译自《WebLab 帮助文件》



# WebLab 中文使用文档

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注:本文中的插图均来自《WebLab 帮助文件》

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# 1.WebLab 简介

伴随着生物数据的激增,出现了大量用于分析这些生物数据的工具和网站。然而安装 和维护这么多生物信息软件是非常困难的,不但非常耗时,而且成本也很高。为了提高生物 信息领域的研究效率,开发一个整合了各种分析工具,具有友好用户界面的多功能平台是非 常有意义的。

开发 WebLab 的目的就是为了给生物医学研究人员提高一个"一站式"的生物信息分析 平台。在 WebLab 上,用户不但可以使用上面的丰富的软件进行生物信息分析,而且可以利 用 WebLab 上强大的数据管理功能,分组策略和数据共享机制来大大的提高工作效率。



如上图所示,WebLab的架构是一个使用代理模式的层次性的拓扑结构。服务器的入口 是一个具有友好web用户界面,它作为一个代理来接受用户的请求。WebLab主要由用户界 面显示层和内部逻辑处理层组成。在接受到入口服务器的请求后,相应的后台服务器就会运 行要求的程序。在分析完成后,便将结果送回入口服务器并被存入入口服务器的数据库中。

一般来说,用户可以把 WebLab 当作一个松散联系的分布系统。

2.用户注册

为什么每个用户都需要一个帐号?

首先说明一点,注册帐号是免费的。注册了账号以后,你就可以将序列和分析结果存入 "my data"。这对于有大量数据要分析的用户来说是非常有用的。

其次,你还可以分别在"my literature","my toolbox"和"my metapackage"中保存和 管理文献,喜欢的工具,meta-packages 等以便于进一步分析。这意味着只要你连上互联网 就可以在地球的任何地方得到你的数据。

如果你的任务需要运行很长时间,不能立即得到结果,你还能监视已提交任务的状态。 而且还易于控制已提交的任务。

你可以根据任务来运行和设计流程(protocol 和 macros)。

可通过分享机制和分组策略来合作研究。

因此,我们强烈推荐用户注册一个账号。你只需要填一个简单的表格点一下注册按钮便可拥 有一个属于自己的账号。

注:填写一个正确的 email 地址是非常重要的。你需要通过 email 来激活你的账号,并 且当你的长任务完成后,服务器会将运行结果发到你邮箱里。

				WebLab	¤ Feedback ¤ Contact ¤ Help						
	Service	Why do I need	an account								
	Program	<ul> <li>For free</li> </ul>	elv registered account, you can s	ave sequence and analysis result in "user data space".							
_	Protocol	It's espe	<ul> <li>For meety regressive account, you can save sequence and analysis result in user data space.</li> <li>It's especially useful if you have many sequences to analyze.</li> </ul>								
_	Macro	You core	You could monitor the status of your submitted work if it needs long time to compute and can't return result immediately.								
-	Utility		,,	· · · · · · · · · · · · · · · · · · ·							
	User Space										
	My Data	1	ACCOUNT REGISTRATION								
	My Literature		* Account:	3-20 characters							
	My MetaPackage		t Carally								
-	My Toolbox		- Email:	valid email address							
-	History		* Password:	5-20 characters							
æ	Account		* Confirm Password:	5-20 characters							
	Login in		* Name:								
	Registration		* Orgnization:								
				Fields with * are requried to fill in.	Submit						

登陆后,用户可以通过点击"My Account"来看自己的账号信息。在这,服务器允许用 户更改账号的基本信息。

					CBI STORE	WebLab	¤ Feedback ¤ Contact ¤ Help
	Service						
	Program		Account:	wangjun			
	Protocol		Empil:	wangiun kathleen@126.com			
	Macro		Linai.	wangjun_kanieen@120.com			
_	Utility		Name:	wangjun			
	User Space		Orgnization:	ecnu			
_	My Data	Sen	d long time job result to	Yes			
	My Literature		Register Date:	2006-10-11			
	My MetaPackage		Negister Date.	2000-10-11			
	My Toolbox		Last Login Time:	2008-03-05 22:54:49			
	History						Edit My Account
	Account						
	My Account						
	My Group						
	Logout						
					CBI S	WebLab	¤ Feedback ¤ Contact ¤ Help
	Service						
	Program		Email:	xxx@xxx.xxx			
在编	Protocol		Password:				
	Macro		Confirm password:				
	User Space		Name:	xxx			
	My Data		Orgnization:	xxx			
	My Literature	Sen	d long time job result to				
	My MetaPackage		email box:	Yes			
	My Toolbox			No			(authorite)
	History	_					submit
&	Account						
	My Account						
	My Group						
	Logout						

对于暂时不想注册的用户,WebLab也提供了"try out"功能。

在没有注册的情况下,用户可通过"try out"体验 WebLab 提供的所有功能。不过,当 你登出后或对话超出时间限制,你的账号信息将会消失。如果你经常使用 WebLab,最好能 注册一个账号并在使用前登陆。



#### 3. 用户空间及数据管理

#### 1). My Data

"My Data"就像用户的网络硬盘。没有注册的用户只能从本地磁盘上上传文件或粘入数据,而每一个注册的用户都有一个用户空间来存储序列进行后续的分析。

便于选择保存的文件进行不同的分析。

不受空间限制的继续做工作。例如,你可以在任何地方用不同的计算机分析这些数据,因为 WebLab 中保存你需要的数据。

分享数据给指定的用户。

**基本操作**:我们为用户提供了一些基本操作来管理自己的文件,包括目录操作,上传文件, 修改,删除,分享和添加评论和标签。

**目录操作:**用户可以创建层次性的目录来保存数据。这对于管理大量数据和分析结果是非常 有利的。此外,用户还可以删除,重命名和移动这些目录。

**文件上传**:有几种上传文件的方法。上传后,用户可以重命名,移动或删除这些文件,也能 改变文件所对应的格式。

几种方法: 在文本框中粘入序列; 从本地磁盘上传; 从 WebLab 内嵌的 resource 模块来获得数据。

注:WebLab包含一个数据格式表,该表中定义了生物医学领域中使用的各种数据格式。 请在上传文件时指定一个恰当的数据格式,因为很多对数据的操作依赖于数据的格式。用户 可以在"My data"中修改数据的格式。

数据操作:对于非二进制文件,用户可通过点击文件名浏览文件内容。

对一些特殊的数据格式,WebLab 提供了一个更直观的浏览方式,这是WebLab 的呈递 机制。目前安装了一些常用数据类型的呈送,包括ClustalW,双重序列比对的输出,KOBAS 结果,Prints 和 Prosite 数据库的检索结果。用户可以通过选择合适的观看方式来更好的理解 这些结果。

			WebLab	¤ Feedback ¤ Contact ¤ Help
	Service	View: Multiple-al	ignment view View Edit Download (Friendly Print)	
	Program			
	Protocol	Choose program:	clustalw2-ppa (Profile Profile Alignment function of clustalw2)	
	Macro			
	Utility	Human Mouse	MVLSPADKTNVKAANGKVGAHAGEYGAEALEKMPLSPPTTKTYPPHP-DLSHGSAUVKGH MVLSGEDKSNIKAANGKIGGHGAEYGAEALERMPASEPTTKTYPPHP-DVSHGSAUVKGH	
	User Space	Dolphin Chicken Frog	MVLS BADYINV KOTNIS KIONHSABY GABALDEMPINERSIYTYESHE - DIGHOSADIYOH MVLGAADXNEW KOTTINI AGHABIY GABTERMPITYEPIKAYIPHE - DIGHOSADIYOH MLGAADXNEW KIIRANIM A LAHCOX KOGANIYAM INVERIYYYES BS - DHINA KOTSA	
	My Data	Snake	MVLTEEDKSRVRAANGPVSKNAELYGAETLTRLFTAYPATKTYFHHF-DLSPGSSNLKTH	
	My Literature	Goldfish	MSLSDKDKAVVKALWAKIGSRADEIGAEALGRMLTVYPOTKTYPSHWSDLSPGSGPVKKH	
	My MetaPackage			
	My Toolbox	Human	GKKVADALTNAVAHVDDMPNALSALSDLHAH <mark>K</mark> LEVDPVNFKLLSHCLLVTLAAHLPAEFT	
	History	Mouse	GKKVADALASAAGHLDDLPGALSALSDLHAHKLRVDPVNFKLLSHCLLVTLASHHPADFT	
-	Account	Dolphin Chicken Frog	SKAVNDALITAAVELUNE DALE DALAS LEDDIAAN EKO POMPENDE OLUS OLUU AAAAA PAAA SKAVNDALITAANE IDALASINE JA SULAANE VOPMPENDE OLUS OLUS OLUV VAAN PAAA SKAVNDALINEASINELDIATSIS KUS DALAAS <mark>U VOPMPENDE OLUS OLUVU</mark> AANE EKO PO	
	My Account	Snake	GKKVIDAITEAVNNLDDVAGALSKLSDLHAOKLEVDPVNFKLLGHCLEVTIAAHNGGPLK GKTIMGAVGDAVSKIDDIVGAISALSELHAFKIBIDPANEKILAHNVIVUTGMIEDGDET	
	My Group	00101100		
	Logout			
		Muman Mouse Dolphin Chicken Frog Snake Goldfish	AVHASLARIASUVELSKY PSVHASLAKTASVSVLISKY PSVHASLAKTAGVSVLISKYR PSVHASLAKTAGVGVLISKYR PSVHASLAKTAGUVAKYR PSVHASLAKTAGUVAKYR PSVHASVAKPEQNLALALSEKYR	

通过点击相应的按钮,用户可以直接的编辑或打印数据文件。

通过点击"do analysis"按钮,用户可以从程序列表中选择需要的程序做进一步的分析。 注:根据指定的数据类型,系统可以将处理该种数据类型的程序列出。因此,不同的数 据类型有不同的程序列表。

			WebLab	¤ Feedback ¤ Contact ¤ Help
	Service	View: Raw View	View Edit Download Friendly Print	
	Program			
	Protocol	Choose program:	clustalw2-ppa (Profile Profile Alignment function of clustalw2)	
	Macro		clustalw2 - ppa (Profile Profile Alignment function of clustalw2)	
	THE CO	CLUSTAL W (1.83	clustalw2-psa (Profile Sequence(s) Alignment function of clustalw2)	
	Utility	00001110 # (1100	distmat(v5.0) (Creates a distance matrix from multiple alignments.)	
	User Space	Human Mouse	ehmmbuild(v2.3.2) (Build a profile HMM from an alignment) Wextractalign(v5.0) (Extract regions from a sequence alignment) Wideaccomparibility alongithm)	
	My Data	Dolphin	Windinatist(v3.6b) (Nucleic acid sequence Distance Matrix program) GBAQLEGE	
	My Literature	Chicken	MVfdnainvar(v3.6b) (Nucleic acid sequence Invariants method)	
	My Meter Beale	Frog	MLfdnaml(v3.6b) (Estimates nucleotide phylogeny by maximum likelihood)	
	му метаРаскаде	Snake	M fdnamlk(v3.6b) (Estimates nucleotide phylogeny by maximum likelihood)	
	My Toolbox	Goldfish	MSfdnamove(v3.6b) (Interactive DNA parsimony)	
	History		fdnapars(v3.6b) (DNA parsimony algorithm)	
<b>&amp;</b>	Account	Human Mouse Dolphin	Galpondi (V3.6b) (Potein phylogeny by maximum likelihood) Galpondi (V3.6b) (Potein phylogeny by maximum likelihood) Galpondi (V3.6b) (Potein glisapor algorithm)	
	My Account	Chicken	GE (protpars(v3.6b) (Protein parsimony algorithm)	
	No. Comment	Frog	GMfseqboot(v3.6b) (Bootstrapped sequences algorithm) ABNEEDVVAANNEPKOPD	
	My Group	Snake	GKfseqbootall(v3.6b) (Bootstrapped sequences algorithm)	
	Logout	Goldfish	GRInfoalign(v5.0) (Information on a multiple sequence alignment ) and provide a set of sequences )	
			pepwindowan(v5.0) (Displays protein hydropathy of a set of sequences )	
		Human	PAVHASLDKFLASVSTVLTSKYR	
		Mouse	PAVHASLDKFLASVSTVLTSKYR	
		Dolphin	PSVHASLDKFLASVSTVLTSKYR	
		Chicken	PEVHASLDKFLCAVGTVLTAKYR	
		Frog	PATHKALDKFLATVSTVLTSKYR	
		Snake	PEVILSLDKFLCLVAKTLVSRYR	
		Goldfish	PEVHMSVDKFFONLALALSEKYR	

#### 注释和标签:

**注释**:注释是用户对文件的描述。它可以帮助用户在短时间内理解文件内容以提高工作效率。 用户可通过添加,编辑或删除注释使文件更容易理解。然后,当把鼠标放到黄色图标上时, 你将会看到关于该数据的简短描述。

					CBI S	Webl	Lab	¤ Feedback ¤ Contact ¤ Help
	Service Program	Edit Comment	Delete Comment	Edit Tag	Attach Tag	Edit Format		
	Macro							
-	Itility	🖻 🦾 📃 My Dat	ta					
	User Space		A/B_hemoglobin HBB_human bio:sec	q:fasta:single:prote in				
	My Data		hba_rat bio:seq:fasta	a:set	This is the h	bb of human.		
	My Literature		B_HBA	1				
	My MetaPackage	🕂 🛄 📃 hom	iework2					
	My Toolbox	E 📄 🖯 CDS	5					
	History	🕂 🧰 📃 hba	3					
æ	Account	🕀 🧰 📄 chai	nge_homework2					
	My Account	- 🔤 🖂 120	04550346010.fasta b	oio:seq:fasta:single:dr	a			
	My Group	- 🔤 📃 120	)4552382861.fasta b	oio:seq:fasta:single:dr	a			
	Logout	📄 🔲 ok.!	Mapping.2008-03-03	3 21:53 PM unknown				
		🔲 🖂 othe	er					
			New Directory	New File	Delete	Move	Rename	
			Share	Cancel Share	Import	Cancel Import	Refresh	

**标签:**除了用经典的树状结构来组织数据文件外,还可通过自定义的标签来浏览"my data"中的数据。

			WebLab	¤ Feedback ¤ News ¤ Contact ¤ Help ¤ Download
	Service	for others protein		
	Program			
	Protocol	Image: Second Seco		
	Macro			
	Utility	protein aaa unknown		
	Resource			
R	User Space	delete tag protein		>>My Data
	My Data			
	My Literature			
	My MetaPackage			
	My Toolbox			
	History			
-	Account			
	My Account			
	My Group			
	Logout			

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通过点击"edit tag"按钮,用户可创建或修改标签。然后通过"attach tag"按钮为文件添加 自定义的标签。

		WebLab	¤ Feedback ¤ News ¤ Contact ¤ Help ¤ Download
	Service	Edit Comment Delete Comment Edit Tag Attach Tag 🗸 Edit Format	
	Program		
	Protocol	+Expand all -Collapse all-	
	Macro	🗄 🗁 📄 My Data	
	Utility	🕂 🦢 📄 emboss test data	
	Resource	Ė- 🔄 🗖 prophet	
	User Space	Protein globins.gribskov unknown      Protein aaa unknown	
	My Data	For others bbb unknown	
	My Literature	P for others Untilled ESearch unknown	
	My MetaPackage		
	My Toolbox		
	History		
&	Account	New Directory         New File         Delete         Move         Rename	
	My Account	Share Cancel Share Import Cancel Import Refresh	
	My Group		
	Logout		
	,		

**分享:** 在"my data", "my literature" and "my metapackage" 中的所有文件都可以分享给你的同 事。

#### 2). My Literature

WebLab 提供了一个"my literature"让用户来管理自己的文献。"my literature"除了具有"my data"具有的功能外,还对全文检索,通过 EndNode 和 PubMed 等参考文献管理工具进行互操作等提供全面的支持。

**文献上传**:用户可以上传文献到指定的目录。目前,我们只接受 txt, pdf, doc 格式文献。 另外,我们支持批量上传。用户最多可一次上传 10 篇英文文献,每个不超过 10M。

				CBI STATES	WebLab	¤ Feedback ¤ Contact ¤ Help
	Service Program	Please upload at pdf(Portable Doo	most 10 English literature files at one tir sument Format) doc(MicroSoft Word)	ne, each of which is no m literature formats are acc	ore than10M.Besides, only txt(Plain Text epted.	Document)
	Protocol	UPLOAD LITER	ATURES FROM LOCAL DISK			
	Macro	Choose file:	Choose File po file selected			
	Utility	choose me.	Choose the home selected			
	User Space	Files	D:\Grid.pdf Delete D:\ig.pdf Delete			
	My Data	(maximum ro)	D:\WS.pdf Delete			
	My Literature					
	My MetaPackage					Upload
-	My Toolbox					
	History					

引用信息:除了文献本身,WebLab还允许用户添加每篇文献的引用信息。

引用信息可提供给用户关于该文献的充分的细节。用户可通过引用信息来检索文献。更为重要的是,所有的引用信息可被导成 Endnote 导入格式,bibtex 等著名的引用格式。

目前,WebLab 在"my literature"中提供获取,删除和导出引用信息等功能。

	Canal	WebLab	¤ Feedback ¤ News ¤ Contact ¤ Help
	Service	Edit Comment Delete Comment Edit Tag Attach Tag  Search: GO >>Advanced Search	
	Program		
	Protocol	+Expand all -Collapse all	
	Macro	E- 🗁 📃 My Literature	
	Utility	🔤 🗖 Text mining for biology - the way forward opinions from leading scientists odf	
	Resource	HTML/time View Citation   Delete Citation   Export Citation	
	User Space	BioCaster detecting public health rumors with a Web-based text mining system.pdf      HTML.view Fetch Caston      G	
	My Data		
	My Literature	LET [ try gR1167.pdf HTML View (Fastion L Delete Citation L Exact Citation	
	My MetaPackage		
	My Toolbox	HTML View (View Citation   Delete Citation   Export Citation	
	History	I linking genes to literature text mining information extraction and retrieval applications for biology off	
-	Account	HTML_View   View Citation   Delete Citation   Export Citation	
	My Account	New Directory Upload Delete Move Rename Download	
	My Group		
	Logout	Share Cancel Share Import Cancel Import Export Citation Refreh	

对于没有引用信息的文献,用户可提供 PubMed id 或文献名通过"fetch citation"功能从 PubMed 中获取引用信息。Weblab 将会把获取的引用信息保存成中间格式。

		WebLab	¤ Feedback ¤ News ¤ Contact ¤ Help
	Service		
	Program	Weblick will feach and there index the situation information for	
	Protocol	weblab will fetch and then index the citation information for	
	Macro	BioCaster detecting public nearth rumors with a web-based text mining system.pdr	
	Utility	- through title	
	Resource	Title: DisCaste datasting public health summer with a Mich, haved text mining sustem.	
	User Space	Submit	
	My Data		
	My Literature	through pubmed ID	
	My MetaPackage	Pubmed ID (like 11748933): (submit	
	My Toolbox		
	History		
&	Account		
	My Account		
	My Group		
	Logout		
			6

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用户可通过"view citation"来浏览引用信息。

注: WebLab 只显示标题,杂志名,出版日期,卷,期,页,摘要,PubMed ID 等信息 而不是所以的引用信息。

		Keedbar Keebbar Kee	ck t
	Service	Citation Information for 🗇 3787.pdf	
	Program		
	Protocol	Cryobiology.2001-Jun;42(4):244-255.	
	Macro		
	Utility	Is cryopreservation a homogeneous process? Ultrastructure and motility of untreated, prefreezing, and poethawed spermatozoa of Diplous nutrative (Cetti)	
	Resource	postnumed spermatozoa of Diplotes partazzo (ceta).	
	User Space	R Taddei, F Barbato, L Abelli, S Canese, F Moretti, J Rana, M Fausto, M Mazzini.	
	My Data	This study subdivides the cryopreservation procedure for Dipiodus puntazzo spermatozoa into three key phases, fresh, preferezing (camples enullibrated in cryoshutions) and postthawed stages, and examines the ultrastructural anomalies and	
	My Literature	motility profiles of spermatozoa in each stage, with different cryodiluents. Two simple cryosolutions were evaluated: 0.17 M	
	My MetaPackage	sodium chloride containing a final concentration of 15% dimethyl sulfoxide (Me(2)SO) (cryosolution A) and 0.1 M sodium citrate containing a final concentration of 100/ Me(2)SO (cryosolution A) und 0.1 M sodium chloride in a containing a final concentration of 100/ Me(2)SO (cryosolution A) and 0.1 M sodium	
	My Toolbox	nuclear membranes of the sperm head were common and the severity of the cryotiniury differed significantly between the	
	History	pre- and the postfreezing phases and between the two cryosolutions. In spermatozoa diluted with cryosolution A, during the	
<b>&amp;</b>	Account	prefreezing phase, the plasmalemma of 01% of the cells was absent or damaged compared with 24% in the fresh sample (P < 0.001). In spermatozoa diluted with cryosolution B, there was a pronounced increase in the number of cells lacking the head plasmatic membrane from the prefreezing to the postthawed stages (from 32 to 52%, P < 0.01). In both cryosolutions,	
	My Account	damages to nuclear membrane were significantly higher after freezing (cryosolution A: 8 to 23%, $P < 0.01$ ; cryosolution B: 5 to 38%, $P < 0.01$ ) with cryosolution A, the after-activation motility profile confirmed a consistent from from from the batter of the first statement of the statement	
	My Group	prefreezing stage, whereas freezing and thawing did not affect the motility much further and 50% of the cells were immotile	
	Logout	by 60-90 s after activation. With cryosolution B, only the postthawing stage showed a sharp drop of motility profile. This	
		damage.	
		PMID: 11748933	
		Conversion 2004 2009 Contaction For Distribution All District Resourced	

用户可以通过单个(每篇文献下面的按钮)和批量(整个文献空间下面的按钮)方式来 导出文献。用户可选择导出的格式。目前 WebLab 支持 Endnote, BibTex, ADS 文献格式, ISI 格式, RIS 格式和 word2007 参考书目格式。



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**索引和检索**:在文献上传的过程中,WebLab 将会提取文献内容建立全文索引并建立标题, 作者,杂志,出版日期等信息的索引。

目前,WebLab使用Lucene 作为文献库的索引和恢复。

注:有时,WebLab 不能提取全文信息和引用信息,此时则不能建立索引(WebLab 会 尽力给出出错的原因)。例如,WebLab 不能对加密的 pdf 文件建立索引。WebLab 使用不同 的图标来标记文献的索引状态,粉红色表示该文献的全文或引用信息没建立索引。

10 <b>1</b>	<b>2 1</b>	1 1 1	I
19 ( <sup>19</sup> 19		) 🔁 🗳	
	E 8		]

对于已成功建立索引的文献,用户通过简单检索和高级检索来搜索相关信息。简单检索 只能按关键词对文献全文搜索。

	Canal	WebLab	Feedback News Contact Help
	Service	Edit Comment Delete Comment Edit Tag Attach Tag 🗸 Search: GO >>Advanced Search	
	Protocol	- +Expand allCollapse all	
	Macro		
-	Utility		
	Resource	Image:	
	User Space	BioCaster detecting public health rumors with a Web-based text mining system.pdf     HTML_View   Fetch Clation	
	My Data		
	My Literature	Ut i gydrifo7.pdf	
	My MetaPackage		
	My Toolbox	HTML_View   View Citation   Delete Citation   Export Citation	
	History	Linking genes to literature text mining, information extraction, and retrieval applications for biology.pdf	
-	Account	HTML_View   View Citation   Delete Citation   Export Citation	
	My Account	New Directory Upload Delete Move Rename Download	
	My Group		
	Logout	Share Cancel Share Import Cancel Import Export Citation Refreh	

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对于高级检索,用户可对全文和引用信息进行复杂的检索。

3			¤ News ¤ Contact ¤ Help
	Service Program Protocol	Full Text Search Full Text: text mining Any Words	
_	Utility	Refine Search	
_	Resource	Title:	
	User Space	Any Words 🔻	
_	My Data	Any Words	
	My Literature	laumalu	
	My MetaPackage	Journal:	
	My Toolbox		
	History	Publish Date:	
<b>&amp;</b>	Account	Specify a date range   from April  To January  Z008  Z008	
	My Account		
	My Group	Under the directory I - account share	
	Logout	,	
		Complete 2004 2008, Contro for Divisionarian All Division Resourced	

搜索的结果如下图所示,检索的关键词被高亮显示。每篇文献的得分是指匹配得分。得 分高的文献显示在前面。



**HTML 预览**:对于存储在"My literature"中的每篇文献,WebLab 提供 HTML 预览功能便 于浏览文献的内容。



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#### 3). My Meta Package

"Meta Package"是用户自己的数据库。用户可在上面建立自己的数据库。目前我们提高两种类型的程序来生成数据库:reverse\_ePCR\_db\_builder 和 formatdb。然后用户可以 blast 他们自己的数据库。这使得实验变得更加的灵活。

注:绿色箭头链向可产生这种数据库的程序。另外,每一个 meta-package 文件不仅仅是一个 文献,而是一个压缩包。用户可下载并解压缩来得到这些文件。

		WebLab × Fee * Con * Help	dback tact p
Ô	Service	Edit Comment Delete Comment	
	Program		
	Protocol		1
	Macro	E-la My MetaPackage	
	Utility	🖻 🎯 📃 blastdb 💌	
	User Space	Image: mail to be a constrained of the second decision of the second decis	
	My Data	🖻 🦢 🖂 reElectronicPCRdt 🏓	
	My Literature	at weblab:metadata:reElectronicPCRdb	
	My MetaPackage		1
	My Toolbox		
	History	New Directory Delete Move Rename	
	Account	Share Cancel Share Import Cancel Import Refresh	
	My Account		
	My Group		
	Logout		

**生成 Meta Package**: 在 Meta Package 中有两个目录: blastdb and reElectronicPCRdb。程序 Formatdb 用来对蛋白和核酸进行格式化得到 blast 数据库。reverse\_ePCR\_db\_builder 用来生 成要求的数据库文件以通过 STS 来检索序列数据库。在这里我们以 reverse\_ePCR\_db\_builder 为例。

注: 如果程序可生成 Meta-package, 则输出路径将自动设为"Meta package"。

			U CBI O	WebLab	× Feedback × Contact × Help
	Service	reverse_ePCR_db_builder -	reverse electronic PCR	database builder	>>add to ToolBox
	Program	This program integrate two programs,	famap and fahash, to pro	duce the required	
	Protocol	database files to perform STS lookup	o against sequence databas	e.	
	Macro	🗏 Input			
	Utility	the imput fasta file:		v (3	
	User Space				
	My Data				
-	My Literature	output, the result will be saved in :	- reElectronicPCRdb	T	
-	My MetaPackage				
-	My Toolbox	Basic Options			
	History	* databaseName:		3	
&	Account	Use compiled-in table to convert input:	off	T	
	My Account	Set word size when building hash tables:		69	
-	My Group	Set discontiguity when building hash		0	
-	Logout	tables:		•	
-		Skip repeats when building hash-file:	no	T	
		Set watermarks for fragment size (in Mb) (version 1 only):		3	
		Set cache size (version 2 only):		0	
		Use format version (1 2, 2 is default):	2	• @	

Run

**使用 Meta Package:** 当用户运行相关的程序时可选用自己的数据库。比如假如我生成了一个蛋白数据库,那么我在运行 blastp 程序时可以从用户创建的数据库中选择该数据库。通过 该 功 能 , 用 户 可 在 他 们 的 实 验 中 选 择 更 加 合 适 的 数 据 库 。

			WebLa	web × Feedback × Contact × Help
	Service	blastp(v2.2.15) - Search pro	otein database using a protein query	>>add to ToolBox
	Program	Compares an amino acid query seque	ence against a protein sequence database	
	Protocol	Input		
	Macro Utility	* Query file:	······	0
	User Space	🗆 Output		
	My Data	* save result in directory:	Work Directory	
	My Literature	* Output file name: (bio:align:blast)	Untitled.blast	8
	My MetaPackage			
	My Toolbox	Basic Options		
	History	* Choose database:	Swissprot protein sequences (swissprot 🔻	0
æ	Account	* Filter low complexity regions:	built-in databases Swissprot protein sequences (swissprot)	
	My Account	* Expect:	Protein Data Bank proteins (pdb)	
	My Group	* Matrix:	user-created databases	
	Logout		hbb	
		Advanced Options		
		Description:	100	
		Alignments:	50	
		Gapped blast:	Т	
		Gap open:		
		Gap extension:		
		Word size:		

Run

4.如何在 WebLab 上工作

1). Utility——一些有用的工具

"Utility"是一些用于生物信息学分析的小部件。这些"Utility"主要由 javascript, Java 插件和其它基于浏览器的客户端程序组成。它们一般运行的时间不是太长不过非常有用。截 至日前,在 WebLab 中共有 66 "utilities",其中大部分都集中在序列编辑,数据可视化等 方面。

注: 在运行 WebLab 上的"utility"之前,请设置浏览器允许运行 Java 和 JavaScript,并要安装 Java 运行环境。

#### 2). Program——构造元件

WebLab 中的程序包含三种不同类型的服务:

•本地程序:这类程序在 WebLab 的计算节点上运行,其中大部分程序来自 EMBOSS, NCBI BLAST 等最通用的生物信息分析软件包。

•Web 服务程序:现在Web 服务在生物信息领域变得越来越热门,因此WebLab也为一些著名的生物信息的网站的web 服务提供了客户端程序。通过我们提供的web 界面你可以向远程web 服务器提交任务。

•基于网格的服务程序: WebLab 也提供一些基于网格的程序来处理像 blast 这样的计算和输入输出密集型服务。

到目前为止,WebLab 上有 264 个程序。用户可通过它们的软件包,功能及字母顺序进行浏览。

程序的运行: WebLab 为不同的程序服务提供了统一的符合感官的界面便于用户的使用。

在程序提交页面,具有相似功能的参数聚成一组。在提交任务以前,用户需要注意下 面几个方面:

•对于输入文件,未注册用户可通过上传文件或直接贴入数据,而注册用户还可以通过"my data"来输入数据。

•注册用户需要指定输出的路径。

•带\*号的参数为必须填的项目。

•如果你不清楚那个参数的意义,可以通过点击右面的"?"获得帮助。

•如果你想知道程序的具体细节,请点击程序名查看程序文档。

在为每个参数输入一个恰当的值后,你就可以点击"Run"来提交任务了。

Service	clustalw2-msa - Multiple Seg	uence Alignment function of a	clustalw2	>>add to To
Program	05 Clustal W is a general purpose mult	tiple alignment program for DNA or	proteins.	
Protocol	clustalw2-msa is used to do the mul	ltiple sequence alignment task.		
Macro	🗏 Input			04
Utility	input sequences:		•	6
User Space	OR upload file from local disk:	Choose File no file selected		
My Data				
My Literature				
My MetaPackage				
My Toolbox				
History	OR paste into window:			
Account				
My Account				
My Group				11
Logout	file for old guide tree:		V	0
		·		•
	Comparison matrix file (optional) for pairwise alignment:		T	0
	E Comparison matrix file (optional) for multiple alignment:		v	•
	02			
	□ Output			
	a * save result in directory:	Work Directory	v	
	sequence alignment file name: ( bio:align:emboss:msf)	Untitled.msf	0	
	Dendrogram (tree file) from clustalw output file: (bio:report:dendrogram)	Untitled.dendrogram	3	
	General settings			
	🗄 fast pairwise alignments			
	🗄 slow pairwise alignments			
	multiple alignments			

当你提交任务时,前端服务器会查找合适的计算节点然后向其发送请求。在接到请求 后,后台服务器便会运行要求的程序。当分析完成后,结果被送回前端服务器。

一个任务可以有五个状态。通过这些工作状态你可以控制在 WebLab 上运行的任务。

当程序顺利跑完后,你可以在"my data"中看到结果文件。 当然你可以在"result"的下拉菜单中选择不同的结果浏览。

### 3). 工作流(Protocol和macro)

• 什么是工作流

生物信息分析是要涉及大量生物信息软件的复杂工作。传统的工具平台缺乏不同 软件间的联系和互用,用户不得不在不同的软件间传递数据并一个个的运行。而 WebLab 提 供的工作流机制可自动的根据一系列规则将相关的软件组合在一起。

• WebLab 上的两种工作流

根据交互能力的不同,WebLab 将工作流分为两种类型。

a). Protocol: 在运行过程中需要用户的介入,它给了用户改变程序参数和执行顺序的 机会。

b). Macro: 它可自动的执行,大大简化了分析工作流程。在输入命名参数后,无需用 户介入便可执行玩整个工作流程。

• WebLab 上的工作流模型

工作流模型在服务器的文件系统中是以 XML 格式表示的,在内存中是以 DAG (有向无环图)。在 DAG 中,矩形节点表示一个程序或 macro——这个表示 WebLab 支持定义递归工作流,你可以使用 macro 作为其它工作流的节点。菱形节点表示算子,边表示数据流。算子控制着工作流的执行顺序。目前在模型中有两种类型的算子。

a). 选择算子: 这类算子将更加输入条件判断下一步要执行的分析。

注:目前在 WebLab 中有一种类型的选择算子——序列类型选择算子,通过该算子判断 序列是蛋白序列还是核酸序列,然后选择不同的分析步骤。

选择算子由选择分支与选择终止组成。分支算子将工作流分成不同的分支,当然只有 其中的一个分支被选择执行。选择终止算子将不同的分支合为一支。

b). 平行算子: 该算子可以使得几个程序同时分析同一输入。这对分析具有相同功能的 不同软件的结果非常有用。

平行算子由平行分支和平行终止组成。平行分支让输入数据流向几个相应的程序。平行终止将几个数据流合在一起。

• 预定义工作流

WebLab 已定义好了几个工作流,包括 DNA 分析,蛋白分析,系统发育分析和代谢通路识别等以方便用户的使用。

#### 工作流的运行:

• Protocol 的运行

下面的例子将示范如何在 WebLab 上运行工作流。例中的工作流仅包含两个程序。第一个为 emma,一个多序列比对的程序。第二个为 cons,它将从 emma 生成的多序列比对中提取保守区域。原则上,你可以点击任何程序来运行,但一般来说,你应该点击起始程序(没有父程序的程序),在该例中通过 emma 来启动整个工作流。

注: 在每个工作流中有且仅有一个起始程序。

a). 工作流程序的提交界面和单个程序的界面类似。唯一的不同就是你可以在页面的上半部看到工作流的 DAG。在填写了合适的参数后,点运行来提交工作流程序。

			CBI CBI	WebLa	b × Feedback × Contact × Help
	Service	demonstration protocol			
	Program Protocol Macro Utility User Space		input		
	My Literature		1-emma(v5.0)		
	My MetaPackage				
	My Toolbox				
	History				
æ	Account		2-cons(v5.0)		
	My Account				
	My Group		×		
		emma(v5.0) - Multiple alignm Input	ent program - interface	to ClustalW progra	m >>add to ToolBox
		* sequence:	-human_hba.fasta	· · · ·	
		Dendrogram (tree file) from clustalw file (optional) :		•	
		E Comparison matrix file (optional):		• 3	
		E Comparison matrix file (optional):		• 0	
		🗄 Output			
		Basic Options			
		H Advanced Options			
			Rup		
b).	你将会看到	下面的界面,点击超链接	医可以看到工作流的	应行状态。	



c). 你会看到表示 emma 的那个矩形填充成粉红色,这表示这个程序以成功运行完。如果程序正在运行,在矩形为橄榄绿,如果出错,则为红色。你可以在下面的表格中查看提交程序的详细运行信息。



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根据上面的步骤你可以选择下一个要执行的程序直到 Protocol 结束。要说明的是在 Protocol 执行的过程中,你可以调整每个程序的参数。

• Macro 的运行

运行 macro 的过程与运行 Protocol 的过程完全不同。唯一的相似点就是在运行 Protocol 中的 a), b), c)步骤仍然是必要的。不过,有一些不同的地方需要注意。

- 在 macro 中,只有一个提交页面。因此在 macro 运行前需要填入所有必须的参数。
- •一旦 macro 被提交,内嵌的工作流引擎将根据相应的 DAG 执行 macro 中定义的 所有程序。
- 在你首次进入查看 macro 运行状态的页面时,在大多数情况下,你的 macro 还没结束。一般都会有几个程序正在运行。在所有的程序执行完或出错结束前,你需要不断的载入该页面查看 macro 的状态。

Macro 最显著的特征是你只需提交一个无需干涉便可运行完整个工作流。

#### 用户自定义工作流

虽然 WebLab 提供了一些预定义的 Protocol 和 Macro,但这对于实际的分析工作来说是远远不够的。因此,WebLab 提供了让注册用户自定义 Protocol 和 Macro 的机制。

注: WebLab 将引导你定义一个正确能运行的工作流。但你要包证你的工作流是有效的, 这是 WebLab 所不能担保的。

• 定义工作流

注册用户即可定义 Protocol 又可定义 Macro。定义的过程是有所不同的。下面是一个构 建 Macro 的例子。因为构建 Macro 比构建 Protocol 相对复杂些,所以当看完这个例子后你 应该就会构建 Protocol 了。

首先,点击"create your Macros"按钮来开始构建工作流。

			WebLab	¤ Feedback ¤ Contact ¤ Help	
	Service	Pre-defined Macros		Create Your Macros	
	Program	MACRO NAME	DESCRIPTION	Ċ -	
	Protocol				
	Macro	(a demo workflow to test	this workflow is used to test the workflow which can have ANDJoiner operator		
	Utility	ANDJoiner)			
	User Space	demo (just a demo workflow)	this workflow is used to test the workflow which can have more than one input		
	My Data		This macro is focused on prediction of protein functions based on sequence similarit	ty, where you have a	
	My Literature	profunction	gene sequence or several one in hand. You may begin with this protocol from nucleotide sequence(s), either cDNAs/ESTs or genomic DNA, as long as there will be protein coding region(s) existed. You will follow family identification, sensitive sites finding, and distant homologue sear processes. Each step will be performed by well-known software or programs. The flow chart will draw a sketch for you to understand		
	My MetaPackage	(Protein function analysis			
	My Toolbox	based on sequence similarity)			
	History		it.		
&	Account	MSAnalysis (Multiple sequences analysis workflow)	This workflow is designed to do some simple analyis for multiple sequences. At first, will be aligned using emma. Then, weblogo, cons and ealistat will give you some sta information for the aligned sequences. Besides, ehmebuild will build a HMM model	the input sequences atistical or intuitive and at last two	
	My Account	,	incidental programs will run to generate sequences based on this model and calibra	te the model.	
	My Group		This workflow is focused on constructing phylogentic tree by Neighbor-Joining meth	od. First, we do	
	Logout	phylogenetic (Construct phylogenetic tree by Neighbor-Joining method)	multiple sequence alignement, then use boostrap resampling for later evaluating the consensus tree. After bootstrap, distance of each sequence is calculated from result alignment. Then, the phylogenetic tree is built using Neighbor-Joining method. Final tree is calculated.	<ul> <li>significance of the of multiple sequence</li> <li>the strict consensus</li> </ul>	

(1). 构建 Macro/Protocal 的第一步是要填写一些关于要构建的工作流的基本信息,包括 名字,标签(简短的描述),详细的描述。

(2). 选择开始程序,工作流(系统预定义的或自己已定义的)或算子。在该例中,我们选择程序 emma。

注: Macro/protocol 的名字由数字,字母和下划线来构成。

			WebLab × Feedback WebLab × Help
ø	Service	ADD USER'S OWN MAC	CRO
	Program		Please use digit alphabet letter and underline as the components of the macro
	Protocol	Name:	macro_example name
	Macro		an example macro
	Utility	Label:	
	User Space		this is only an illustration workflow
	My Data		
	My Literature		
	My MetaPackage	Description:	
	My Toolbox		
	History		
&	Account	Type of Start Activity:	program 💌
	My Account	Start program:	emma(v5.0)
	My Group		
	Logout		(Next Step)
			~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

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(3). 点击 "next step",设置所选程序的参数。你可以看到你正在构建的 Macro/Protocol 当前的 DAG。

在 Macro 执行前,通过复选框选择你想调整的参数,也可对参数默认值进行修改。

注:对于没有默认值的必须参数,WebLab 将替你选中。因为假如没有这些参数,Macro 不能正确的运行。

通过点击"save parameters and continue"接着构建工作流,点击"finish activity selection" 完成创建。现在我们选中"save parameters and continue"。

Please select the parameters which you want to justify before submitting the macro, and then provide the default
value. For the mandatory parameters having no default value, we have checked the boxes for you and recommend
that you hold them; otherwise your macro may not work normally during the execution.

emma(v5.0)	- Multiple a	lignment progra	am - interface to	ClustalW	orogran
------------	--------------	-----------------	-------------------	----------	---------

	* output format:	Clustal	T	
1	* Do alignment using an old dendrogram:	N	•	
	* Protein pairwise alignment matrix:	blosum	¥	0
8	* DNA pairwise alignment matrix:	iub	v	0
	* Protein multiple alignment matrix:	blosum	v	0
3	* Nucleotide multiple alignment matrix:	iub	-	0
	* Slow pairwise alignment: gap opening penalty :	10.0		0
3	* Slow pairwise alignment: gap extension penalty :	0.1		0
1	* Fast pairwise alignment: similarity scores: K-Tuple size :	1	v	0
1	* Fast pairwise alignment: similarity scores: gap penalty :	3	v	0
4	* Fast pairwise alignment: similarity scores: number of diagonals to be considered :	5	v	6
1	* Fast pairwise alignment: similarity scores: diagonal window size :	5	v	0
3	* Fast pairwise alignment: similarity scores: suppresses percentage score :	N		
3	* No residue specific gaps:	N		0
3	* List of hydrophilic residues:	GPSNDQEKR		0
_	* No hydrophilic gaps:	N		0

(4). 现在你进入了扩展工作流的页面。在此你也能看到你当前构建工作流的 DAG。

在页面的上面,选择工作流中已有的一个源程序和一个目标程序。目标程序可为新程序 或一个结束算子来形成一个新的指向路径。在页面的下面,可选择去除工作流中已有的程序 节点。

注: 你无法删除有后子节点的程序节点。

Service
Program
Protocol
Macro
Utility
User Space
My Data
My Literature
My MetaPackage
My Toolbox
History
Account
My Account
My Account
Logout

				CBI ST	<sup>our</sup> /,	ebLab	¤ Feedback ¤ Contact ¤ Help
	Service	MACRO:	AN EXAMPLE MACRO				
	Program Protocol Macro Utility User Space My Data My Literature My MetaPackage My Toolbox	From:	Activity selected: 1-emma(v5.0)		Target:	Activity which will accept emma(v6.0) output as input Operator which is already in the macro:	•
	History						Add it
&	Account My Account		.0)				
	My Group Logout	Remove:	Leaf node activity selected:				(remove it)

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多注意一下这一步。

注: WebLab 将对子节点能否接受父节点的输出做基本的判断。如果子节点的输入与父节点的输出矛盾,下拉菜单的该程序被标为红色。不过,如果你认为这个流程是合理的,请在选择这个标为矛盾的程序时不要犹豫。

				CBI CBI CBI CBI	W	<sup>eb</sup> on th ebL	ab	¤ Feedback ¤ Contact ¤ Help
	Service	MACRO:	AN EXAMPLE MACRO					
	Program					Activitity		
	Protocol					which will		
	Macro					accept	cons(v5.0)	-
	Utility					output as	btwisted(v5.0)	<u> </u>
	User Space	From:	Activity selected: 1-emma(v5.0)		Target:	operator	cai(v5.0) chaos(v5.0) charge(v5.0) checktrans(v5.0)	D
-	My Data					which	chips(v5.0)	
-	My Literature					is already	cirdna(v5.0)	
_	My MetaPackage					macro:	clustalw2-msa	
	My Toolbox						clustalw2-psa	
	History						codcmp(v5.0)	(Add it
&	Account		(codcopy(v5.0) coderet(v5.0) 1-emma(v5.0) compseq(v5.0)					
	My Account						cpgplot(v5.0)	
-	My Group Logout	Remove:	Leaf node activity selected:	•			cusp(v5.0) cutseq(v5.0) dan(v5.0)	(remove it)
							degapseq(v5.0)	ų
			Copyright© 2004-2008. Center for Bio	Informatics All Rights	s Reserve	ed.	ueseseq(05.0)	м

注:当选择分支作为父节点时,你需要确定一个判断值以运行不同的程序。对 SeqTypeConditioner 来说,判断值是 "protein" 和 "dna"。

					CBI	your M	' <sub>ªb or</sub> /eb	Lab	¤ Feedback ¤ Contact ¤ Help
	Service	MACRO:	AN EXAMPLE	MACRO					
	Program Protocol Macro Utility User Space My Data My Literature My MetaPackage My Toolbox History	From:	Activity selected: Conditioner determine values:	3-choice branch-Se	eqTypeConditioner 🔹	Target:	Activity which will accept choice branch output as input: Operator which is already in the macro:	(fprotdist(v3.6b)	
-	Account								Add it
	My Account My Group Logout				1-emma(v 2-fseqboot(v 3-choice bra	v3.6b)			
		Remove	Leaf node activity selected:		•				(remove it)
			Copyrigh	nt© 2004-2008, Center	for BioInformatics All Rig	hts Rese	rved.		

然后点击 "add it",进入新选择程序的参数设置页面。重复上面的两个步骤知道完成工 作流的构建。 对 Protocol 来说,点击"finish Protocol"完成 Protocol 的构建。 对 Macro,在点击"finish activity selection"后,还有重要的事要做。



(5). 为了每一个 Macro 程序在运行中都能得到恰当的输入,你需要为每个程序选择输入 参数的类型。这里有三种输入参数的类型。

- user provided: 在提交 Macro 时,用户需提供该类型参数的值。也就是说这些参数是 Macro 的全局输入参数。
- pipe: 这种类型的参数或者接受其它程序的输入或者使用 "user provided" 参数。在下部中 WebLab 就会引导你为 pipe 类型的参数指派数据源。
- do not use: 在 Macro 执行中,这些参数是可以不用的。一般来说,这些参数不是必 须参数。

注:WebLab 给每一个输入参数都指定了一个默认类型。 指定完参数类型后,点 "save selection"按钮。

		Wel	bLab	¤ Feedback ¤ Contact ¤ Help
	Service	Please select the source of the input parameters for activity		
	Program			
	Protocol	user provide: User will provide the input before the workflow execution. If you have more than one through the "branch" operators, please select one parameter as "user provided" and others as "pir	e activity to share one input	parameter
	Macro	pipe: Accept other activity's output or input as the input value.		
	Utility	do not use: Do not need to provide the input value during the workflow execution. And obviously, as "do not use"	you can not mark a manda	tory parameter
	User Space	1-emma(v5.0)		
	My Data			
	My Literature			
	My MetaPackage	•		
	My Toolbox			
	History	2-fseqboot(v3.6b)		
&	Account	1 - emma(v5.0) (Multiple alignment program - interface to C	lustalW program )	
	My Account	Input Parameter Selection	0	
	My Group	• • sequence:	<b>(</b> )	
	Logout	O O Dendrogram (tree file) from clustalw file (optional) :		
		O O O Comparison matrix file (optional):	0	
		Comparison matrix file (optional):	6	
		2 - fseqboot(v3.6b) (Bootstrapped sequences algorithm)		
		• sequence:	•	
			0	
		O O O O O O O O O O O O O O O O O O O	0	
		Veignts file:	•	
		(save selection)	,	

(6). 现在进入 Macro 构建的最后一步。在本步中,为 pipe 类型的参数指定数据源。

注: WebLab 为每个 pipe 参数都指定了一个默认的数据源。

现在,点击"Save IO Pipe Association"完成 Macro 的构建。

		WebLab	¤ Feedback ¤ Contact ¤ Help
ی ا ا ا ا ا ا ا ا ا ا ا ا ا ا ا ا ا ا ا	Service Program Protocol Macro Utility User Space My Data My Literature My MetaPackage My Toolbox History Account	User provide: User will provide the input before the workflow execution. If you have more than one activity to share one through the "branch" operators, please select one parameter as "user provided" and others as "pipe". pipe: Accept other activity's output or input as the input value. do not use: Do not need to provide the input value during the workflow execution. And obviously, you can not mark a mas "do not use". 1-emma(v5.0) Please associate possible values to the "pipe" input parameters you just selected 1 - emma(v5.0) (Multiple alignment program - interface to ClustalW program )	input parameter andatory parameter
	My Account	Input Parameter Selection	
	My Group	O * sequence: value: 1-emma(v5.0)-seque	ince 🔞
_	Logout	<ul> <li>Dendrogram (tree file) from clustalw file (optional) :</li> </ul>	<b>()</b>
		Comparison matrix file (optional):	<b>()</b>
		Comparison matrix file (ontional)':	0
			•
		2 - fseqboot(v3.6b) (Bootstrapped sequences algorithm)	
		Input Parameter Selection	
		* sequence:     * sequence:     * sequence:     value:	ioutfile eq
		File of input categories:	
		O O Weights file:	6
		(Save IO Pipe Association) Copyright© 2004-2008, Center for BioInformatics All Rights Reserved.	

#### • 删除和编辑工作流

你可以通过点击"remove"来删除相应的用户自定义的 Protocol 或 Macro。而且你还可以通过"edit"按钮来编辑相应的工作流。



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编辑过程是工作流创建过程的一个延伸。你可以在此通过"remove it"删除特定的节 点和加入新的节点。如果你修改的是 Macro 工作流,在最后还要设置参数的类型及 pipe 参 数的数据源。

				S S S S S S S S S S S S S S S S S S S	BI	WebLab	¤ Feedback ¤ Contact ¤ Help
	Service	MACRO:	AN EXAMPLE MACRO				
	Program					Activity which	
	Protocol					will	
	Macro					fseeboot(v3.6b)	▼
	Utility	From	Activity selected: 2-fseaboot(v3.6b)	-	Tarnet	output as input:	
	User Space	Trom.			Targot	Operator which	
-	My Data					the macro:	
	My Literature						
	My MetaPackage						Add it
	My Toolbox						
	History			1-em	ma(v5.	.0)	
æ	Account						
	My Account				*		
	My Group			261			
	Logout			2-fseqb	poot(V3	3.6D)	
		Remove:	Leaf node activity selected:	🔻			remove_it

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4). 任务控制——你是你的任务的主人!

#### 任务状态

一个任务可以是如下五个状态之一:

•submitted:当用户输入参数发送请求运行程序,一个任务被创建被设为"submitted" 状态。

• running: 当通过参数验证并存入数据库,请求被推进入任务调度,任务的状态改为 "running"。

•in queue:如果拥有请求程序的所有节点都在高负荷运行,任务状态设为"in queue"。

- finished: 任务顺利完成,结果存入"my data",状态改为"finished"。
- failed:如果由于某些原因造成任务失败或非正常退出。状态改为"failed"并记录和显示详细的警告信息。

#### 任务历史

注册用户可以在"History"中监视提交任务的最新状态。

						CBI CBI	NebLab			¤ Feedback ¤ Contact ¤ Help
	Service	total count: 1824			Pa	geSize: 5 🔽 Ord	er: Start Time 🔻 Type	Desc	•	
	Program		100							
	Protocol	WORKFLOW	JOB ID	SERVICE	STATUS	INPUT FILE	OUTPUT FILE	TIME	TIME	MESSAGE
	Macro							2008-		
	Utility		56406	inforce(vE 0)	Finished	1205061014269 footo	Untitled.infoseq.2008-03-	03-09	1.00	
	User Space		50400	moseq(vo.o)	Fillished	1200001914200.18518	09 19:25 PM	19:25 PM	1.05	
							Untitled.dendrogram.2008-	2008-		
-	My Data	3802 demonstration protocol	56320	emma(v5.0)	Finished	hba15.fasta	03-08 20:53 PM Untitled msf 2008-03-08	03-08	1.0s	
-	My Literature	demonstration_protocol					20:53 PM	PM		
-	My MetaPackage		56319 emm				Untitled.dendrogram.2008-	2008-		
	My Toolbox	3801		emma(v5.0)	Fail	human hba.fasta	03-08 20:45 PM	03-08		<b>(</b> )
	History	demonstration_protocol					20:45 PM	20:45 PM		•
- <u>8</u> -	Account							2008-		
-0			56235	cons(v5.0)	Finished	abiview.msf	Untitled.fasta	03-08	1.0s	
-	My Account							15:32 PM		
-	My Group							2008-		
_	Logout		55097	clustalw2-	Finished	bbo15 facto	hba.msf	03-06	1.00	
			00907	msa	Fillistieu	nua i o.iasia	hba.dendrogram	20:42	1.05	
								PIN		
					1 2	3 4 5 6 7 8 9 10	11 12 13 14 15 16 1	7 18 19	20	21 > >>

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#### 任务控制

对于一些运行了很长时间的任务,你可以选择杀掉该进程。 注:你最多可同时运行 30 个任务。

						CBI Sol Your	VebLab		н н н	Feedback Contact Help
	Service	total count: 1825			Pa	geSize: 5 🔻 Ord	ler: Start Time 🔻 Type	Desc	•	
	Program Protocol	WORKFLOW	JOB ID	SERVICE	STATUS	INPUT FILE	OUTPUT FILE	START TIME	RUN TIME	ERROR MESSAGE
	Macro Utility User Space		56474	blastp(v2.2.15)		human_hba.fasta	Untitled.blast.2008-03-10 14:59 PM	2008- 03-10 14:59 PM		
	My Data My Literature		56406	infoseq(v5.0)	Finished	1205061914268.fasta	Untitled.infoseq.2008-03- 09 19:25 PM	2008- 03-09 19:25 PM	1.0s	
	My MetaPackage My Toolbox History	3802 demonstration_protocol	56320	emma(v5.0)	Finished	hba15.fasta	Untitled.dendrogram.2008- 03-08 20:53 PM Untitled.msf.2008-03-08 20:53 PM	2008- 03-08 20:53 PM	1.0s	
<b>&amp;</b>	Account My Account	3801 demonstration_protocol	56319	emma(v5.0)	Fail	human_hba.fasta	Untitled.dendrogram.2008- 03-08 20:45 PM Untitled.msf.2008-03-08 20:45 PM	2008- 03-08 20:45 PM		•
	My Group Logout		56235	cons(v5.0)	Finished	abiview.msf	Untitled.fasta	2008- 03-08 15:32 PM	1.0s	
					1 2	3 4 5 6 7 8 9 10	11 12 13 14 15 16 1	7 18 19	9 20	21 > >>

# 5). 我的工具箱

工具箱中存放你最爱的服务或程序。"my toolbox"是一个类似"my data"的用户空间。 注册用户可用它来方便的收集和管理 WebLab 中的程序, Protocols, macros 和 utilities。

	Constant	WebLab	¤ Feedback ¤ Contact ¤ Help
	Service	- +Expand all -Collapse all-	
	Program		
	Protocol	⊡-i_ My ToolBox	
	Macro	E 🔤 🔲 analysis	
	Utility		
	User Space		
	My Data		
	My Literature	phylogenetic weblab.service.protocol	
	My MetaPackage	A jalview weblab:service:utility	
	My Toolbox		
	History 💟		
&	Account	New Directory         New Tool         Delete         Move         Rename	
	My Account		
	My Group		
	Logout		

#### 使用工具箱

WebLab 上所有服务的提交页面上都有一个 "add to Toolbox" 按钮。如果你任务这个服务有用,点击此按钮便可将其加入工具箱。

				WebLab	¤ Feedback ¤ Contact ¤ Help
	Service	seqret(v5.0) - Reads and w	rites (returns) sequences		>>add to ToolBox
	Program	🗏 Input			U
	Protocol	Use feature information:		v	
	Macro Utility	🕀 * sequence:	(	v @	
	User Space	Start of each sequence to be used:			
	My Data	End of each sequence to be used:			
	My Literature	_			
	My MetaPackage	Output section			
	My Toolbox	* save result in directory:	Work Directory	<b>v</b>	
	History	* outseq: (bio:seq:fasta)	Untitled.fasta	6	
4	Account	Advanced Options			
	My Account	Read one sequence and stop:	[	v	
	My Group				
	Logout		Run		

6). 资源——获取源数据

WebLab 提供 resource 模块供用户方便的提取生物数据库中大量的数据。而且,还可将 这些数据保存入"my data"中供进一步分析。

					WebLab	¤ Feedback ¤ News ¤ Contact ¤ Help
	ervice rogram rotocol lacro tility esource ser Space ly Data ly Literature ly MetaPackage	WebLab provides a few to conveniently.	interfaces through BioMart is a que Cancer Resean Please click her	h which users can acce ary-oriented data manageme ch (OICR) and the European re to enter the query page for	A comprehensive plant transcription facto contains 26 402 TFs predicted from 22 sp	e resource
M H An M L	ly Tectarackage ly Toolbox listory ccount ly Account ly Group ogout	Plant T	ranscription Fa	Human Proteome Organiza China. More than 100 labs One major goal of HLPP is and the important liver prot Please click here to query to	five model organisms with available who sequence and 17 plants with available ES has extensive annotation at both family at Please click here to query PlantTFDB inte WebLab. Attion starts the Human Liver Proteome Proj from 18 countries and regions participated to study the binasy protein-protein interacti ein complexes. HLPP integrated in WebLab.	e genome 5T sequences. It nd gene levels. grated in ect directed by in this project. ons between liver
		SRS Choose database: UniProtKB Through: Accession FASTA no • format: no • Each line one Accession Number or ID	Number			Paget Saurch
					(	Keset Search

#### 提取数据

目前,WebLab 提供提取 BioMart, planttfdb, hlpp 和 SRS 中数据的用户界面。

• BioMart

BioMart 是 OiCR 和 EBI 共同开发的一个数据检索管理系统。 通过 BioMart 获得数据,你需要首先选择要检索的数据库。



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然后 BioMart 为你收集相关的属性和过滤。

				Ble WebL	.ab	¤ Feedback ¤ News ¤ Contact ¤ Help			
ø	Service		Celegans_gene_ense	set 🔹					
	Protocol								
	Macro		Attrib	oute					
	Utility	⊟ Features							
	User Space	GENE:	Ensembl Transcript ID	Ensembl Peptide ID	Description				
	My Data	Chromosome Name	📃 Gene Start (bp)	Gene End (bp)	Strand				
	My Literature	Transcript Start (bp)	Transcript End (bp)	📃 Gene name	📃 Gene DB				
	My MetaPackage	External Transcript ID	External Transcript DB	Ensembl CDS length	Ensembl cDNA leng	th			
	My Toolbox	Ensembl Peptide length	Transcript count	SC content %	Biotype				
	History	I EXTERNAL:							
8	Account	<ul> <li>         ■ PROTEIN:         <ul> <li>             ■ GENOMIC REGION:         </li> </ul> </li> </ul>							
	My Account	⊞ Structures							
	My Group								
	Logout	± Sequences							
		Ciltor							
		chromosome_name:							
		id_list_filters:	•						
		◯ only ◯ excluded							

在选择一些属性和过滤后,BioMart 会给出结果。此外,你可以设置文件名,指定数据格式,选择存储数据的目录。你也可以选择保存检索条件。然后点击"save to my data",结果就会存入你的数据空间。

Band and	WebLab	¤ Feedback ¤ News ¤ Contact ¤ Help
Service	Save Data	
Program	Your File Name: myresult.out	
Protocol	Specifiv File Format: unknown	
Macro		
Utility	Select the directory you want to save:  -other v	
User Space	(Save to My Data)	
My Data		
My Literature	Attribute: ensembl_gene_id chromosome_name percentage_gc_content	
My MetaPackage	Filter: chromosome_name = V	
My Toolbox	Results:	
History	B0348.5 V 51	
Account	B0348.6 V 44 B0348.4 V 37 B0348.2 V 33	
My Account	B0348.1 V 39	
My Group	1360-95.2 V 30 Y38(09.1 V 33	
Logout	Y38C9B.3 V 42	
	F56E10.2 V 38	
	F56E10.3 V 31	
	F56E10.1 V 40	
	Y38C9A1 V 35	
	Y38C9A.2 V 36	
	W03F9.1 V 41	
	W03F9.2 V 40	
	W03F9.10V 39	
	Service Program Protocol Macro Utility User Space My Data My Literature My MetaPackage My Toolbox History Account My Account My Group Logout	Your Jab on the web         Service         Program         Protocol         Macro         Utility         User Space         My Data         My Toolbox         My Toolbox         My Toolbox         My Toolbox         My Account         My Account         My Account         My Group         Y38C9B.2 V         V38C9B.1 V         1 goout

• PlantTFDB

PlantTFDB 是 CBI 开发的一个综合的植物转录因子数据库。检索 PlantTFDB 的过程与检索 BioMart 类似。不同的是在这我们还提供 blast 功能。

4	Service	Choose your query condition
	Program	Field
-	Protocol	Gene_Model
-	Macro	Family
-	Utility	Domain_ID
	Resource	Domain Description
·		Expression
	User Space	Protein_Length
	My Data	
-	My Literature	CDS Sequence
	My MetaPackage	
	My Toolbox	Filter
	History	
Ъ	A	Gene_Model:
	Account	Family: like
	My Account	
	My Group	Domain_ID: like 🔻
	Logout	
		Domain_Description: like
		Expression:
		Protein_Length: > •
		All_Text: like •
		Do Blast
		Program: blastp
		Sequence:
		Expect_Threshold: 0.1 •

• SRS

序列检索系统 SRS 是世界上第一个整合,分析和显示生物数据的生物信息学工具。 在此,我们提供两种检索方式。

・SRS ID/AC 检索

用户需要选择数据库,数据格式,填入感兴趣的序列的编号。每行填一个序列编号。

OR THROUGH SRS	
Choose database:	UniProtKB
Through:	Accession Number
FASTA format:	yes 🔻
	P69905
Each line one	
Accession Number or ID	
	(Reset) (Up ad

•SRS 关键字检索

选择数据库和数据格式,输入关键字进行检索。

OR USE SRS KEYWORDS SEARCH					
Choose database:	UniProtKB				
FASTA format:	no				
One or several keywords:	If the number of result entries is no more than 100, all of them will be displayed; otherwise, only 100 entres are provided.				
	Search				

检索结果如下图所示。用户可选择感兴趣的序列并保存。

			<b>)</b>	WebLa	web <b>b</b>	¤ Feedback ¤ Contact ¤ Help
	Service	number of entries: 26		Page	Size: 10 🔻	
-	Program					
	Protocol	save selection sequences				
	Macro	ENTRY NAME	PRIMARY	DESCRIPTION	SEQUENCE LENGTH	
	Utility	UNIPROT:OLF1_APILI	Q26419	Olfactory receptor-like protein HbA1 (Fragment).	165	
	User Space		Q7Z6G4	HBA2 (Fragment).	31	
	My Data					
	My Literature	UNIPROT:Q148I4 BOVIN	Q148l4	Similar to brain acyl-CoA hydrolase isoform hBACHa.	338	
	My MetaPackage					
	My Toolbox	UNIPROT:P95636 RHOPA	P95636	4-hydroxybenzoyl-CoA reductase HbaC subunit.	774	
<b>&amp;</b>	Account	UNIPROT:P95635_RHOPA	P95635	4-hydroxybenzoyl-CoA reductase HbaB subunit (4- hydroxybenzoyl-CoA reductase, first of three subunits) (EC 1.3.99.20).	163	
	My Account		P95637	4-hydroxybenzoyl-CoA reductase HbaD subunit (4- hydroxybenzoyl-CoA reductase, third of three subunits)	327	
-	My Group	UNIFRUI.F95057_RHOFA		(EC 1.3.99.20).		
	Logout	UNIPROT:Q9RFR5_RHOPA	Q9RFR5	Transcriptional activator HbaR (Hydroxybenzoate anaerobic degradation regulatory protein HbaR, Crp/Fnr family).	241	
		UNIPROT:A7M7S6_MOUSE	A7M7S6	Hemoglobin X, alpha-like embryonic chain in Hba complex (Fragment).	156	
		UNIPROT:Q78PA4_MOUSE	Q78PA4	Zeta globin (Hemoglobin X, alpha-like embryonic chain in Hba complex).	142	
		UNIPROT:A8KBN4_DANRE	A8KBN4	Hbae1 protein.	143	
				<< < 1	23>>>	

5. 和同事一起工作——分组策略及分享机制

### 1). 概述

生物学研究者通常需要和合作者分享他们的分析数据,感兴趣的文献和工作经验。为 了便于组内的合作研究,WebLab 提供了分享和分组机制。组内成员之间几乎可以方便的分 享任何 WebLab 上的东西。

## 2). 分组——你不是一个人在工作

#### WebLab 的分组机制

组是一群用户的集合。每一个注册用户可以点击"My Group"查看组的状态。你可以检查你所创建组(上面的粉红框内)和参加组(下面的绿框内)的详细信息。

				WebLab	¤ Feedback ¤ Contact ¤ Help
Service			Us	er Created Group	
Program	NAME	DESCRIPTION		>>Creat	a Your Group
Protocol		BEGORI HON			Action
Macro	test	test group	📥 k	ongl 🖱 xiaoqiao 🦱 wangjun 🆱 qingwa 🆱 gaoge 🖱	delete edit
Utility			aiygu	nia	
User Space	xiaoqiao	SSS	🚨 x	aoqiao 🚔 qingwa 📥 zhaosq 🛎 liuxq	delete edit
My Data			Us	er Attended Group	
My Literature	NAME	DESCRIPTION	CREATOR	MEMBERSHIP	ACTION
My MetaPackage			•		
My Toolbox	test	test group	aingwa 🍊	alvgunia	' quit
History Account	xiaoqiao	555	aingwa	🛎 xiaoqiao 🚔 qingwa 🚔 zhaosq 🏝 liuxq	quit
My Account					
My Group					
Logout 💟					

#### 创建组

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每一个注册用户都有权创建并管理自己的组。点击"Create Your Group"进入创建组页面。

					WebLab	¤ Feedback ¤ Contact ¤ Help
	Service			Us	er Created Group	
	Program	NAME	DESCRIPTION		MEMBERSHIP	>>Create Your Group
	Protocol		DEGORIFICIA			
	Macro	test	test group	🥌 ko	ongl 🌥 xiaoqiao 🌥 wangjun 🌥 qingwa 🌥 gaoge	e 🥌 🛛 delete edit
	Utility			aiygu	lia	
	User Space	xiaoqiao	SSS	🚨 xi	aoqiao 🚔 qingwa 🚔 zhaosq 🚔 liuxq	delete edit
	My Data			Us	er Attended Group	
	My Literature	NAME	DESCRIPTION	CREATOR	MEMBERSHIP	ACTION
	My MetaPackage			•		
	My Toolbox	test	test group	aingwa 🍊	alvounia	gaoge 📟 🛛 quit
	History			•		
æ	Account	xiaoqiao	888	🎽 qingwa	🛎 xiaoqiao 🛎 qingwa 🌥 zhaosq 🋎 liuxq	quit
	My Account					
	My Group					
	Logout					

按照一下步骤创建自己的组:

•填写组的基本信息:包括组名及组的简短描述。

•添加组员:输入组员的账号(每次一个),加入组中。在创建组的过程中,你可以动态的修改组员列表。注意,一个组内最多不得超过15个成员。

注意:如果你想分享该组的数据和知识请记着把自己加入该组中。

•点击"save group"完成组的创建。

			WebLab	¤ Feedback ¤ Contact ¤ Help
	Service	CREATE NEW O	GROUP	
	Program	Name:	weblab_group	
	Protocol			
	Macro	Description:	the group is used to share literature in weblab development group	
	Utility	Description.		
	User Space		Please input the user name:	
	My Data			
	My Literature		Member list: (maximum 15)	
	My MetaPackage		liuxq_Delete	
	My Toolbox	Membership:	luojc Delete	
	History		zhaosq Delete	
&	Account		kongl Delete gaoge Delete	
	My Account		wangj Delete	
	My Group			
	Logout			Save Group

#### 组操作

- •作为所创建组的管理员,你可以点击"delete"删除相应的组,或点击"edit"修改 组的基本信息和添加删除组员。
- •如果你发现参加的组非常无聊,可以点击"quit"退出该组。

注:组操作会改变 WebLab 系统中分享的数据和知识信息。

					CBI S	WebLab	¤ Feedback ¤ Contact ¤ Help
	Service			U	ser Created Gro	up	
	Program	NAME	DESCRIPTION			MEMBERSHIP	Create Your Group
	Protocol		DEGORIFHON		•		Action
	Macro	test	test group	2	kongl 🍮 xiao	qiao 🆱 wangjun 🆱 qingwa 🦱 gaoge 🤅	delete edit
	Utility			aly	gunia		
	User Space	weblab_group	the group is used to share lite weblab development gr	oup	luojc 📥 kong	I Å wangj Å zhaosq Å liuxq Å gaog	je <u>delete</u> edit
	My Data						
	My Literature			Us	er Attended Gro	up	
	My MetaPackage	NAME	DESCRIPTION	CREATOR		MEMBERSHIP	ACTION
	My Toolbox	test	test group		📥 kongl 📥	xiaoqiao 🚨 wangjun 🚨 qingwa 🚨 gao	oge 🚨 🛛 quit
	History		•	qiligwa	alygunia		
&	Account						
	My Account						
	My Group						
	Logout						

#### 分享数据, 文献和 MetaPackage

数据, 文献和 MetaPackage 的分享模型是链接分享。在数据库中只存在一分拷贝和他的分享链接信息。分享内容的所有改动都能被提供者和分享者同时看到。

•如何分享数据, 文献和 MetaPackage

选择目录 My Data, my literature 或 my MetaPackage, 然后点"share"分享。

注:用户既不能分享根目录,也不能导入根目录。

	Central	WebLab	¤ Feedback ¤ Contact ¤ Help
	Service	Edit Comment         Delete Comment         Edit Tag         Attach Tag         Edit Format	
	Program		
	Protocol		
	Macro	🗄 🍃 🥅 My Data	
	Utility	E test data	
A	User Space		
	My Data	Image:	
	My Literature	🔤 🔄 mdr3_fugu.fasta bio:seq:fasta:set:protein	
	My MetaPackage	🗏 🖶 📃 Untitled.pair bio:align:emboss:pair	
	My Toolbox	- 🞼 🖂 1180937824600.fasta bio:seq:fasta:set	
	History	- 😽 🥅 Untitled.msf bio:align:emboss:msf	
-	Account	Untitled.dendrogram bio:report:dendrogram	
	My Account		
	My Group	New Directory New File Delete Move Rename	
	Logout	Share Cancel Share Import Cancel Import Refresh	

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选择目录及权限(只读,读写)分享给其它组或用户。

•只读权限只允许授权用户读取数据而不能修改文件或向分享目录写入文件。

•读写权限允许用户读,修改文件并能向分享目录写入文件。

		WebLab	¤ Feedback ¤ Contact ¤ Help
	Service		
-	Program	Read only	
-	Macro	Please select the group: weblab_group  Read and Write	
-	Utility	Share	
	User Space		
	My Data		
根捷	子子李类度的	的不同,分享的目录被标记成不同的颜色。	
		分享给单个用户。	
		分享给整个组。	
		既分享给单个用户又分享给一个组。	
如果	<b>人想取消分</b> 事	享,点击"cancel share"按钮。	

		WebLab	¤ Feedback ¤ Contact ¤ Help
ő	Service	Edit Comment Delete Comment Edit Tag Attach Tag 🔻 Edit Format	
	Program		
	Protocol	+Expand all -Collapse all	
	Macro	🗄 🗁 🥅 My Data	
	User Space	e 📴 📄 test data e 📴 📄 II	
	My Data	🔤 🖂 osht01.fasta bio:seq:fasta:set	
	My Literature	- 📴 📄 P61981.fasta bio:seq:fasta:protein	
	My MetaPackage	🔤 📴 6dna.fasta bio:seq:fasta:set:dna	
	My Toolbox	- 🔢 📄 1201487229077.fasta bio:seq:fasta:dna	
	History	- 🔢 🖂 1201487298108.fasta bio:seq;fasta:dna	
&	Account	- 🛄 🗧 rice	
	My Account	🛛 🖂 🕞 oba human fasta bio seo fasta single protein	
	My Group	D nha rat fasta biorsen fasta set	
	Logout	D nha mouse fasta hio sen fasta sat	
		bha7 fac hin can facto cat	
		New Directory New File Delete Move Rename	
		Share Cancel Share Import Cancel Import Refresh	

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你可以获得你所分享数据的所有信息。点击"cancel share"停止某个分享。

				WebLab	¤ Feedbac ¤ Contact ¤ Help
	Service	Account Based Sha	aring		
9	Brogram	SHARED DIR	ACCOUNT	PRIVILEGE	ACTION
	Protocol	cirdna	xiaoqiao	Read only	cancel share
	Macro	blast	xiaoqiao	Read only	cancel share
	Utility				
	User Space	Group Based Shari	ng		
	My Data	SHARED DIR	GROUP	PRIVILEGE	ACTION
	My Literature	ePCR	test	Read and Write	cancel share
	My MetaPackage				
	My Toolbox				
	History				>>Back to My Data
æ	Account				
	My Account				
	My Group				
	Logout				

•如何导入数据, 文献和 MetaPackage

当知道某人分享给你或你所属的组东西,可通过点击"import"按钮来查看与你有关的分享信息。

		WebLab	¤ Feedback ¤ Contact ¤ Help
	Service	Edit Comment Delete Comment Edit Tag Attach Tag 🔻 Edit Format	
	Program		
	Protocol	+Expand all -Collapse all-	
	Macro		
	Utility	🖻 🦢 📃 My Data	
	User Space	P 🔤 📄 test data	
	My Data	🌃 📃 osht01.fasta bio:seq:fasta:set	
	My Literature	💹 📃 P61981.fasta bio:seq:fasta:protein	
	My MetaPackage	🔤 📴 6dna.fasta bio:seq:fasta:set:dna	
	My Toolbox		
	History	- 🔯 🖂 1201487298108 fasta bio:sec:fasta:dna	
-	Account	- Con Horsen Solar	
	My Account	🖳 🔤 nha human fasta bio seo fasta single protein	
	My Group		
	Logout		
		m 🛂 📋 hba7.tas bio:seq:fasta:set	
		New Directory         New File         Delete         Move         Rename	
		Share Cancel Share Import Cancel Import Refresh	

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你可以查看与你有关的所有分享的详细信息,然后选择导入你感兴趣的数据。

					CBI Solution	We	<sup>on the web</sup>		¤ Feedback ¤ Contact ¤ Help
	Service	Account Based Import							
9	Program	AVAILABLE D	IR	FROM ACCOUN		PRIVILEGE		ACTION	
	Protocol	rotocol arabidopsis		bobbaby		Read only		Import	
	Macro	L							
	Utility			Gro	up Based Import –				
	liser Space	AVAILABLE DIR	AS MEM	BER OF GROUP	FROM ACCOU	NT	PRIVILEGE	ACTION	
	User Space	water	web	lab_group	liuxq	liuxq		Import	
	My Data								
	My Literature							>>My (	Data
	My MetaPackage								

导入的目录根据分享粒度和权利的不同被标上不同的颜色。

导入的目录是分享给单个用户的只有读权限的目录。

■■■■ 导入的目录是分享给单个用户的有读写权限的目录。

导入的目录是分享给一个组的只有读权限的目录。

导入的目录是分享给一个组的有读写权限的目录。

注:对于 Metapackage, 你既可以在"My MetaPackage"中看到导入的资源, 又可以在相应 程序的提交界面的上把其作为输入。

#### 分享知识:分发工作流

工作流的分享机制与数据, 文献和 MetaPackage 的分享机制不同。

- •工作流的分享是基于单个工作流(macro或 Protocol)而不是一个目录。
- 由于 WebLab 提供递归的工作流设计,为了避免影响分享者的递归工作流,WebLab 用分发代替了分享。分发工作流意味着一旦用户导入工作流,则他得到的是这个工 作流的一分拷贝而不是一个链接。你可以对此工作流做任何改动而不会改变分发者 的工作流。
- 如何分发工作流

注册的用户可以分发任何自定义的或导入的工作流。

			)	CBI South	WebLab	¤ Feedbad ¤ Contact ¤ Help			
	Service	Pre-defined Macros				Create Your Macros			
-	Program	MACRO NAME			DESCRIPTION				
	Protocol	AND loiperTest							
	Macro	(a demo workflow to test	this workflow is us	ed to test the workflow whi	ch can have ANDJoiner operator				
	Utility	ANDJoiner)			-				
	User Space	demo (just a demo workflow)	this workflow is us	ed to test the workflow whi	ch can have more than one input				
_	My Data		This macro is focused on prediction of protein functions based on sequence similarity, where you have a						
	My Literature	profunction	gene sequence or several one in hand. You may begin with this protocol from nucleotide sequence(s), either cDNAs/ESTs or genomic DNA, as long as there will be protein coding region(s) existed. You will follow family identification, sensitive sites finding, and distant homologue search processes. Each per will						
-	My MetaPackage	(Protein function analysis							
-	My Toolbox	based on sequence similarity)	be performed by well-known software or programs. The flow chart will draw a sketch for you to understand it.						
	History								
æ	Account MSAnalysis (Multiple sequences analysis workflow) workflow) a digned using emma. Then, weblogo, cons and ealistat will give you some statistica information for the aligned using emma. Then, weblogo, cons and ealistat will give you some statistica					the input sequences tistical or intuitive and at last two			
-	My Account		This work for the for	io mininari lo gonoralo ocq.		d First we de			
-	Logout	phylogenetic	multiple sequence	alignement, then use boo	strap resampling for later evaluating the	significance of the			
-	Logout	(Construct phylogenetic tree by Neighbor-Joining method)	consensus tree. A alignment.Then, the tree is calculated.	ter bootstrap, distance of e le phylogenetic tree is buil	each sequence is calculated from result of turner to the sequence is calculated from result of the sequence is turner to the sequence of the	of multiple sequence y, the strict consensus			
		EmbedMacro (a demo workflow which is used to test embedded macro)	this workflow is us	ed to test the workflow whi	ch has other macros as component activ	rity			
		phylogenetic_max_parsimony (Construct phylogenetic tree by maximum parsimony method)	imony This workflow is focused on constructing phylogentic tree by maximum-parsimony method. First, we do multiple sequence alignement, then use bootstrap resampling for later evaluating the significance of the consensus tree. After boostrap, the phylogenetic tree is built using maximum parsimony method. Finally, the strict consensus tree is calculated.						
		User Customized Macros		Distribute Macrogh	Cancel Distribute Macros	Import Macros			
		MACRO NAME		DE	SCRIPTION	ACTION			
		RNA_analysis (rna_analysi	s) rna fold			Remove Edit			

选中的工作流可以分发给某个用户或你所参加的组。

注: 在工作流的分发上没有权限选项。

		WebLab	¤ Feedback ¤ Contact ¤ Help
	Service		
	Program		
	Protocol	You want to distribute RNA_analysis to group	
	Macro	Please select the group: weblab group group	
	Utility	Heade science and group.	
	User Space	Distribute	
周相	分发粉度的	1不同 分发的工作流被标上不同的颜色	

根据分发粒度的不同,分发的工作流被标上不同的颜色。

分发给单个用户。 分发给整个组。

既分发给单个用户又分发给一个组。

如果你想停止分发,只要点击"cancel distribute macro"或"cancel distribute Protocol" 按钮便可。

			WebLab × Feedback					
	Service	Pre-defined Macros	Create Your Macros					
_	Program	MACRONAME	DESCRIPTION					
	Protocol							
	Macro	ANDJoinerTest (a demo workflow to test	this workflow is used to test the workflow which can have ANDJoiner operator					
-	Utility	ANDJoiner)						
	User Space	demo (just a demo workflow)	this workflow is used to test the workflow which can have more than one input					
	My Data		This macro is focused on prediction of protein functions based on sequence similarity, where you have a					
	My Literature	profunction	gene sequence or several one in hand. You may begin with this protocol from nucleotide sequence(s),					
-	My MetaPackage	(Protein function analysis	follow family identification, sensitive sites finding, and distant homologue search processes. Each step will					
	My Toolbox	based on sequence similarity)	be performed by well-known software or programs. The flow chart will draw a sketch for you to understand					
-	History							
æ	Account	MSAnalysis (Multiple sequences analysis workflow)	This workflow is designed to do some simple analyis for multiple sequences. At first, the input sequences will be aligned using emma. Then, weblogo, cons and ealistat will give you some statistical or inutitive information for the aligned sequences. Besides, ehambuild will build a HMM model and at last two incidental procents will us to concern sequences beard on this model and calibrate the model					
-	My Account		incidental programs will full to generate sequences based on this model and camprate the model.					
-	My Group	phylogenetic	This workflow is focused on constructing phylogentic tree by Neighbor-Joining method. First, we do multiple sequence alignement, then use boostrap resampling for later evaluating the significance of the					
-	Logout	(Construct phylogenetic tree by Neighbor-Joining method)	consensus tree. After bootstrap, distance of each sequence is calculated from result of multiple sequence alignment. Then, the phylogenetic tree is built using Neighbor-Joining method. Finally, the strict consensus tree is calculated.					
		EmbedMacro (a demo workflow which is used to test embedded macro)	this workflow is used to test the workflow which has other macros as component activity					
		phylogenetic_max_parsimony (Construct phylogenetic tree by maximum parsimony method) This workflow is focused on constructing phylogentic tree by maximum-parsimony method. First, we c multiple sequence alignement, then use boostrap resampling for later evaluating the significance of consensus tree. After boostrap, the phylogenetic tree is built using maximum parsimony method. First the strict consensus tree is calculated.						
		User Customized Macros	Distribute Macros Cancel Distribute Macros Import Macros					
		MACRO NAME	DESCRIPTION ACTION					
		RNA_analysis (ma_analysi	s) ma fold Remove <b>fail</b>					

你可以看你所分发的工作流的所有信息。点"cancel distribute"按钮停止分发。

Constant		CBD CBD CBD CBD CBD CBD CBD CBD	bLab	¤ Feedback ¤ Contact ¤ Help
Service				
Program	Account-Based Distributed Macro:			
Protocol	ACCEPTER	MACRO NAME	ACTION	
Macro	I			
Utility	Group-Based Distributed Macro:			
	ACCEPT GROUP	MACRO NAME	ACTION	
User Space	weblab_group	RNA_analysis	cancel distribute	
My Data	•			•
My Literature			>>macro	o home
My MotoDackage				

• 如何导入工作流

当知道有人分发给你或你所属的组工作流后,点击"Import Macros"/"Import Protocols" 按钮来查看与你有关的分发信息。

			A C U JOY	WEDLAD	¤ Help		
9	Service	Pre-defined Macros		с	reate Your Macros		
_	Program	MACRONANE		CRIPTION			
	Protocol	MACRONAME	Des	BCRIPTION			
	Macro	ANDJoinerTest (a demo workflow to test	this workflow is used to test the workflow which ca	this workflow is used to test the workflow which can have AND Joiner operator			
_	Utility	ANDJoiner)					
	User Space	demo (just a demo workflow)	this workflow is used to test the workflow which ca	an have more than one input			
_	My Data		This macro is focused on prediction of protein functions based on sequence similarity, where you have a gene sequence or several one in hand. You may begin with this protocol from nucleotide sequence(s), either cDNAs/ESTs or genomic DNA, as long as there will be protein coding region(s) existed. You will follow family identification, sensitive sites finding, and distant homologue search processes. Each step will be performed by well-known software or programs. The flow chart will draw a sketch for you to understand it. This workflow is designed to do some simple analyis for multiple sequences. At first, the input sequences will be aligned using emma. Then, weblogo, cons and ealistat will give you some statistical or intuitive information for the aligned sequences. Besides, ehmmbuild will build a HMM model and at last two incidental programs will run to generate sequences based on this model and calistates the model.				
_	My Literature	profunction					
_	My MetaPackage	(Protein function analysis based on sequence similarity)					
_	My Toolbox	based on bequence onniany)					
	Account My Account	MSAnalysis (Multiple sequences analysis workflow)					
_	My Group Logout	phylogenetic (Construct phylogenetic tree by Neighbor-Joining method)	This workflow is focused on constructing phyloge multiple sequence alignement, then use boostrap consensus tree. After bootstrap, distance of each alignment.Then, the phylogenetic tree is built usin tree is calculated.	ntic tree by Neighbor-Joining method. resampling for later evaluating the si sequence is calculated from result of 1g Neighbor-Joining method. Finally,	. First, we do ignificance of the multiple sequence the strict consensus		
		EmbedMacro (a demo workflow which is used to test embedded macro)	this workflow is used to test the workflow which has other macros as component activity				
		phylogenetic_max_parsimony (Construct phylogenetic tree by maximum parsimony method)	This workflow is focused on constructing phyloge multiple sequence alignement, then use bootstrag consensus tree. After boostrap, the phylogenetic the strict consensus tree is calculated.	ntic tree by maximum-parsimony meth p resampling for later evaluating the s tree is built using maximum parsimon	nod. First, we do iignificance of the y method. Finally,		
		User Customized Macros	Distribute Macros	Cancel Distribute Macros	Import Macros		
		MACRO NAME	DESCR		ACTION		
		RNA analysis (ma analysis)	s) ma fold		Romovo E di		

你可以查看与你有关的所有分发的详细信息,然后选择你感兴趣的工作流导入。

						CBI	your I	ebLa	web	¤ Feedback ¤ Contact ¤ Help
	Service		Account Based Import							
•	Program		AVAILABLE MAC	RO FROM ACCOUNT			ACTION			
	Protocol				0	One Brandlesset				
	Macro				Grou	p Based Imp	oort			
	Utility		AVAILABLE MACRO	AS MEME	BER OF GROUP	FROM AC	COUNT		ACTION	
	User Space	!_	RNA_analysis	web	lab_group	liu:	«q		<u>Import</u>	!
	My Data								>>	Macro Home
	My Literature									

一旦你导入了某个工作流,它就和你自己定义的工作流一样,你可以编辑,删除和分发。