

Minutes from Discussion XSPAN Workshop 11-09-02

User Feedback after Demo:

A lot of data on existing databases is only accessible by accession numbers
Only these terms are warehoused - but must beware as these change occasionally
Makes sense to include accession numbers with terms in warehouse

- U3: Need these facilities within 1-2 years:
chick developmental biology
own chicken community
development of chick resources (all)
sequence
micro-arrays
in-situ hybridisations
high throughput gene expression data - 1/2 million clones
no anatomy DB
ideally adopt mouse & drosophila
need nomenclature
- JB: To get something up and running not too difficult. Depends on required granularity - coarse easy - fine - very difficult.
- U4: Can XSPAN not help by providing core?
- U3: How can it be progressed?
- U4: What for - adult or developmental?
- R: In long run - will become major model organism.
- JB: Birds most similar/homogenous as an Order.
- U3: Want to be able to compare chicken with mouse and human. e.g. have developmental mutant with defect in limb development (signalling). 16 genes - what next - look at other species. No timing at this stage. No information about genes really i.e. what can be got from other species.
- JB: XSPAN can help to get you to other organisms.
- U3: Looking at patterns of expression and location of expression compared with anatomical site and path.
- U4: GIESHA Arizona) = archive of patterns of gene expression in chicken.
No anatomy at all and not annotated.
- U3: Very detailed descriptions& staging of chick embryos but not in useful electronic form.
- JB: No controlled vocabulary to organise named tissues. Would not be difficult to put.
- U3: Willing to get funding to get chicken community on line to plug into XSPAN.
- U4: XSPAN must respond to all species communities - as communities. They will want to work these things out for themselves as a community.
- JB: Natural way to do it is through DB curators.

- BW: Work being done to put synonyms into MADB. No procedures/principles for creating new ones - can do this? (XSPAN facilitating)
- JB: MADB nomenclature at mature stage.
- U4: XSPAN will have to cope with differences in nomenclature that are not yet developed e.g. chick - why not use XSPAN to help it be done i.e. interfaces allow easy development of de-nova nomenclatures.
(GF note: i.e. becomes a standardisation facilitator)
- BW: Meta-thesaurus in UMLS links nomenclatures within systems e.g. MeSH & ICD9. Mouse nomenclature should go into UMLS.
- U4: UMLS not used in the same way as OMIM therefore payoff less than OMIM.
- BW: Very small part of OMIM terminology in UMLS.
- U5: Drosophila (IMAGO) has some anatomy
- U4: Gene expression data will become a molecular anatomy if comparisons are between gene expression areas - not anatomy - will XSPAN handle this?
- JB: i.e. not looking at tissue homologies but rather protein expression patterns - no reason why we can't incorporate this i.e. GXD - all tissues that express a gene.
- U4: May want to ask - show me the genes expressed in this pattern in another species
- U3: e.g. area X gene expression breaks down to 2 areas A & B - name after gene expression
e.g. HOT37 gene expression domain
 |
 tissue called
Problem - can't see structure macroscopically only access to gene expression
- U4: This works well as relates between species
- JB: Can name geometry crudely, very precisely (e.g. GXD) or cop out completely (e.g. MGEDB). GXD approach would be as much as you can expect.
- U4: This doesn't address U3's problem - as people learn more about molecular anatomy they will want to use it.
- AB: i.e. developing an alternative anatomy
- BW: What will the DBs look like - current ones are spatio-temporal?
- U4: Don't need spatio-temporal - just refer to gene expression domain. May need to use standard anatomical term to refer to wider area & can just refer to GED. This will happen with MAGD. Domains will become part of the framework like anatomical terms.
- JB: How will you distinguish between messenger & protein domains?
- U4: May not need to - some one - some other.
- WN -> U3: What kind of service would you like from XSPAN?

U3: e.g. problem - start off with 10 genes in chicken - unknown - want to take one property - which one should you look at first? Look at other species to see if any other organism has expression of these genes.

JB: 1. What is a homologue
2. Where is it expressed and when

U4: Would you prefer to use existing DB of homologues or would you like to do search terms & criteria yourself?

U3: Would like to be able to establish accepted links but ...

U5: Would you like to match by expression pattern or sequence?

U4: Sequence may not give homologues & gene expression patterns - may be more useful.

JB: Ultimately user will have to make judgement using pointers with not too many false positives

U3: e.g. 3 genes are part of a family - very interesting to look at then during development. Absolutely fundamental - must have tools that allow users to draw homologies between genes. Can't disentangle gene homology & anatomical expression / similarity).

JB: Accept that there are algorithms that will determine homologies.

U4 -> U3: e.g. has mutant phenotype & may be interested in similar mouse mutant. Ask - are the same structures affected & in the same way. Will XSPAN extend to address this phenotype matching?

JB: Not yet - but open to suggestion.

U4: XSPAN may be able to get in at the beginning. There are competitors - know of grant application in the States - turned down. (BW also knows of one) Will XSPAN look outwards & make effort to find out about them? A lot of people have concerns in this area, so should look for people doing the same.

AB: We will collaborate if we find them.

U4: How do you plan to integrate with Go?

JB: Some anatomists sit on Go. Can submit own if good. If better one comes along - should be standard & should be used.

AB: Go does not have anatomy.

JB: Refers to bits of anatomy. I am in touch with Go.

AB: Every intention of communicating with them.

U3: Make sure not wasted effort - which will happen if you don't work with communities. Lots of other places trying to provide solutions. Go is the standard.

AB: There is space for anatomies in Go.

U4: Please send out written feedback to participants.

AB: Will do when we have enough data.