACRKRVA 187

kklgl1npk11ELSMGMSgDfelAIeaGsT1VRvGsaIFGeRdypkpkp<-*
+++g + 1 LSMGMSgDfelAI GsT+VRvGs+IFG+R+y +k+
sequence 188 EAIGKAETDLDLSMGMSGDFELAI SCGSTHVRVGSTIFGARNYANKE 234
```

Search

Quick links

[Whole genome function views](#)
[Gene expression tools](#)
[cSNP tools](#)
[Upload multiple gene IDs](#)
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[My Workspace](#)
[HMM scoring](#)
[Downloads](#)
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Enter your Email:

PANTHER FAMILY INFORMATION

Family: PROLINE SYNTHETASE CO-TRANSCRIBED BACTERIAL HOMOLOG PROTEIN (PTHR10146)

Subfamilies: [1](#)

PANTHER Links:



[Tree](#) [MSA](#)

GO Molecular Function: [catalytic activity](#)

GO Biological Process: [metabolic process](#)

↳ [primary metabolic process](#)

↳ [cellular amino acid and derivative metabolic process](#)

↳ [cellular amino acid metabolic process](#)

GO Cellular Component:

PANTHER protein class:

Pathway Categories: No pathway information available

Genes: [45](#)

HMM Length: 273

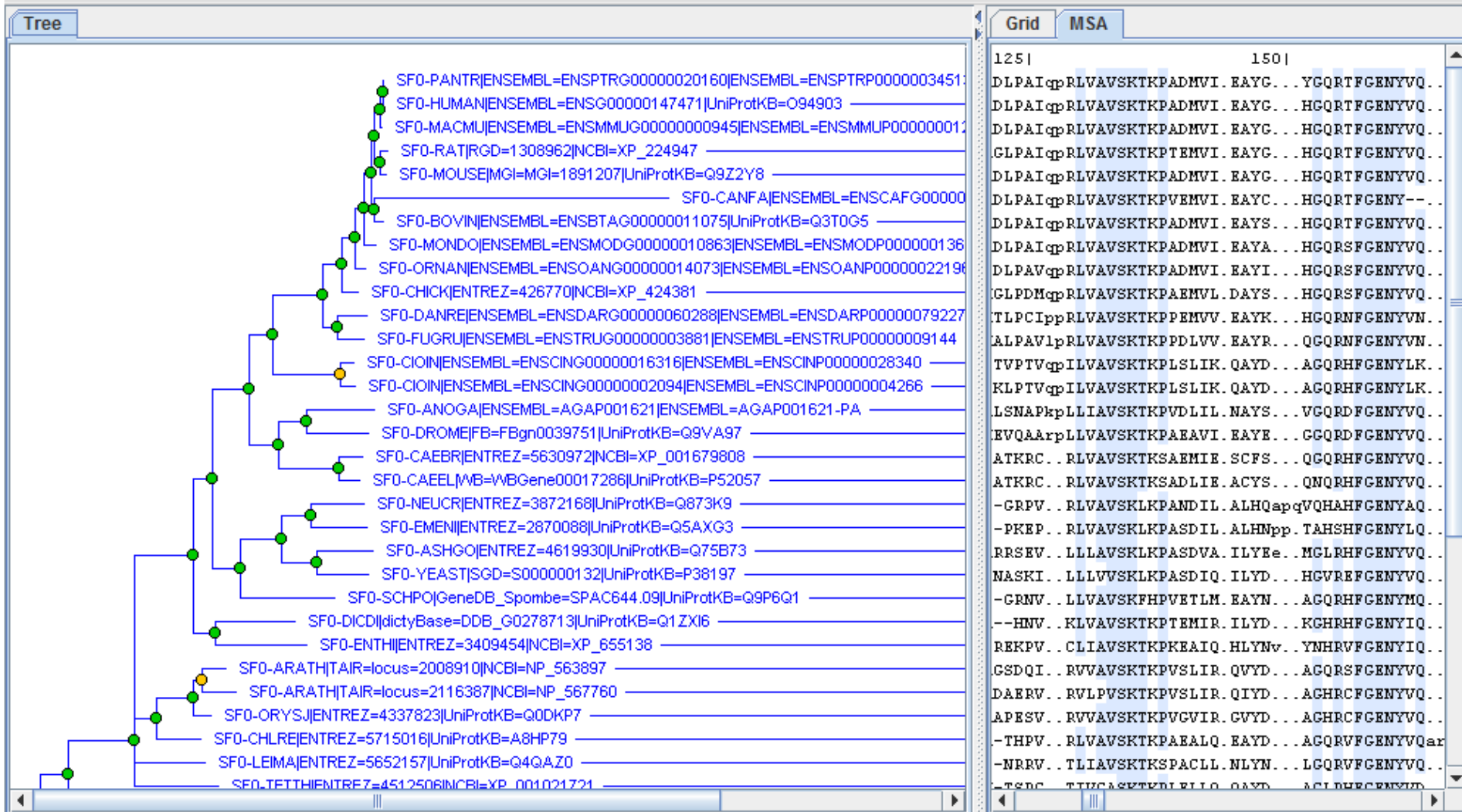
Downloads: [HMM](#) (HMMER format)

GENES ASSIGNED TO THIS FAMILY

Species	Count
Anopheles gambiae	1
Aquifex aeolicus vf5	1
Arabidopsis thaliana	2

Family Name : PROLINE SYNTHETASE CO-TRANSCRIBED BACTERIAL HOMOLOG PROTEIN (PTHR10146)

Tree MSA



Resource federation: InterPro

EMBL-EBI

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BioMart

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Protein Focus

Killer toxin Protein (KP4)

EBI > Databases > InterPro

InterPro protein sequence analysis & classification

InterPro is an integrated database of predictive protein signatures used for the classification and automatic annotation of proteins and genomes. InterPro classifies sequences at superfamily, family and subfamily levels, predicting the occurrence of functional domains, repeats and important sites. InterPro adds in-depth annotation, including GO terms, to the protein signatures.

Current release: **37.0 30 April 2012** (see [Release Notes](#) for further details)

Search

InterPro:

>

Do a sequence search of InterPro, via [InterProScan](#)

Extract large datasets by querying our [BioMart](#)

You can access our data programmatically, via [Web Services](#)

Use the updated [InterProScan Web Service](#)

News

We are delighted to announce the release of InterProScan 5RC1: the first release candidate of InterProScan version 5. To obtain a copy of this release candidate, please visit [Running InterProScan 5](#) for complete documentation regarding downloading, installing and using InterProScan 5RC1.

A recently published paper describing new developments with the InterPro database is available at Nucleic Acids Research ([doi: 10.1093/nar/qkr948](#))

A paper describing InterPro's approach to Gene Ontology curation has also recently been published and is available at Database ([doi: 10.1093/database/bar068](#))

Not as easy as it may sound...

- Specific protein families may not be consistent across resources
- Most families (MSAs, trees, HMMs) in these resources are not manually curated
 - Domains in Pfam-A are curated
 - TIGRfams are curated
 - HAMAP families are curated

http://www.expasy.org

Query all databases [help](#)

Visual Guidance

Categories

- proteomics
- genomics
- structural bioinformatics
- systems biology
- phylogeny/evolution
- population genetics
- transcriptomics
- biophysics
- imaging
- IT infrastructure
- drug design

Resources A..Z

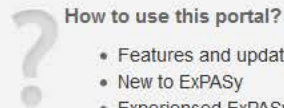
Links/Documentation

ExPASy is the **SIB Bioinformatics Resource Portal** which provides access to scientific databases and software tools (i.e., *resources*) in different areas of life sciences including proteomics, genomics, phylogeny, systems biology, population genetics, transcriptomics etc. (see **Categories** in the left menu). On this portal you find resources from many different SIB groups as well as external institutions.

Featuring today

SuperTree

Build phylogenetic supertrees
[\[details\]](#)



How to use this portal?

- Features and updates
- New to ExPASy
- Experienced ExPASy users: what is different

Popular resources

-  UniProtKB
-  SWISS-MODEL
-  STRING
-  PROSITE

Latest News

UniProt Knowledgebase release 2013_08 - 2013-07-24

UniProtKB/Swiss-Prot Release of 24-Jul-2013 contains 540,732 sequence entries...[More](#).
UniProtKB/TrEMBL Release of 24-Jul-2013 contains 41,451,118 sequence entries...[More](#)

Protein Spotlight: the intricacy of a smell - 2013-07-22

We all need a nose. Inside this part of an animal's body lie millions of olfactory receptors awaiting smells that they will send on to the brain. In turn, our brain will say whether the smell is good, or bad...[More](#).

[\[More news\]](#) [\[SIB news\]](#)

 [help](#)

Visual Guidance

Categories

[proteomics](#)[genomics](#)[sequence alignment](#)[similarity search](#)[characterisation/annotation](#)[structural bioinformatics](#)[systems biology](#)[phylogeny/evolution](#)[population genetics](#)[transcriptomics](#)[biophysics](#)[imaging](#)[IT infrastructure](#)[drug design](#)

Resources A..Z

Links/Documentation

[SIB resources](#)[External resources](#) - *(No support from the ExPASy Team)*

Tools

- [Alignment tools](#) • Four tools for multiple alignments • [\[more\]](#)
- [boxshade](#) • MSA pretty printer • [\[more\]](#)
- [ClustalW](#) • Multiple sequence alignment • [\[more\]](#)
- [ClustalW - PBIL](#) • Multiple sequence alignment program • [\[more\]](#)
- [ClustalW2](#) • Multiple sequence alignment program • [\[more\]](#)
- [Codon Suite](#) • codon-based sequence analysis • [\[more\]](#)
- [Decrease redundancy](#) • Sequence redundancy reduction • [\[more\]](#)
- [DIALIGN](#) • Local multiple sequence alignment • [\[more\]](#)
- [GENIO/logo](#) • RNA/DNA & Amino Acid Sequence Logos • [\[more\]](#)
- [Kalign - EBI](#) • Fast and accurate multiple sequence alignment • [\[more\]](#)
- [Kalign - SBC](#) • Fast and accurate multiple sequence alignment • [\[more\]](#)
- [LALIGN](#) • Pairwise alignment • [\[more\]](#)
- [MADAP](#) • clustering for genome annotation data • [\[more\]](#)
- [MAFFT - CBRC](#) • Multiple sequence alignment • [\[more\]](#)
- [MAFFT - EBI](#) • Multiple sequence alignment • [\[more\]](#)
- [MaxAlign](#) • Gap removal from alignments • [\[more\]](#)
- [Multalin](#) • Multiple sequence alignment • [\[more\]](#)
- [MUSCLE](#) • Multiple alignment server • [\[more\]](#)
- [Newick Utilities](#) • high-throughput phylogenetic tree processing • [\[more\]](#)
- [Phylogibbs](#) • regulatory sites discovery • [\[more\]](#)
- [SIBsim4](#) • spliced sequence alignment • [\[more\]](#)
- [T-Coffee](#) • sequence and structure multiple alignments • [\[more\]](#)
- [T-Coffee - EBI](#) • Multiple sequence alignment program • [\[more\]](#)
- [T-Coffee - WUR](#) • Multiple sequence alignment program • [\[more\]](#)
- [WebLogo](#) • Sequence logos • [\[more\]](#)

proteômica

Categories

proteomics

protein sequences and identification
mass spectrometry and 2-DE data
protein characterisation and function
families, patterns and profiles
post-translational modification
protein structure
protein-protein interaction
similarity search/alignment

genomics

structural bioinformatics

systems biology

phylogeny/evolution

population genetics

transcriptomics

biophysics

imaging

IT infrastructure

drug design

Resources A..Z

Links/Documentation

Databases

 **neXtProt** • human proteins • [\[more\]](#)
 **PROSITE** • protein domains and families • [\[more\]](#)
 **STRING** • protein-protein interactions • [\[more\]](#)
 **SWISS-MODEL Repository** • protein structure homology models • [\[more\]](#)
 **UniProtKB** • functional information on proteins • [\[more\]](#)
 **UniProtKB/Swiss-Prot** • protein sequence database • [\[more\]](#)
 **ViralZone** • portal to viral UniProtKB entries • [\[more\]](#)

 **EMBNet services** • bioinformatics tools, databases and courses • [\[more\]](#)
 **ENZYME** • enzyme nomenclature • [\[more\]](#)
 **GlycoSuiteDB** • glycan database • [\[more\]](#)
 **GPSDB** • gene and protein synonyms • [\[more\]](#)
 **HAMAP** • UniProtKB family classification and annotation • [\[more\]](#)
 **MetaNetX** • Metabolic Network Repository & Analysis • [\[more\]](#)
 **MIAPEGelDB** • MIAPE document edition • [\[more\]](#)
 **MyHits** • protein domains database and tools • [\[more\]](#)
 **PANDITplus** • protein families and domains resources • [\[more\]](#)
 **PaxDb** • protein abundance database • [\[more\]](#)
 **Prolune** • Popular science articles (in French) • [\[more\]](#)
 **Protein Model Portal** • structural information for a protein • [\[more\]](#)
 **Protein Spotlight** • Informally written reviews on proteins • [\[more\]](#)
 **SugarBind** • pathogen sugar-binding • [\[more\]](#)
 **SWISS-2DPAGE** • proteins on 2-D and SDS PAGE maps • [\[more\]](#)
 **SwissSidechain** • non-natural amino-acid sidechains • [\[more\]](#)
 **SwissVar** • variants in UniProtKB entries • [\[more\]](#)
 **TCS** • interaction specificity in two-component systems • [\[more\]](#)
 **UniMES (UniProt metagenomic samples)** • UniProt Metagenomic and Environmental Sequences • [\[more\]](#)
 **UniParc (UniProt sequence archive)** • UniProt sequence archive • [\[more\]](#)
 **UniPathway** • metabolic pathways for the UniProtKB • [\[more\]](#)
 **UniRef (UniProt sequence clusters)** • UniProtKB sequence clusters • [\[more\]](#)
 **World-2DPAGE Constellation** • set of 2DPAGE resources • [\[more\]](#)
 **World-2DPAGE Repository** • gel-based proteomics data • [\[more\]](#)

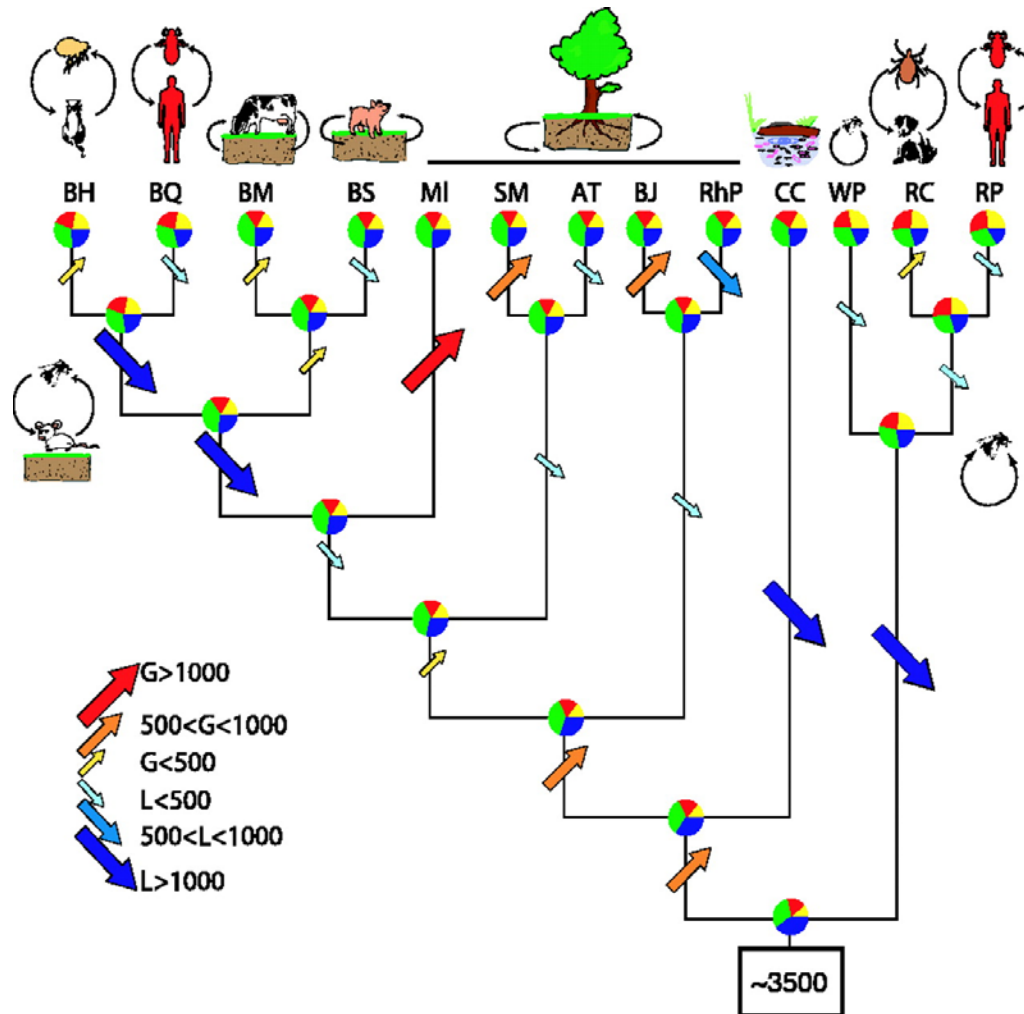
Tools

 **SWISS-MODEL Workspace** • structure homology-modeling • [\[more\]](#)
 **SwissDock** • protein ligand docking server • [\[more\]](#)
 **2ZIP** • Prediction of leucine zipper domains • [\[more\]](#)
 **3of5** • find user-defined patterns in protein sequences • [\[more\]](#)
 **AACompIdent** • protein identification by aa composition • [\[more\]](#)
 **AACompSim** • amino acid composition comparison • [\[more\]](#)
 **Agadir** • Prediction of the helical content of peptides • [\[more\]](#)
 **ALF** • simulation of genome evolution • [\[more\]](#)
 **Alignment tools** • Four tools for multiple alignments • [\[more\]](#)
 **AlilAl** • protein sequences comparisons • [\[more\]](#)
 **APSSP** • Advanced Protein Secondary Structure Prediction • [\[more\]](#)
 **Ascalaph** • Molecular modeling software • [\[more\]](#)
 **big-PI** • predict GPI modification sites • [\[more\]](#)
 **Biochemical Pathways** • Biochemical Pathways • [\[more\]](#)
 **BLAST** • sequence similarity search • [\[more\]](#)
 **BLAST (UniProt)** • BLAST search on the UniProt web site • [\[more\]](#)
 **BLAST - NCBI** • Biological sequence similarity search • [\[more\]](#)
 **BLAST - PBIL** • BLAST search on protein sequence databases • [\[more\]](#)
 **Blast2Fasta** • Blast to Fasta conversion • [\[more\]](#)
 **boxshade** • MSA pretty printer • [\[more\]](#)
 **CFSP** • Protein secondary structure prediction • [\[more\]](#)
 **ChloroP** • chloroplast transit peptides & cleavage sites • [\[more\]](#)
 **Click2Drug** • Directory of computational drug design tools • [\[more\]](#)
 **ClustalO (UniProt)** • Align two or more protein sequences • [\[more\]](#)
 **ClustalW** • Multiple sequence alignment • [\[more\]](#)
 **ClustalW - PBIL** • Multiple sequence alignment program • [\[more\]](#)
 **ClustalW2** • Multiple sequence alignment program • [\[more\]](#)
 **Coiled-Coils prediction** • Prediction of coiled coils regions • [\[more\]](#)
 **COILS** • Prediction of Coiled Coil Regions in Proteins • [\[more\]](#)
 **ColorSeq** • Color Protein Sequence • [\[more\]](#)
 **Compute pI/MW** • theoretical pI and Mw computation • [\[more\]](#)
 **CPHmodels** • Protein homology modeling • [\[more\]](#)
 **CSS-Palm** • Prediction of palmitoylation sites in proteins • [\[more\]](#)
 **DAS-TMfilter** • Prediction of transmembrane regions • [\[more\]](#)
 **Decrease redundancy** • Sequence redundancy reduction • [\[more\]](#)
 **DIALIGN** • Local multiple sequence alignment • [\[more\]](#)
 **DictyOGlyc** • GlcNAc O-glycosylation sites in D. discoideum • [\[more\]](#)
 **DisEMBL** • Prediction of disordered protein regions • [\[more\]](#)

Além de construir filogenias

- inferência de genes compartilhados e não compartilhados entre organismos de um mesmo grupo permite inferir “ganhos” e “perdas” de genes ao longo da evolução
- Exemplo: proteobactérias alfa

Fig. 4. Net gene loss or gain throughout the evolution of the {alpha}-proteobacterial species



Boussau, Bastien et al. (2004) Proc. Natl. Acad. Sci. USA 101, 9722-9727