Summary of Arabidopsis Bioinformatic Survey sent to Arabidopsis mailing list on 16th February 2010

Compiled by N. Provart, nicholas.provart@utoronto.ca, 18 March 2010

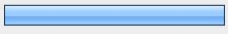
Question 1 – What is your geographic location?

1. What is your geographic location?	Response Percent	Response Count
North America	39.8%	117
South America	1.4%	4
Asia (incl. China, India, Japan, Australia)	8.2%	24
Europe, including Russia	**48.3%**	**142**
Africa / Middle East	2.4%	7
answered question		294
skipped question		1

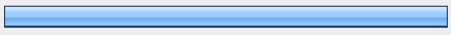
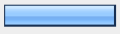
Question 2 – What is your position?

2. What is your position?	Response Percent	Response Count
graduate student	15.0%	44
principal investigator	**45.9%**	**135**
post-doctoral fellow	20.7%	61
research associate	10.5%	31
industry scientist	3.7%	11
government researcher	4.1%	12
answered question		294
skipped question		1

Question 3 – What's your bioinformatic skill level?

3. What's your bioinformatic skill level?			
		Response Percent	Response Count
excellent - I develop code and perform analyses on a regular basis		8.8%	26
competent - I am comfortable using most online sites and command line interfaces		**46.3%**	**136**
casual - I use online resources, occasionally with some frustration		44.9%	132
		answered question	**294**
		skipped question	**1**

Question 4 – Which of the following organisms do you work with on a regular basis?

4. Which of the following organisms do you work with on a regular basis?			
		Response Percent	Response Count
Arabidopsis thaliana		**92.6%**	**249**
close Arabidopsis relatives		12.3%	33
Oryza sativa / rice		12.6%	34
Zea mays / maize		8.2%	22
Populus trichocarpa / poplar		4.1%	11
Medicago truncatula or alfafa		5.2%	14
Hordeum vulgare / barley		4.5%	12
other biomass species		6.3%	17
other agronomically important species		22.7%	61
		answered question	**269**
		skipped question	**26**

Question 5 – What sort of sites do you use on a regular basis?

5. What sort of sites do you use on a regular basis?

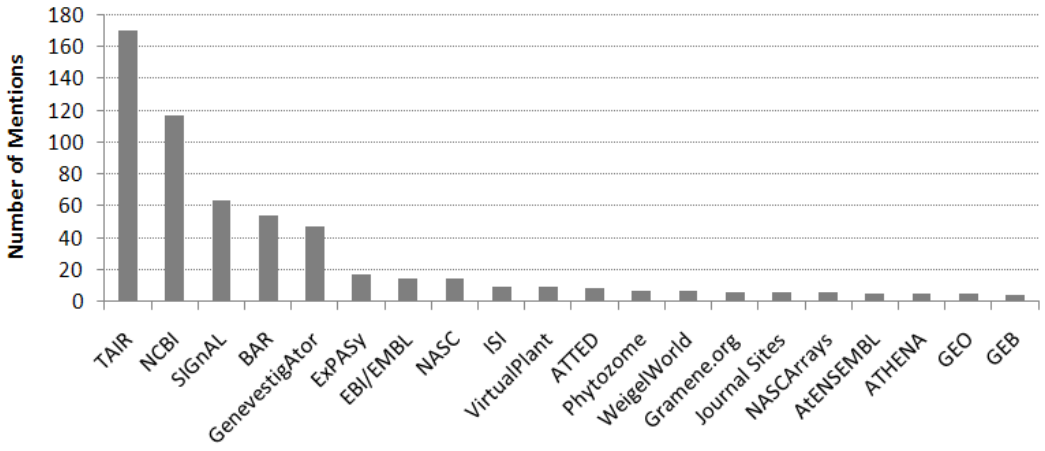
	Response Percent	Response Count
Literature and sequence databases (e.g. PubMed, GenBank, online journals)	**97.0%**	**260**
Gene models, annotation details (e.g. TAIR)	93.7%	251
Knockout collection databases (e.g. SIGnAL)	67.9%	182
Gene expression databases and analysis tools (Genevesigator, BAR, NASCArrays, WeigelWorld, PLEXdb etc.)	75.7%	203
Promoter and cis-element repositories (Athena, AGRIS etc.)	31.7%	85
Proteomic resources, including subcellular localization	23.5%	63
Metabolomic resources	10.4%	28
Protein Structure databases	18.3%	49
Other (please specify what you use or would like to see)	6.3%	17
	answered question	**268**
	skipped question	**27**

Other

ATTED, ACT, Genemania, expression angler; BioMart/ GrameneMart / Cis-element identification/; Inparanoid (orthology finding); epigenomic and small RNAs databases; expasy; gene prediction and cis-element analysis; genevestigator; Germplasm database – NASC; MAtDB, TransFac, SimpleSearch, NASC; more phylogenetic analysis sites e. g. super Phytozome; NASC Ensembl, underlying Ensembl db; SALK; epigenetics db – AnnoJ; NCBI; online phylogeny; patent search databases; sequence analysis; Small RNA databases e.g. mirBase; Systems biology sites - Biomodels database, VirtualCell, etc; VirtualPlant

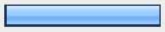
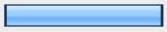
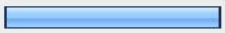
Question 6 – What are your current favourite/most useful sites (please provide name and/or URL, and comments)?

6. What are your current favourite/most useful sites (please provide name and/or URL, and comments)?	Response Percent	Response Count
1.	100.0%	217
2.	86.6%	188
3.	64.1%	139
4.	44.7%	97
5.	26.3%	57
answered question		217
skipped question		78



Other tools mentioned were with 3 instances: Diurnal at OSU, Google Scholar, PLACE, PlantCARE, PlantGDB, Sirocco, TIGR; with 2 instances: ACT, AGRIS, Aramemnon, Brassica.org, iHop, MaizeGDB, Medicago.org, MetaCyc, Phyre, Plantbiology at MSU, PLEXDB, PredictProtein, PRIMe, Primer3, rcsb.org, rsat.ulb.ac.be, SMS, Transfac, UCSC Genome Browser; and with 1 instance: MetGenMAP, AGFP, AnnoJ, AthaMap, BarleyGenomics at WSU, BioConductor, BioGRID, Bioinformatix, Biology Workbench, BioMart, Biosynlab.com, Blast2GO, CBS in Denmark, Chlamydomonas DB in Golm, Clustal, CressExpress, Cytoscape, Elegans at U. Kentucky, Epigenomics site at UCLA, Faculty of 1000, GALAXY, Gatsby, Genscan, girinst.org, GrainGenes, IDT, IVT, JGI website, KEGG, maizesequence.org, MapMan, MASCOT, MatDB, MEME, MIPS, miRBase, MPSS, Noble Foundation site, PDB, PFAM, PhosphAt, PlantP, PlantsT, PlantTA, PlantFDB, PLAZA, PopGenIE, PTFDB, RNA in Sweden, SGN, SMD, SolGen, SolGenomics, sRNA at UEA, STAMP, STRING, SWAMI, TAIL, TargetP, Thomas Girke's R website, TMHMM, TopCons, TTFD, VISTA, WebMap, Weeder, Wikipathway.

Question 7 – Ongoing funding is an issue for many bioinformatics resources. Would you be willing to (choose one or more of the following options)

7. Ongoing funding is an issue for many bioinformatics resources. Would you be willing to (choose one or more options)		Response Percent	Response Count
donate funds occassionally to keep the a given resource functioning? *Wikipedia model.*		17.7%	44
have access to a limited subset of information for free and then full access if you had a subscription? *Freemium model used for many online services such as Doodle.com etc.*		31.5%	78
be willing to pay a surcharge on materials ordered from stock centres? The surcharge would go towards funding online resources for the plant community via some mechanism. *This is a funding model used to finance e.g. emergency service for telephones (911 surcharge model).*		**52.8%**	**131**
have big plant research centres pay into a pool but smaller centres would not have to pay for use. *Sugar daddy model.*		31.9%	79
help maintain/code/annotate for free? *2nd Wikipedia model.*		20.2%	50
none of the above? Granting agencies, private benefactors or corporate sponsors should fund these kind of resources as they enable science. *This is the greater good model but how to deal with the fact that national governments are funding the world's use of many online resources?*		44.0%	109
	Comments		33
	answered question		**248**
	skipped question		**47**

Comments (33 responses)

Government grant bodies require the deposition of marterial into databases as a requirement for funding. If grants would allow costs to be figured in then a fee for use could be adopted. If it is not possible, then the government granting agencies have to provide a means of making data available. However, much research where web resources are used are not grant funded so a lot of exploratory data mining would not be possible if fees were restrictive.

Have federal agency to pay for the maintenance of the service.

Needs to be a model that allows grant funds to be used. Eg donations would not be allowed by finance departments, but fees are fine. I think fees for seeds etc could be much higher without affecting ability to access.

Open Access databasesa and tools have been incredibly important in stimulating much of the very exciting biology of recent years. Movement away from this would be a seriously retrograde step.

Use model, you may have IPs of hits/use of site. Get agreement for national funding agencies to top slice funding according to useage.

If I have to pay, then the money has to come from grants. Why not have the granting agency pay directly for the resource?

I strongly feel that granting agencies need to prioritize maintenance of bioinformatics reseources.

Charge for-profit organizations and large centres more, or ask for donations.

As a graduate student in a small lab, I'm not in a position to donate very much personally, and don't control any aspect of the lab's expenditures.

Who actually donates to Wikipedia?

Not a wealthy lab, like many, so feel fees should be kept reasonable.

It pains me to think that bioinformatics resources could devolve to a state in which there are 'haves' (labs with funding) and 'have nots' (labs with funding lapses) that have differential access to information. This is (should be!) anathama in the scientific community.

It can be sponsored by consortium of countries.

Minimum core service government, 2nd tier by a pol of money raised from foundations and companies etc, super apps by individual foundations/companies ...with clear image benefits to them.

The option must be more fair pointing to pay in basis of research centres size making that small centres pay a small fee. In that way all make a contribution!

We could add usage fees to our grant budgets.

I am at a PUI (public) and use the resources to teach a bioinformatics class. It is vital that the resources remain free to train future researchers in bioinformatics both in the classroom and in my laboratory. I cannot afford to contribute.

Stock centers are already in trouble, adding costs to stocks will make it worse.

If contributing to these were more accepted (as publishing) the willingness to spend time to create code would be easier to justify. Could also allow advertising (the Google model) Also, charging for publication could support some products. If OpenAccess is so important, these tools should be as available to the general public. Therefore, encouraging granting agencies to support such endeavors, especially as a small part of a larger project may encourage the development of these items. That is, instead of having one major project for developing a useful tool, support (or require) it's incorporation as part of a project. Of course, the critical thing will be a repository to organize these things.

Would pay for services that were really useful to me.

Most of the data sets in sites I use were generated with public funds, and should continue to be made accessible. The anticipated decline and termination of TAIR funding, for instance, is a travesty.

How would you pay for it? could you get a site or lab license?

BBSRC and others should top slice into key resources.

National governments should as a matter of extreme URGENCY fully fund these resources. Not to do so is to not understand the vital nature of them to the modern researcher. These nations will benefit from researchers work as science and technological advances have been acknowledged by all these governments as the only way to sustain their economies post globalisation. You fund it or you wither and die. It's a straight-forward choice to the current "rapidly de-industrialising" nations' governments.

There should be a international funding of this DBs by a group of funding agencies.

E.g. TAIR funding has to be put on an international basis.

There must be a transnational solution. This works for EMBL/GrenBank/DDBJ, so zhere should be a chance for plant gemonics as well.

I would include fees for subscriptions in grant aplications.

I would NOT agree to any of the other models above.

Science is not national...

Combining TAIR funding with the stock centers is the best model and likely the one that is most sustainable

I think organizations should pay a subscription fee based on size (journal subscription model)

The funds I use to support would come from NSF anyway!

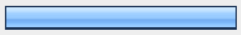
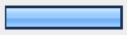
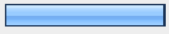
Question 8 – If a fee-based model were in place for a given site, clearly the fee would depend on the utility of the site. If the site were *really useful* (you use the site at least once per week), how much would you be willing to pay at most for that site?

8. If a fee-based model were in place for a given site, clearly the fee would depend on the utility of the site. If the site were *really useful* (you use the site at least once per week), how much would you be be willing to to pay at most for that site?			
		Response Percent	Response Count
$5 per year		8.4%	20
$10 per year		17.2%	41
$50 per year		**47.5%**	**113**
$200 per year		19.7%	47
more per year (please specify)		7.1%	17
	answered question		**238**
	skipped question		**57**

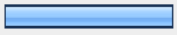
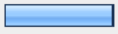
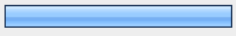
Question 9 – How likely would you be to use a site that requires some sort of login…

9. How likely would you be to use a site that requires some sort of login...						
	I'd avoid it	I'd use it occasionally	I'd use it if necessary	I'd favour another site with similar info but no login requirement	Rating Average	Response Count
if login were required every time?	9.4% (23)	11.1% (27)	**55.3% (135)**	24.2% (59)	2.94	244
if login were required once, but you'd be remembered next visit and wouldn't need to login again	3.5% (8)	18.3% (42)	**62.6% (144)**	15.7% (36)	2.90	230
					Comments	38
				answered question		**248**
				skipped question		**47**

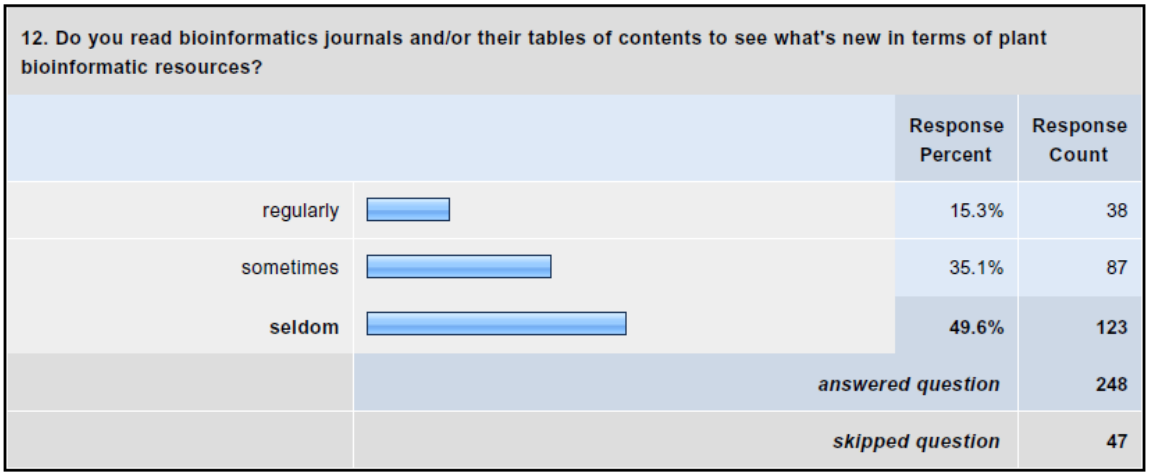
Question 10 – Sometimes a given resource is no longer funded, but the underlying data are still useful (e.g. PLACE). What should happen with such data?

10. Sometimes a given resource is no longer funded, but the underlying data are still useful (e.g. PLACE). What should happen with such data?		Response Percent	Response Count
I'd support the creation of an Open Access repository of biological databases		**45.7%**	**113**
There's probably a newer initiative out there somewhere - it should incorporate older data		22.7%	56
A larger repository should take over the database		31.6%	78
	answered question		**247**
	skipped question		**48**

Question 11 – Biological data are often stored on many different sites. How would you prefer to access data?

11. Biological data are often stored on many different sites. How would you prefer to access data?		Response Percent	Response Count
I'd prefer a central spot		32.9%	82
As long as each separate resource is useful and well designed, I don't mind using many sites		20.9%	52
Info should be shared between resources if possible, such as TAIR / BAR / Genevestigator / NASCArrays / GABI PD / SIGnAL		**45.0%**	**112**
I like the challenge of the hunt, and don't care if I have to peruse many sites		0.0%	0
As long as the sites provide webservices, I can create my own mashup		1.2%	3
		Comment	18
	answered question		**249**
	skipped question		**46**

Question 12 – Do you read bioinformatics journals and/or their tables of contents to see what's new in terms of plant bioinformatic resources?



12. Do you read bioinformatics journals and/or their tables of contents to see what's new in terms of plant bioinformatic resources?

	Response Percent	Response Count
regularly	15.3%	38
sometimes	35.1%	87
seldom	49.6%	123
answered question		248
skipped question		47

Question 13 - Please enter any general comments you have on where you think plant bioinformatics should be heading in the next couple of years, pet peeves, ideas for creative funding etc. Thanks! *(58 respondees)*

A central place such as TAIR for access to bioinformatic resources centered on a theme is great. It is also critical to have a central repository for the primary data (e.g. microarrays, metabolites, etc.) that all resources can share. I find the cis-acting regulatory element analyses programs are not as easily accessed and the TAIR site is not keeping up with new bioinformatic advances in these analyses. I think it is important to put WATCH OUT FOR messages with some of the analysis output. With the easy access to these programs some people use them without understanding the underlying data or applied algorithm and thus can misinterpret the data. For example, just recently I was using eFP browser looking at root expression data and I saw a nice increase in the expression of my gene of interest in response to a particular treatment. However, because I had read related papers and went to the original supplemental data file, I knew that protoplasting itself induces this gene and so used extreme caution in any interpretation.

A central repository is a great idea, but how do you fund / manage / maintain that, I believe the speed of change makes this a poor use of limited funding in the plant community. Another problem with making a single database of tools for the plant community is that some of the most useful tools are not plant-specific. So constraining to one site might lead some plant biologists to miss many wonderful tools that are useful in plants, but developed for other organisms. One option is a publication-monitored model. It would be great if a journal could be developed (not necessarily plant specific) that would provide space for all tools published in that journal in a central location. Then creation of a tool could go through peer-review and have a common space, easily linked to the original paper.

Aiming to be usable to the non-expert. I find many of the available resources unfathomable and very poorly explaine, help files are often useless. Perhaps more communication and standardisation between the creators of resources would help in that serch methods woud becoem more standardised and uniform and easier to grasp.

All the tools out there are of enormous importance for our daily scientific life, but no always appreciated well (e.g. when it comes to support them financially). One difficulty is the duplication of similar data and approaches with somehow different focus, thus it is difficult for the user to get the feeling where you can get the best analyses or information for a particular problem.

As a researcher at a small college, I don't have much funding to pay for access to sites. An institutional site license model might be work considering -- it's a hassle for each of the individual labs to process payment. Also, how would you handle educational use (e.g. course assignments)?

As a wet biologist I like bioinformatics when it can be used by me to enhance my wet work. For this to happen the data needs to be simply presented and web-browsable, but with the underlying data available to be able to confirm its accuracy. I consider myself computer-savvy, but anything that involves writing/changing code or running things on Linux machines or shells is useless to me.

As is I think the system rewards individual creativity. I would hate to see that diminished with more centralization of data and effort. Good luck!

Bioinformatics is becoming essential to every biologist and its use is becoming ever more prevalent. For something so essential we should all have to pay a fee to access/use such data so that grant funds can be shuttled to funding actual research.

Bioinformatics is very important, since in plant sciences funding is less in total except for some crops. Developing bioinformatics tools help us to understand different phenomena and the usage of the sequence information...

Centralized resources of info would be best, I hate having to visit 5 sites to compile info on a gene/protein

Easy comparison of homologues between species for expression analysis etc. conservation. Better more comphrehensive annotation of gene famalies in Arabidopsis

Finding the most current bioinformatic resources can be daunting for people who don't specialize in bioinformatics but use it only as a tool to gain information about their favorite gene (family). A central repository that contains basic information and links to more specialized databases seems to be the most useful strategy for "the rest of us". Up to now, TAIR fulfills this role. To pull the rug out from underneath TAIR is a terrible idea and will leave many "casual bioinfomaticists" out in the cold.

Freemium isn't great, but it could tide us over until Public Good prevails. NB Treaty obligations on Access and Benefit Sharing under the Convention on Biological Diversity (CBD) could force open access to

information such as Arabidopsis data for signatory developed countries, as part of the technology-sharing obligation. This could work for us, as we stand ready to help the gov'ts fulfill their obligations for small funding.

gene annotations need to be improved and updated regularly. Make it easier for researchers to improve the data (Wiki style- but would need moderation)

Gotta keep TAIR running and open to all. It is essential for all plant researchers and genomics researchers in other kingdoms as by far the best sequence and most complete annotation of a plant genome. We need to keep adding to the data. It must be accessible to all (high school etc.) like GenBank/EMBL/DDBJ is.

I beg that we do not forget the critical role of these resources in good undergraduate education. Undergraduates can and should be aware of, and able to use these resources. Restrictions of the types described in this survey WILL prevent this. I also urge strongly against a culture in which some investigators have more access to resources than others. As a community, we should continue to strive for open access to bioinformatics data for ALL.

I don't know if my perspective is of any sort of value as I am a post doc and do not have any sort of spending power. However, I would PERSONALLY be willing to pay up to $50 a year to fund websites such as TAIR to keep it open.

I don't mind using different web sites but it would be useful if there was an up-to-date catalogue of such resources.

I really only use SigNal, BAR and Genevestigator because they are easy (intuitive) to navigate or have decent instructions. I think TAIR is awful because you have to know exactly what you are looking for.

I strongly support the keeping of something like TAIR that gives you a central place to go where you can access data from and/or link to other key sites.

I support the establishment of a government funded permanent plant bioinformatics institute to serve the community needs.

I think asking people for an annual fee is a fair way to go. Even if the government isn't going to fund a particular resource directly, having people pay the fee out of their grant is just indirectly charging the government. It also distributes the funding source so no one person is responsible for renewing a grant. As long as plant biology grant are being awarded there will be a need for bioinformatics resources and the people with these grants would be the ones coughing up the money. But of course, offer a waiver for people who don't have the money, such as grad students without a grant or fellowship. On a more technical note, I would like to see the bioinformatics resources incorporate more web APIs so programmers can easily access data from those sites. And even better, if all the major sites (tair, maizeGDB, etc) used the same API. That way my code that, for example, retrieves information about particular genes, works for arabidopsis the same way it works for maize. Even if the sites never merge, if

they could all use some sort of common programming interface it would make the lives of programmers much easier.

I think it is all too divisive and as long as folk keep pursuing new, shiny, better at the expense of validated, solid, secure then we are all screwed.

I think plant bioinformatics must introduce their work to the PI in an "friendly" manner.

I think Plant communities will need to come together to think about how to organise data at an international level and this is more likely to be funded ie not an Arabidopsis database but perhaps plant clades or comparative sites. On possible useful model might be that of ELIXIR at the EU level.

I use my list of favourite sites frequently. The best ones are where the data has been properly checked eg UniProt. I find NCBI sequence data sometimes mislabelled. Quality of data is very important. Also, ease of going from one dataset on one website to another dataset on another website via links within the webpage, Again Uniprot and NCBI are good for this. As for funding, I think strenuous attempts should be made to obtain it from governments and sponsoring bodies. If that is not enough, subscription by users looks inevitable. But it should be as cheap as possible. Ideally it should all be free and open access but data needs constant updating and management and that is best achieved by paying someone to do it well. Thanks.

I would be willing to pay for one site with most essential information, e.g. TAIR, but not lots of different sites with bits and pieces of information.

I would like to see all plant genomes in a single database, based on TAIR. I think that way there can be a clear argument for funding as it would be relevant to food security & biomass etc. Sequence viewer is my favorite tool, and I find that I just don't have the same access to other plant genomes (such as poplar) as they lack such a high quality sequence browser. I do not favor services that are not free to access because such important tools should not just be availible to those who can pay.

If one would have to pay in one way or the other for "central infrastructure" it must be ensured that the money is spent for the ressource and the ressource only which -if we are talking big money- would need to be audited. Definitely there should be no competition with innovative services provided by the community with a mediocre solution by the core infrastructures. (Think about what would have happened if TAIR would have continued with Microarrays, we would likely have never had a big market for Genestigator, BAR, and others) Also if I paid I would like to get some bang for the buck. We are happily paying for Genevestigator, as this is useful for some people and I think it is fast (I don't need it myself), but paying for some slow services I wouldn't want. Thinking of this: maybe I would even welcome paying a couple 1000 $ for some services, because cancelling my subscription would make an impact and I would have a say what is being done.

Information on plant genetics has grown enormously the past decade. As a result many information are there to provide clues to biological questions. The question is how fisible it is to combine all this

information through bioinformatics. Current tools have done a superb job in the compilation of many of the data (Genevestigator, TAIR), but still the information lies within. I believe what we should expect in the near future is intelligent software that will be able to combine information from many data sources and answer to questions posed by the researchers. An example would be to see the effect of a chemical on Arabidopsis, by compiling genomic, proteomic, metabolomic, anatomic and other available data to give us an idea of plant responce. I am not talking just about systems biology exercised by the average to expert bioinformaticians, but also for the general plant scientist. Thank you for performing this survey. It comes at the right time where we should sit back and think creatively on how we can make the enormous data available more useful.

It is an emerging field and a basics for understanding biological research and therefore an important tool to studentes, researchers and professors. The funding should not be reduced as may laboratories rely on it.

its merely frustrating that most published bioinformatics tools simply do not work. therefore 1) part of the review process of publications including software tools (and even if they are only mentioned in the text) must be to check whether the tool actually works (online). 2) if for download and install it must run 3) no proprietary tools should be allowed, all open source.

Keep TAIR funded!! More trivial-to-use web services, e.g., cressexpress More data available in XML, e.g., NASCArrays

Keep TAIR well funded !!!!

Many of us are acting as reviewers. We need to use this power to support integrated bioinformatics in almost each project. And we need to tell our granting agencies that structured access to data collections is a MUST in functional genomics, not only for the Monsantos but als for academia. It is a waste of money to produce data that can not be used after the end of the project!

More focus on comprehensive data access (eg. GEO) and less on one off tools for looking at a single gene.

My students are really the ones who should be answering this questionnaire. I will forward it to them.

One neccesary think is to put all protein entries with the same code (a new one) instead of the 3-4 different codes we have now. Thanks

Open-Ended Response

plant bioinformatics research should be funded sustainably

Plant bioinformatics is more important now than ever before, and the current high quality and improving resources is playing a really major role in driving the subject forward. For future research underpinning food security is vitally important. Central agencies and/or charities (Rockefeller, Wellcome) must provide the underpinning funding, but user fees for seeds etc could increase (I think

$50-$100 for a seed stock is reasonable). This will work better than charging for access to the databases (and is easier to justify on grants). This could be in addition to a subscription fee if essential.

Produce pipelines for analyzing next gneration sequencing data, databases for storing this data, and visualization tools for making it digestable

Resources for tobacco are important to me. Centalised tools for Q-PCR analysis would be useful, to create some uniformity and community standards in the way data are treated.

Surely necessary, should be taught to students

TAIR is a fantastic model. As I move into other species, I am disappointed that similar resources aren't available. I hope we can eventually move to a system (Ensemble-like?) where the same resources can be found in a similar format for every organism.

TAIR is an essential resource. If it does not have adequate funding, plant biology will be severely affected in a negative way.

TAIR mainenance, not expansion of roles

Text mining. Keeping up on primary research is a serious commitment given the huge amount of research published weekly. Making these search systems 'smarter' could have significant effects on the efficiency of individual research.

Thanks for any initiative to maintain/centralize/optimize/update the data universe!

The closing of TAIR would severely limit my research capacity. I hope the site and data can be continued.

The funding available for bioinformaticians is much smaller than the demand. The most frequent complaint I hear from biologists is that they are waiting for their data to be analysed by bioinformaticians (usually they are understanding, realising that there is not enough resource availale). There is a need not just for algorithm/tool development but also for bioinformaticians to analyse the data being generated by biologists. Although it is not easy, it is possible to get funding for algorithm/tool development. This (along with the need for bioinformaticians to publish in their own right) has led to the proliferation of multiple algorithms/tools each claiming to be better than previous tools, often without adequate evidence. Sometimes the amount of near duplication is ridiculous. But how do you get funding for bioinformaticians to 'just' analyse the data.

The idea of letting the stock centres take a small surcharge on orders is great. The lines are quite cheap as it is, even when you order collections. Also, this way there wouldn't be a need to change funding structures, which is probably very difficult. At the same time, we need stock centres and bioinformatic resources that are going to stay in business for long periods of time to allow the best possible use of data and dissimination of knowledge. This is absolutely paramount.

The plantbio community should replicate the UCSC system. BioMart is terrible! Why doesn't someone import plant genome data into a UCSC style system? It ought to be easy and cheap -- the software is already written.

The reality is that the funding is less than it used to be, so core resources must be prioritised and the 'it would be nice' category of toys needs to be mothballed. There is only so much money. I think our biggest problem is we lack an obvious product for the majority of the work that we do. Why fund us when you can fund work which may result in a product/data that benefits people more directly?

The solution is probably to share costs between users (a slight fee on orders from stock centers) and funding sources for research.

There should be a world wide effort to amalgamate the information and facilitate the integration of individual databases and tools. Anyone funded to produce new tools or data or who publishes them should be obliged to make them easily accessible.

United Nations funding and access for all

We all want something for nothing. But this is no longer possible All the worldwide funding agencies should provide a single central database in perpetuity. These should be funded according to proportion of usage directly from national agencies. But sites should not survive if they don't evolve, or use is geared to the few. There are too many species specific sites. Need to have global ones for all species with common resources, where onotologies, databases are curated to ensure consistency. One database can be curated by funding agencies with bioinformaticians in individual countries. i.e. if say they need 20 people, 35% may be in USA 35% in EU 30% in other countries China/Japan/India S. America Australia. (or proportioned according to usage). The site should be mirrored in all countries participating to ensure speed of access, this is where national funding can come in. But all those working on the project should be collegiate and have regular meetings (Skype etc…) Last comment if I have a class of students that I need to show them how to do something I am not going to pay $$$ for many logins etc….. this will reduce the use of the database for future generations etc… etc…. Hope this all makes sense. Bests GB

We really still need TAIR foremost. I think better GO term annotations would help many, many studies. We need a genome browser like the UCSC site. A webpage listing all of the bioinformatics websites out there and what they are used for would be very helpful.