Review of available software tools that can be used to support selective breeding programs in the Seafood CRC

AUSTRALIAN SEAFOOD COOPERATIVE RESEARCH CENTRE

CRC AUSTRALIA

Australian Government
Fisheries Research and Development Corporation

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Background

The Australian Seafood Cooperative Research Center is developing a Theme Business Plan to support and coordinate a cooperative approach to aquaculture genetics research in the CRC. One of the needs identified in the development of this plan is the provision of tools and technologies to facilitate the planning and implementation of selective breeding programs. This is already a target for the oyster industry and will develop as an important need for a range of other aquaculture production sectors. Such tools will be important in order to "respond to, take advantage and meet the increased demand for seafood". A common requirement for selective breeding programs is good software management tools. These tools are essential in order to keep track of individuals and important information relating to them (pedigree, treatment, trait data, marker information, estimated breeding values etc) and to streamline genetic analysis and decision making.

Need

Some examples of useful software tools needed to support breeding programs in the CRC would be:

- Models to simulate selective breeding programs and to determine economic weights of key traits and optimise the breeding program design accordingly.
- Relational database systems for effective, reliable recording, storage and output of relational data (pedigree, phenotypes, genotypes etc.)
- Pedigree analysis software or procedures
- Genetic analysis software or procedures
- Software that assists development of multiple trait selection indices incorporating economic weights for key target traits
- Software that helps guide mate selection (including optimum contribution selection tools)

Each breeding program in the Seafood CRC will ultimately need to know:

- What type of software do other established breeding programs (in aquaculture and other primary production) require and use?
- What software is already available, from where and from who? What problems do the
- tools address and what do they enable?
- Which software tools are applicable or easily adapted to aquaculture?
- What level of adaptation would be required for the adoption of existing tools into aquaculture and what resources (skills) would this need?
- Which tools could address common problems across different aquaculture sectors?
- What level of skill is needed to operate the software?
- Does the software have good documentation and do the developers offer support
- services?
- Is the software freely available, available at a price, available to partners or maintained as a trade secret?
- Might it be useful to link to other breeding companies or organizations (aquatic, livestock or forestry) to access existing tools or expertise for developing such tools?

- Are there initiatives underway or being planned that aim to develop useful new software for aquaculture and might the CRC be able to link to such initiatives?

Objective

To assist the Seafood CRC in the development of the genetics theme business plan by reviewing available software tools that can be used to support selective breeding programs in the Seafood CRC.

Methods and results

1. The following key contacts (quantitative geneticists and animal breeders) have been identified. Most of these contacts have been surveyed or interviewed for the review others were identified as sources of more detailed information by the review. Interviews and surveys have been used to collect information regarding the availability and utility of existing software and the existence of initiatives to develop such software:

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6	Peer Berg	Dainish Institute for Agricultural Science		
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27	Per Madison	Dainish Institute for Agricultural Science, Aarhus University		
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Enter contact details				
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34	Mike Coffey	SAC Edinburgh Genetic Evaluation Services	Mike.Coffey@sac.ac.uk	0131 535 3241
35	Pedigree Systems Ltd	Pedigree Systems Ltd	requestinfo @ pedsys.com	+44 (0)1422 843975
36	PIC	Pig Improvement Company		
37	CCSI	Canadian Centre for Swine Improvement	info@ccsi.ca	(613) 233-8872
38	Darrell Anderson	Department of Animal Sciences, Purdue University	darrell@nationalswine.com	765-463-3594
39	Peter Brand	Canadian Dairy Network	brand@cdn.ca	(519) 767-9660
40	Paul L. Charteris	Institute of Veterinary, Animal and Biomedical Sciences, Massey University		
41	James Morgan	National Sheep Improvement Program	lmm@earthlink.net	(479) 444-6075
42	Freddy Fikse	Interbull	Freddy.Fikse@hgen.slu.se	+46-18-671994
43	MLC's Signet Breeding Services	MLC's Signet Breeding Services	signet@mlc.org.uk	01908 844195
44	Bruce Greaves	Strategic Forestry Research Pty Ltd & School of Plant Science, University of Tasmania		
45	Peter Kube	CSIRO Marine and Atmospheric Research Tasmania	Peter.Kube@csiro.au	0362325241
46	National Instruments	National Instruments		(800) 531-5066
47	Oracle	Oracle		+1.650.506.7000
48	Kevin Beard	Australian Dairy Herd Improvement Scheme (ADHIS)	kevin.beard@dpi.vic.gov.au	92174200
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58	Statistics Community			
59	Stephen D. Kachman	University of Nebraska, Lincoln		
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63	Harry Johansen	Akvaforsk Genetics Centre (AFGC)	harry.johansen@afgc.no	
64	Tony Reverter	University of New England, Armidale		
65	H. Palmer	Scottish Agricultural College		
66	Thomas Gitterle	CENIAQUA & Akvaforsk Genetics Centre (AFGC)	thomas.gitterle@afgc.no	

2. One other software review was found (Ignacy Misztal, Software packages in animal breeding). This was found on the internet and most likely published during or after 1994 as a proceedings for a conference (eg,. World Congress on Genetics Applied to Livestock Production).
3. A MS-Access database has been created to collate, store and report on the information that is being collected (database attached).
4. Details from the interviews and survey responses have been entered into the database
5. Almost 70 software programs have been identified. The database contains information on the type of software, source, contacts, users, status, support, cost, ease of use, species applied to, IP status, applicability, usefulness, web address, flexibility etc.
6. A number of queries have been created to allow for easy interrogation of the database.

NB 1: The author has populated the database to the best of his ability with the time budgeted for this review. There may be some software that the author has not documented and there may be some factual errors in the information contained here (ie. some information was derived direct from the author of the software, some from web sites and papers, some from users of the software). However, the database will be a useful starting point for the Seafood CRC and can be populated with more information and corrected as new information comes to hand. Clearly more detailed information will need to be collected for "short-listed" software before the Seafood CRC decides on which software should be used.

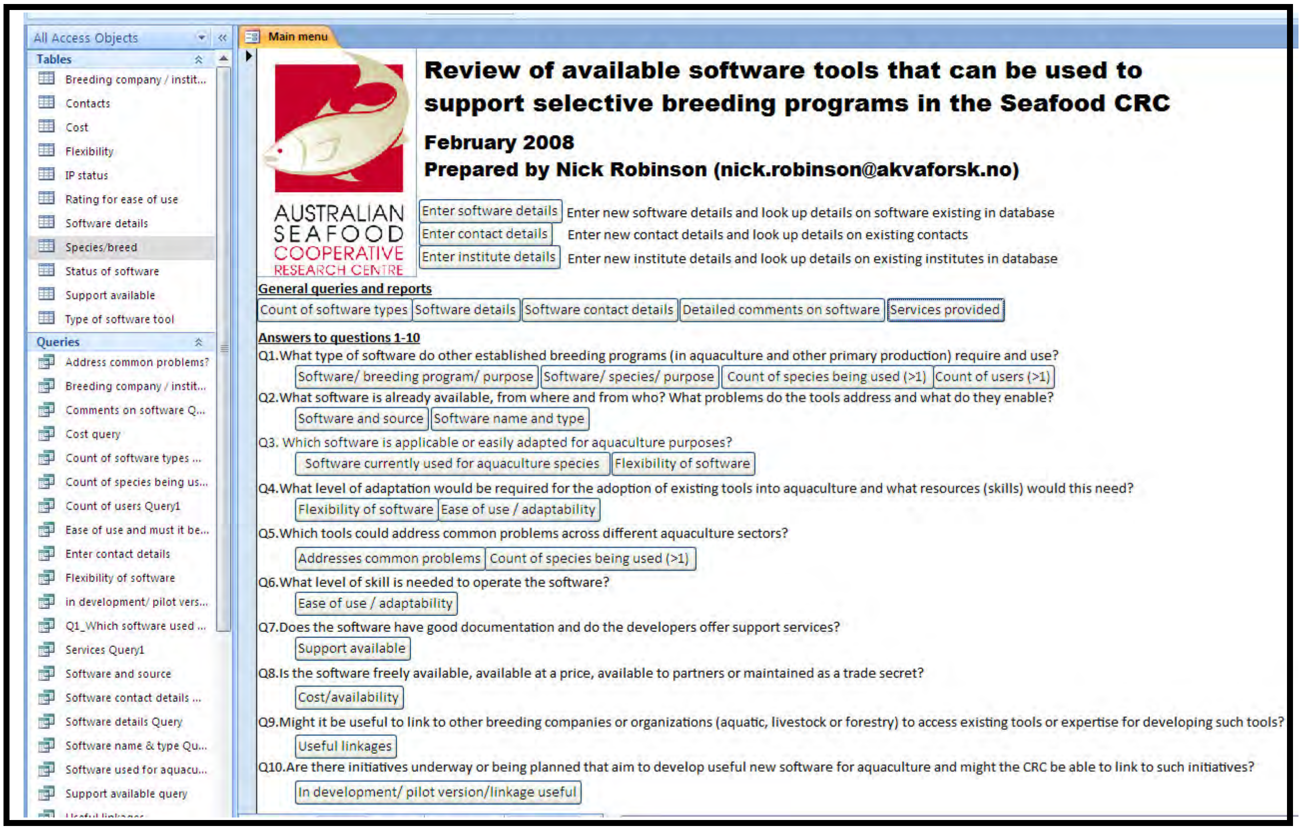
NB 2: There will be some in-house software that is maintained as a trade secret by some of these organizations, and so it might not be possible to obtain complete details on all software.

NB 3: Many of those interviewed have asked if they can obtain access to the report or parts of the report. Some interviewed have asked that we do not pass on to others knowledge about the tools that they use. Therefore, it would be best if we only passed on information about the software and not specifics about the users of the software.

NB 4. I have only investigated the main areas of interest for selective breeding as outlined in the proposal for this review. There will be other software requirements (eg. for molecular population genetics such as Arlequin or Genpop or QTL mapping such as QTLexpress) that fall outside this scope and have not been investigated for this review.

Contents and navigation around the database.

1. Open the database in MS Access 2007 (the database will also be saved and distributed in an earlier version of MS Access). The database should show the main menu as displayed below.



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Enter new software details and look up details on software existing in database

Enter new contact details and look up details on existing contacts

Enter new institute details and look up details on existing institutes in database

General queries and reports

Answers to questions 1-10

Q1.What type of software do other established breeding programs (in aquaculture and other primary production) require and use?

Q2.What software is already available, from where and from who? What problems do the tools address and what do they enable?

Q3. Which software is applicable or easily adapted for aquaculture purposes?

Q4.What level of adaptation would be required for the adoption of existing tools into aquaculture and what resources (skills) would this need?

Q5.Which tools could address common problems across different aquaculture sectors?

Q6.What level of skill is needed to operate the software?

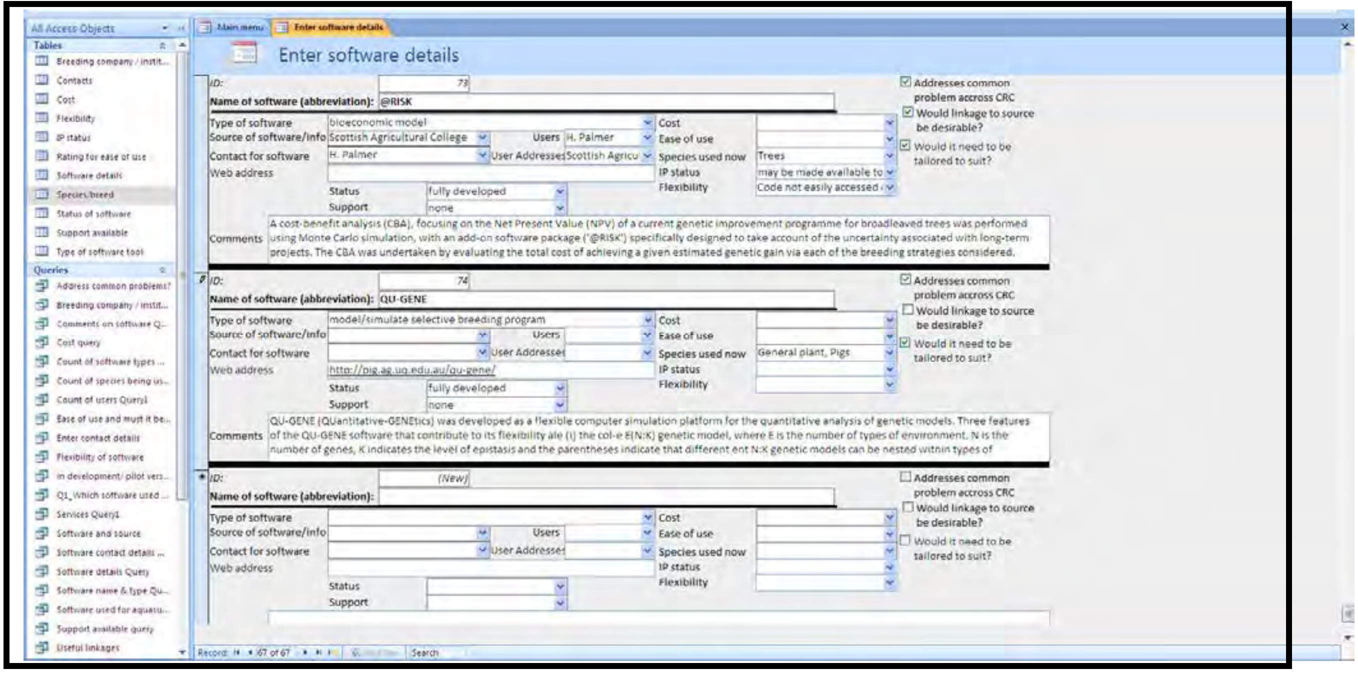
Q7.Does the software have good documentation and do the developers offer support services?

Q8.Is the software freely available, available at a price, available to partners or maintained as a trade secret?

Q9.Might it be useful to link to other breeding companies or organizations (aquatic, livestock or forestry) to access existing tools or expertise for developing such tools?

Q10.Are there initiatives underway or being planned that aim to develop useful new software for aquaculture and might the CRC be able to link to such initiatives?

2. The best way to view the full details of entries in the database is to click the "Enter software details" button on the main menu screen. The "Enter software details" form will open up as displayed in the picture below and you can use the scroll bar to browse the existing entries or to add new entries.



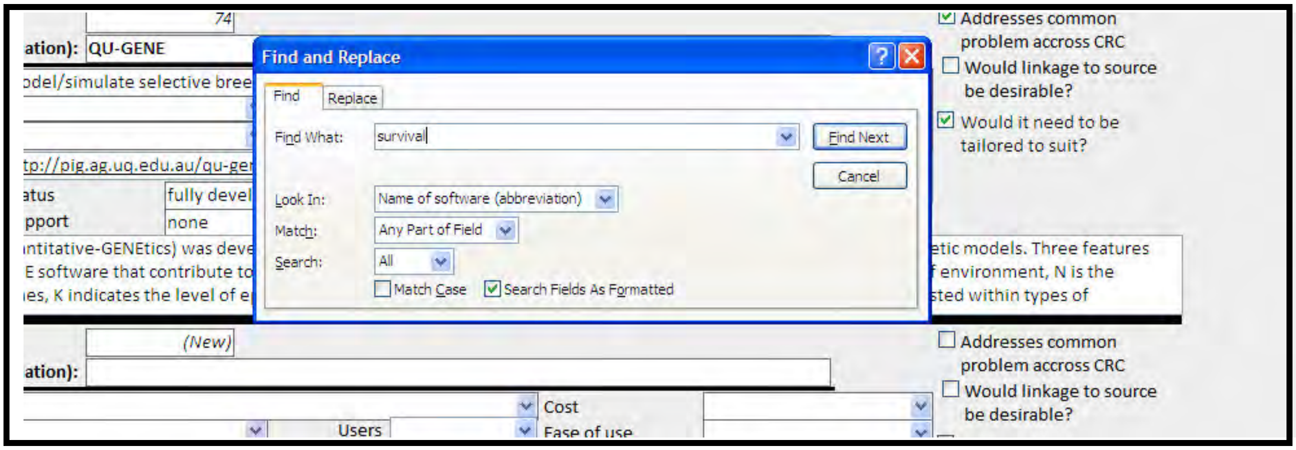
Enter software details

ID: 73
Name of software (abbreviation): @RISK
Type of software: bioeconomic model
Source of software/info: Scottish Agricultural College
Users: H. Palmer
Contact for software: H. Palmer
User Addresses: Scottish Agricu
Web address:
Status: fully developed
Support: none
Cost:
Ease of use:
Species used now: Trees
IP status: may be made available to
Flexibility: Code not easily accessed
☑ Addresses common problem accross CRC
☑ Would linkage to source be desirable?
☑ Would it need to be tailored to suit?
Comments: A cost-benefit analysis (CBA), focusing on the Net Present Value (NPV) of a current genetic improvement programme for broadleaved trees was performed using Monte Carlo simulation, with an add-on software package ('@RISK') specifically designed to take account of the uncertainty associated with long-term projects. The CBA was undertaken by evaluating the total cost of achieving a given estimated genetic gain via each of the breeding strategies considered.

ID: 74
Name of software (abbreviation): QU-GENE
Type of software: model/simulate selective breeding program
Source of software/info:
Users:
Contact for software:
User Addresses:
Web address: http://pig.ag.uq.edu.au/qu-gene/
Status: fully developed
Support: none
Cost:
Ease of use:
Species used now: General plant, Pigs
IP status:
Flexibility:
☑ Addresses common problem accross CRC
☐ Would linkage to source be desirable?
☑ Would it need to be tailored to suit?
Comments: QU-GENE (QUantitative-GENEtics) was developed as a flexible computer simulation platform for the quantitative analysis of genetic models. Three features of the QU-GENE software that contribute to its flexibility ale (i) the col-e E(N:K) genetic model, where E is the number of types of environment. N is the number of genes, K indicates the level of epistasis and the parentheses indicate that different ent N:K genetic models can be nested within types of

ID: (New)
Name of software (abbreviation):
Type of software:
Source of software/info:
Users:
Contact for software:
User Addresses:
Web address:
Status:
Support:
Cost:
Ease of use:
Species used now:
IP status:
Flexibility:
☐ Addresses common problem accross CRC
☐ Would linkage to source be desirable?
☐ Would it need to be tailored to suit?

3. Ctrl-F can be used to find particular software etc, just click in the field where you want to find the information before using the command.



Find What: survival

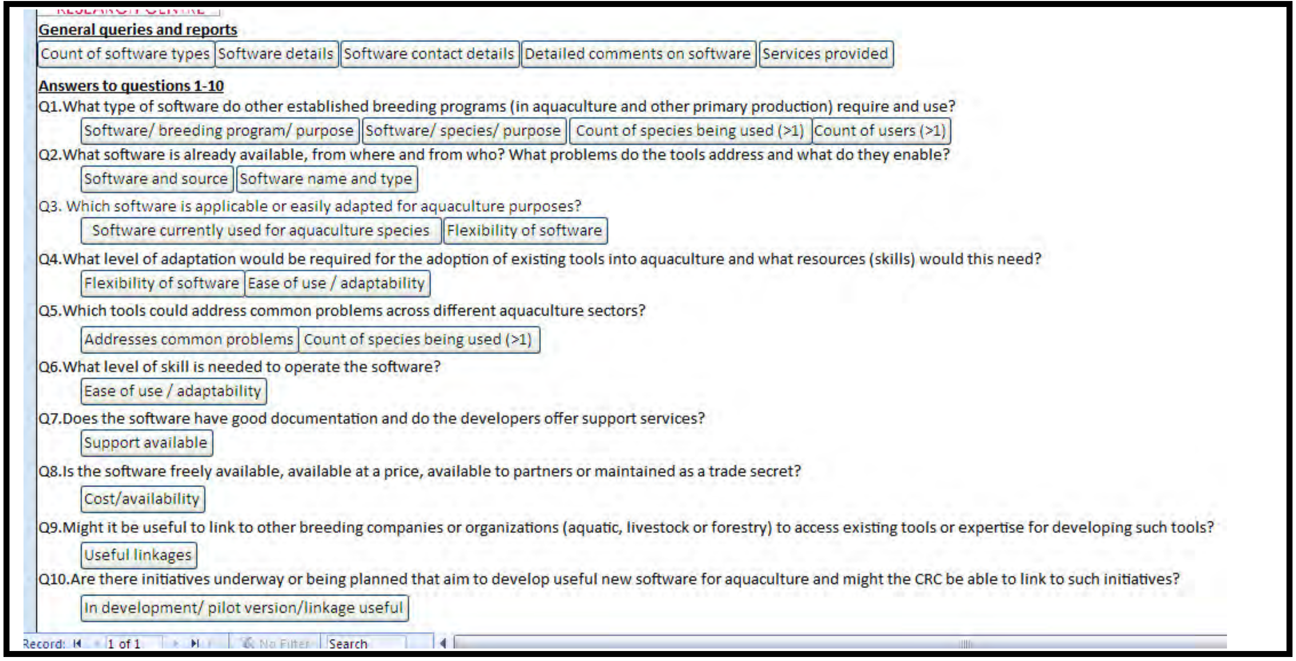
Look In: Name of software (abbreviation)

Match: Any Part of Field

Search: All

☐ Match Case ☑ Search Fields As Formatted

4. Close the form by clicking the close box to go back to the main menu.
5. You can add new breeding companies, contacts or categories by double clicking on the various tables on the left side of the database window or by clicking the “enter contact details” or “enter institute details” buttons on the main form.
6. Key questions for the review can be answered by clicking on the buttons under each question (eg. “Software/ breeding program/ purpose”). More general information is also available under the heading “General queries and reports”. Just click the buttons on the main menu to view these (eg. “Count of software types”).



General queries and reports

Count of software types | Software details | Software contact details | Detailed comments on software | Services provided

Answers to questions 1-10

Q1.What type of software do other established breeding programs (in aquaculture and other primary production) require and use?

Software/ breeding program/ purpose | Software/ species/ purpose | Count of species being used (>1) | Count of users (>1)

Q2.What software is already available, from where and from who? What problems do the tools address and what do they enable?

Software and source | Software name and type

Q3. Which software is applicable or easily adapted for aquaculture purposes?

Software currently used for aquaculture species | Flexibility of software

Q4.What level of adaptation would be required for the adoption of existing tools into aquaculture and what resources (skills) would this need?

Flexibility of software | Ease of use / adaptability

Q5.Which tools could address common problems across different aquaculture sectors?

Addresses common problems | Count of species being used (>1)

Q6.What level of skill is needed to operate the software?

Ease of use / adaptability

Q7.Does the software have good documentation and do the developers offer support services?

Support available

Q8.Is the software freely available, available at a price, available to partners or maintained as a trade secret?

Cost/availability

Q9.Might it be useful to link to other breeding companies or organizations (aquatic, livestock or forestry) to access existing tools or expertise for developing such tools?

Useful linkages

Q10.Are there initiatives underway or being planned that aim to develop useful new software for aquaculture and might the CRC be able to link to such initiatives?

In development/ pilot version/linkage useful

7. The database is written in Access 2007. I will also save it as an earlier Access version, although it may lose some features in this format.
8. You can also search for particular programs or details in the forms, queries or tables of the database by hitting the binoculars (find button).

Special software considerations for species in aquaculture

Aquaculture breeding program requirements are distinctly different to the requirements for plant and land-based livestock breeding programs in a number of ways. Differences occur in the biology of species used, breeding environment and in industry structure. These differences lead to different requirements for software. In the past the most relevant software and quantitative genetics theory developments for aquaculture have come from developments made specifically for livestock breeding (eg. dairy and beef cattle). But the software we use for breeding needs to address problems that are specific to aquaculture, account for differences in biology, environment and industry structure and exploit any possible advantages posed by the unique situation in aquaculture.

First, much larger families can generally be produced for fish and shellfish than for livestock, and because aquatic species need to be handled quickly when out of the water, there is an even greater need for rapid and automated measurement of traits for aquaculture species. This creates some special software and technical requirements for quickly capturing and entering information into databases in the field.

Second, the nature of livestock and aquaculture industries and their selective breeding arrangements are generally very different. Most aquaculture breeding programs operate with a central breeding nucleus that supplies genetically improved seedstock to the whole industry (sometimes via seed multipliers). The central breeding nucleus sends out some animals for testing and also measures and tests the breeding candidates and their siblings themselves. In contrast, for grazing livestock like dairy cattle, information is collected from a number of herd recording centres and milk testing laboratories. Data is then processed by quantitative geneticists such as those working for the Australian Dairy Herd Improvement Scheme (ADHIS) who perform the genetic evaluations for the whole industry in Australia. Bull semen is then priced on the basis of the genetic evaluations and is sold by independent suppliers such as Genetics Australia to farmers. In this system a bulls genetic merit is evaluated from the milking performance of his daughters. The software requirements for genetic evaluation and choice of mate pairs for these different breeding structures are therefore very different, partly due to differences in industry structure and partly due to the specific task of measuring milk production in cows to evaluate bulls.

Gjedrem (2005) has described the key differences between typical livestock and aquaculture breeding programs. These differences are as follows:

1. The reproductive cycle of aquaculture species is often complex and frequently not fully understood and therefore it is difficult to reliably control optimal mate pairing and avoid inbreeding. This is particularly so for marine species. There is a need for aquaculture breeding software that can be used in the field as the situation unfolds to guide mate pairing.
2. Gjedrem also highlights that “there is also very little reliable information about phenotypic and genetic parameters of economically important traits” for most species. These parameters are needed for formulating the breeding objective which is “a linear combination of breeding values for each trait weighted by their relative economic importance”. Therefore it is often necessary with aquaculture breeding programs to start with a very simple breeding objective (eg one trait that is well understood, simple to select and gives demonstrable benefits such as growth rate). There is a need to estimate realized heritability and correlations and to build up information for a range of traits as the breeding program progresses.

3. One advantage with aquaculture species is that when the species have external fertilization, and artificial control is possible, it is possible to have a lot of flexibility in mating. This is often not possible for livestock. More options become possible for genetic improvement and evaluation because of these features.
4. Interspecific hybridization is often possible for aquaculture species. This can add some complexity to breeding programs and can in some instances result in exciting possibilities to be exploited such as heterosis, hybrid infertility etc.
5. Chromosome manipulation is often possible for aquaculture species. There are possibilities to produce polyploids, single sex crops, completely homozygous clones etc. But the effect of such manipulations needs to be carefully considered and modeled (eg. What will be the ultimate economic outcomes?)
6. Production and rearing is a lot cheaper than for farm animals.
7. Larvae cannot be tagged or marked like the offspring of farm animals. Ie. families must be reared separately until tagging or modern technology used to determine pedigrees.
8. Fish are generally small and of low economic value compared to livestock. Ie. may be less efficient and profitable to establish breeding programs for.
9. Rapid accumulation of inbreeding is a problem that needs to be actively avoided for some of the above reasons.

When software has been developed for farm animals, these differences and the ability of the software to cope with these factors needs to be considered. For instance, due to the possibility for rapid accumulation of inbreeding for some aquaculture species breeding programs, software that allows for implementation of techniques such as “optimal contribution selection” becomes important.

Broad options available for the Seafood CRC

The Seafood CRC is in a good position as a range of software is already available and being used by the aquaculture, livestock and plant industries around the world. Typically, the software that is used has been developed by teams of quantitative geneticists over many years. Because of the time, expense and specialist expertise associated with the development of such software it would probably be unwise for the Seafood CRC to develop its own software if reasonably priced alternatives already exist that could be adapted to the purpose. So the breeding programs that will be established by the Seafood CRC have several different options available for genetic analysis and for acquiring access to appropriate software:

1. Establish a National Breeding Company that will coordinate the management and analysis of genetic data and be closely associated (and be supported from) commercialisation strategies within multiple aquaculture sectors. This would provide all Australian breeding programs access to specialist aquaculture breeding software and expertise. Operating across a number of sectors the service would be cost efficient and be able to provide a better variety of expertise and software solutions. This option has been highlighted in the Seafood CRC Breeding for Profit theme business plan. Such a national company might be able to develop a mutually beneficial arrangement with a specialist aquaculture breeding company overseas. The National Breeding Company would then benefit from the advantages that the overseas partner has (established software tools and systems, specialist knowledge and expertise applied to a range of aquaculture species).

2. Enter into a service contract with an established service provider who uses a system that can be adapted for all of the species in question. The potential service providers in Appendix 4 could be investigated if this option is chosen. This may come at a cost to the CRC or in some cases may necessitate strategic research linkages with the software developers.
3. Many industry bodies (eg. ADHIS) have their own purpose built software that is very sophisticated and well suited to address problems in their industry. It might be attractive to some of these industry bodies if they could recuperate some of the development costs by selling a service or a database shell that could be used by the seafood CRC.
4. Employ a quantitative geneticist to make use of and adapt existing software for use with all of the Seafood CRC species.
5. Employ one or a team of quantitative geneticists to develop systems and software needed from scratch (a long and expensive project).

There is only one instance where a national breeding company exists to support multiple aquaculture sectors. Australia is unique in that there are many species for which breeding programs have or are being developed. Other countries have had a tight focus on one or a couple of key species. In Norway where the selective breeding has reached a relative mature commercialization phase for Atlantic salmon, new opportunities are beginning to be explored for other species (eg. Atlantic cod). Either exisiting research institutes or commercial selective breeding companies perform the genetic evaluations for most industries. In Norway, two main companies supply the industry with selected Atlantic salmon seed (Aquagen and Salmobreed). Both these companies utilize AKVAFORSK for research and special project work. AKVAFORSK's daughter company, the Akvaforsk Genetics Centre (AFGC) performs evaluations for Salmobreed, while Aquagen have an agreement with Norway's pig and cattle breeding companies to share quantitative genetic expertise. AFGC consults across the world and runs breeding programs for a number of different species in aquaculture (Atlantic salmon, Atlantic cod, rainbow trout, tilapia, shrimp, carp, sea bass, sea bream etc). AFGC, would therefore be similar in many ways to the National Breeding Company proposed for Australia. AFGC have well established software systems that they use to tackle problems across the range of species they work with. AFGC might therefore be a potentially valuable partner to consider in the National Breeding Company model as they could provide access to specialist knowledge, software and business models.

Software types and options

Appendix 1, and the buttons in the database in answer to question 1, outline the software used by the breeding companies and institutes contacted for this review. Here I summarise these findings:

Pedigree analysis

There is not a lot of specific software out there for this purpose. Records are kept as part of the trait relational databases for most programs. The relationships are taken into account when performing genetic evaluations and when performing mate selection. There is little reason to produce pretty pictures etc mapping out the pedigree structure. These sorts of programs are mainly needed if the animals are not tagged and if DNA typing is used to determine parentage. A thorough economic analysis needs to be done before breeding programs head down this track.

The efficiency of doing this will be highly dependent on the variance in family sizes and survival until genetic evaluation.

FAP by John Taggart predicts the resolving power of specific parental data sets (nuclear and mitochondrial) for unambiguously discriminating among families / groups of families. Assigns family of origin to progeny from genotype (nuclear and mitochondrial) data.

Vitassign by Marc Vandeputte is a useful program to use when assigning pedigree using marker information. In parentage assignment by exclusion, using multiple and very polymorphic loci, genotyping errors are a major cause of non-assignment. Using stochastic simulations, Vandeputte tested the possibility to allow for mismatches at one or more allele as a way to recover assignment power. This was very efficient provided the set of loci used had a high assignment power (> 99%) and the error rate was not too high (below 3–4%). In these cases, most of the theoretical assignment power could be recovered. Some groups such as Syaqua incorporate pedigree assignment programs into their relational database.

Trait recording relational databases

Trait relational databases are a key requirement for any breeding program. These databases are normally very specific to the species in question and in the past have been built largely from scratch. The sort of database backbone systems used include MySQL and Oracle. User friendly front-ends can be built into such systems. The design, maintenance and upgrading of these relational databases is important and can be expensive and ongoing. Specialist ongoing support is needed to keep the database alive and well.

A number of services are now available where database building, maintenance and even genetic evaluations can be performed at a price (eg. SAC-EGENES, BREEDPLAN, etc). These are based on database shells and analysis pipelines developed for livestock. Significant re-development would most likely be needed for aquaculture species. None-the-less, this avenue of database provision needs to be further investigated.

Genetic evaluation

Genetic evaluation is ofcourse a key component for any breeding program. A large number of options are available here. Most popular among fish breeders are PEST & VCE, DMU, Mixed99 and SAS solutions. DMU, Pest/VCE and SAS can estimate variance components as well as yield breeding values. DMU doesn't handle very large data sets though.

Mate selection

An important requirement for optimizing genetic response while minimizing inbreeding. Needs to be flexible and easily worked for the fish situation. This is for very practical reasons. (eg. for abalone, the precise timing of spawning is difficult to control, so a list of prioritized matings needs to be generated quickly on the spot as animals spawn). There are two main available alternatives used by fish selective breeders here (EVA and OCSelect), but other options might be available through research or commercial collaborations (eg. the AFGC in-house system which is used with a number of species).

Simulation including full bioeconomic models, of selective breeding programs

These are useful tools for the planning of breeding programs to optimize their economic effects (both for industry and for the selective breeding company). Such models predict the genetic response and economic effects of the breeding program. Normally, all the parameters used in the model can be varied so that best and worst case assumptions can be accounted for and optimal plans (eg. traits, trait weighting, numbers of families etc) can be determined. The models are needed because such calculations are complex (can't be done on the back of an envelope) and because many factors influencing the genetic response and economics are probabilistic (it is necessary to draw values from a distribution in order to determine the average outcome and variation in outcomes through repeated running o the simulation model).

The author of this report has a model he has developed himself that is being applied to some of the selective breeding programs in the Seafood CRC (AKVAFORSK model). This is a simple bioeconomic model that considers the effects of selecting one trait at a time. The model could be adapted in the future to account for multi-trait selection. A manuscript describing use of this model is currently under review for Aquaculture. @RISK looks to be similar to the AKVAFORSK model, but its availability could not be determined.

Economic weights and selection indices
There doesn't seem to be much software available to help here (Desire, Finish spreadsheets, models used for sawn timber). DESIRE is designed to help you explore the possible outcomes of a breeding program, in terms of predicted genetic gains for a number of traits. When we set desired gains, this restricts the possible range of genetic change for other traits. DESIRE is "a dynamic tool to help you surf the n-dimensional (n-trait) space of possible outcomes from a simple breeding program. It does this by showing 2- dimensional slices of this space. The algebra behind DESIRE is largely drawn from Pim Brascamp's paper: "Brascamp, E.W. 1984. Selection indices with constraints. Animal Breeding Abstracts 52:645-654."" As mentioned below, full bioeconomic simulation models such as that of AKVAFORSK's are useful for formulating these indices as well (see section above on these). A Finish model is under development and might prove very useful. A MS excel model developed for the sawn timber industry could be useful if it was adapted by somebody to the aquaculture situation (this might be being done by Peter Kube at CSIRO).

Probably the best option is to contract out the work to formulate the index to specialists who have had experience in this area. The final breeding objective will depend on the genetic parameters for the traits of interest (eg. heritability), the economic effects of improvement for each of the traits and correlations between traits. The more traits you add to the index, the less improvement you will see for any single trait. As an overall rule with selection on *equally important and independent traits*, the genetic gain in any one trait expected with selection based on an overall selection index

$= \frac{1}{\sqrt{n}} * \textit{gain obtained if selection directed to that trait alone}$ (Hazel and Lush 1942)

Although the overall economic effect may be greater with more traits, it might be possible for the selective breeding program to capture more of the market (achieve more uptake by growers and be more profitable) by focusing on fewer traits. This is because uptake of selected stock might be greater when the benefits from the selective breeding program are more obvious and easily demonstrable (eg. improvement on a single trait for which improvement is easily demonstrated such as growth rate). This improved uptake adds to the economic benefit to industry and needs to be accounted for in economic models. Also, it costs to measure any new traits. Some traits are much more expensive to measure than others. Traits like growth rate are cheap and quick to measure, disease resistance is expensive, lengthy, complicated and indirect to measure. All these considerations need to be made as well.

AKVAFORSK is working with the Economics Department at a University in Norway and software is being developed that will assist with the formulation of breeding objectives. Bioeconomic simulation models are useful tools that can be used for optimising economic weights and selection indices.

Variance component estimation

This is normally done using ASREML, DMU, PEST & VCE or SAS by most selective breeding programs. Some members of the CRC probably already have ASREML licences. ASREML performs a mixed model analysis. ASREML is said to be more user friendly than DMU, it has more modules (eg. survival analysis etc) than the other alternatives, is probably more advanced than the other alternatives and contains modules for marker information as well. ASREML is relatively more costly, but many institutions in Australia have it and use it already under license. Documentation for ASREML is all publically available and you can clearly see how it works. Add-ons are available so that it can be used with S-plus or R (one license). A non-commercial license costs approx 195 pounds sterling. The program requires a good statistical knowledge and is not particularly user friendly.

Automation of data collection

As described above, software that can automate and increase the efficiency and accuracy of data collection will be essential for aquaculture breeding programs. A number of options are available including Vatjus-Micro Oy and Labview.

Labview enables a PC to collect electronic data from various devices (including PIT tag readers) and/or the keyboard, displays the data on screen in whatever format you choose, writes the data to a file, and keeps on screen tallies of a session. The program is robust, easy to use, and highly flexible. Data capture programs can be quickly written for any application required in the breeding programs.

Vatjus-Micro Oy is a "Digital table" used in Finland on-site which is connected to a computer. It automatically reads pit tags and records body weight and length, and sends information to a computer. Other traits such as appearance, colour etc can be manually entered through a waterproof keyboard. The system also includes software so that when you read the pit tag it can tell you who the fish should be mated with (ie. it connects to data you supply).

Survival analysis

Survival analysis is complex and requires specialist treatment. This form of analysis is quite unique to aquaculture breeding programs. AKVAFORSK and AFGC have run a series of projects over many years on this topic for salmon, trout, shrimp etc. It would take many years to develop the knowledge and tools that would be needed for this type of analysis and collaboration or consultation with experts in this area would be desirable. A group in Austria have developed a software package that might be useful.

Future considerations in the choice of software

There are a number of detailed considerations that quantitative geneticists will need to make before choosing software (see "Software packages in animal breeding", a review prepared by Ignacy Misztal at University of Illinois for an example). Species orientation (dairy, beef, pigs, salmon etc), year released and year last updated, development system (DEC Unix, PC DOS, Sun UNIX, PC OS/2, RS/6000 Unix, Convex Unix, IBM CMS), usefulness and clarity of comment lines in source code, detail in manual, MME solutions with large data sets, repeatability with large data sets, trouble shooting agreements etc.

Answers to key questions

Most of the key questions outlined under the "need" section above can be answered by pressing the database buttons under each question. The database prepared for this review should contain information about most of the software that exists, is being used or might be useful for aquaculture breeding programs. It is designed to be a "living" database where new information and developments can be added. It is a resource that the CRC can use to help with the development of its business plans and breeding programs.

Summary and recommendations

This review gives an overview of the options for software that are currently available, being utilized or of potential use for selective breeding programs in aquaculture. Access to this software varies and can be free, by purchase, accessed through a service or in some instances might be gained through a collaborative agreement. Most of the software that is required for selective breeding takes years of time and many thousands of dollars to develop. Aquaculture and aquatic species pose unique problems for selective breeding, and therefore software developed for livestock or plants normally require some degree of adaptation before they could be validly applied to species in aquaculture. The software options considered here need to be evaluated in the context of what quantitative, programming, database or modeling skills will be available to the breeding programs in the Seafood CRC and how the breeding programs will be run (eg. whether run out of a National Breeding Company dealing across sectors, in collaboration with an experienced multisector breeding company that already has well developed software tools, or run on a sector-by-sector basis with relatively few available genetic skills and resources). Once the model for operation of the breeding programs is decided, further details on a short-list of software options, (their applicability to the situation, cost, availability, support, effectiveness etc) will need to be determined and detailed. This information is best collected by quantitative geneticists involved in running the breeding programs, as decisions should also be influenced by the particular skills and preferences that the users of these software tools may have.

Therefore my main recommendations are as follows:

1. Utilize existing expertise and software that can be adapted to the task.
2. Quantitative geneticists should utilize and add to the database initiated for this review to generate a shortlist of software needed.
3. Further detailed information gathering for shortlisted software should be performed at a later stage once the size and scope of the breeding programs or national breeding company running the programs is known.

Appendix 1. Software and general purpose of software as grouped according to breeding company or institute performing the analysis. Contents of the first two columns have been shaded to protect confidentiality of the companies involved.

R			
Breeding company / institute.user (breeding company or institute)	**Breeding company / institute.country**	**Software details.Name of software (abbreviation)**	**Software details.Type of software.Value**
[redacted]	[redacted]	MYSQL relational databases with MS Access interface	trait recording relational database
[redacted]	[redacted]	EVA	mate selection
[redacted]	[redacted]	Biomark data collection tab with P3 software	automation of data collection
[redacted]	[redacted]	MTDFREML (Multiple Trait Derivative Free REML, Boldman and Van Vleck)	genetic evaluation
[redacted]	[redacted]	Pedigree viewer	pedigree analysis from tag record

R			
Breeding company / institute.user (breeding company or institute)	**Breeding company / institute.country**	**Software details.Name of software (abbreviation)**	**Software details.Type of software.Value**
[redacted]	[redacted]	SAS	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	SAS	genetic evaluation
[redacted]	[redacted]	MTDFREML (Multiple Trait Derivative Free REML, Boldman and Van Vleck)	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	Optimum contribution selection software	mate selection
[redacted]	[redacted]	AKVAFORSK data collection software	automation of data collection
[redacted]	[redacted]	R	general statistical or analysis tools
[redacted]	[redacted]	Formulation of economic weights	economic weights & selection indices
[redacted]	[redacted]	Analysis of complex survival data	survival analysis
[redacted]	[redacted]	Analysis of complex survival data	genetic evaluation
[redacted]	[redacted]	AKVAFORSK Bioeconomic simulation software for selective breeding design	bioeconomic model
[redacted]	[redacted]	Photofish	automation of data collection
[redacted]	[redacted]	R	bioeconomic model
[redacted]	[redacted]	ASREML	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	MYSQL relational databases with MS Access interface	trait recording relational database
[redacted]	[redacted]	AFGC mate selection program	mate selection
[redacted]	[redacted]	PEST & VCE	variance component estimation (heritability, correlations etc)

R			
Breeding company / institute.user (breeding company or institute)	**Breeding company / institute.country**	**Software details.Name of software (abbreviation)**	**Software details.Type of software.Value**
[redacted]	[redacted]	PEST & VCE	genetic evaluation
[redacted]	[redacted]	SAS	genetic evaluation
[redacted]	[redacted]	DMU	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	SAS	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	AKVAFORSK data collection software	automation of data collection
[redacted]	[redacted]	DMU	genetic evaluation
[redacted]	[redacted]	BREEDPLAN	trait recording relational database
[redacted]	[redacted]	BREEDPLAN	genetic evaluation
[redacted]	[redacted]	OVIS	genetic evaluation
[redacted]	[redacted]	In-house economic weight and selection index calculation C++	economic weights & selection indices
[redacted]	[redacted]	In-house relational database C++	trait recording relational database
[redacted]	[redacted]	Interbull & Interbeef	genetic evaluation
[redacted]	[redacted]	MYSQL relational databases with MS Access interface	trait recording relational database
[redacted]	[redacted]	ASREML	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	ADHIS	trait recording

R

Breeding company / institute.user (breeding company or institute)	Breeding company / institute.country	Software details.Name of software (abbreviation)	Software details.Type of software.Value
[redacted]			relational database
[redacted]	[redacted]	ADHIS	genetic evaluation
[redacted]	[redacted]	SAS	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	SAS	genetic evaluation
[redacted]	[redacted]	ASREML	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	DMU	genetic evaluation
[redacted]	[redacted]	DMU	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	The Survival Kit	survival analysis
[redacted]	[redacted]	ASREML	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	LabVIEW	automation of data collection
[redacted]	[redacted]	CSIRO Oracle Database	trait recording relational database
[redacted]	[redacted]	ADAM	model/simulate selective breeding program
[redacted]	[redacted]	SAS	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	SAS	genetic evaluation
[redacted]	[redacted]	PEST & VCE	genetic evaluation
[redacted]	[redacted]	Pedigree viewer	pedigree analysis from tag record

R			
Breeding company / institute.user (breeding company or institute)	**Breeding company / institute.country**	**Software details.Name of software (abbreviation)**	**Software details.Type of software.Value**
[redacted]	[redacted]	ASREML	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	PEST & VCE	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	Winwedge	automation of data collection
[redacted]	[redacted]	Vitassign	pedigree analysis from genotype
[redacted]	[redacted]	ASREML	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	Own models for selective breeding programs-MathCad	model/simulate selective breeding program
[redacted]	[redacted]	OCSelect and GenCont	mate selection
[redacted]	[redacted]	Image capture system - MediaCybernetics	automation of data collection
[redacted]	[redacted]	FAP (Family Assignment Program)	pedigree analysis from tag record
[redacted]	[redacted]	FAP (Family Assignment Program)	pedigree analysis from genotype
[redacted]	[redacted]	SAC-EGENES commercial databases in Edinburgh	trait recording relational database
[redacted]	[redacted]	TM- Bayesian Threshold Model for Genetic Evaluation	genetic evaluation
[redacted]	[redacted]	MS-Excel own scripts	automation of data collection
[redacted]	[redacted]	FAP (Family Assignment Program)	mate selection
[redacted]	[redacted]	SAS	genetic evaluation
[redacted]	[redacted]	DMU	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	AFGC mate selection program	mate selection
[redacted]	[redacted]	PEST & VCE	genetic evaluation

R			
Breeding company / institute.user (breeding company or institute)	**Breeding company / institute.country**	**Software details.Name of software (abbreviation)**	**Software details.Type of software.Value**
[redacted]	[redacted]	SAS	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	AKVAFORSK data collection software	automation of data collection
[redacted]	[redacted]	DMU	genetic evaluation
[redacted]	[redacted]	PEST & VCE	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	Home made scripts	trait recording relational database
[redacted]	[redacted]	Mixed99	genetic evaluation
[redacted]	[redacted]	DMU	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	DMU	genetic evaluation
[redacted]	[redacted]	Vatjus-Micro Oy	automation of data collection
[redacted]	[redacted]	Finish spreadsheet	economic model
[redacted]	[redacted]	EVA	mate selection
[redacted]	[redacted]	Pedigree Systems Ltd	pedigree analysis from tag record
[redacted]	[redacted]	Pedigree Systems Ltd	trait recording relational database
[redacted]	[redacted]	DMU	genetic evaluation
[redacted]	[redacted]	AKVAFORSK data collection software	automation of data collection
[redacted]	[redacted]	Photofish	automation of data collection
[redacted]	[redacted]	SAS	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	SAS	genetic evaluation
[redacted]	[redacted]	PEST & VCE	genetic evaluation

R			
Breeding company / institute.user (breeding company or institute)	**Breeding company / institute.country**	**Software details.Name of software (abbreviation)**	**Software details.Type of software.Value**
[redacted]	[redacted]	PEST & VCE	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	AFGC mate selection program	mate selection
[redacted]	[redacted]	DMU	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	@RISK	bioeconomic model
[redacted]	[redacted]	TGRM® Mate Selection Service (Total Genetic Resource Management)	mate selection
[redacted]	[redacted]	SyGrow	bioeconomic model
[redacted]	[redacted]	SyAqua Relational Database-Oracle database	pedigree analysis from tag record
[redacted]	[redacted]	SyAqua Relational Database-Oracle database	pedigree analysis from genotype
[redacted]	[redacted]	GenMate	mate selection
[redacted]	[redacted]	BLUPF90	genetic evaluation
[redacted]	[redacted]	MTDFREML (Multiple Trait Derivative Free REML, Boldman and Van Vleck)	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	MTDFREML (Multiple Trait Derivative Free REML, Boldman and Van Vleck)	genetic evaluation
[redacted]	[redacted]	SyAqua Relational Database-Oracle database	trait recording relational database
[redacted]	[redacted]	OCSelect and GenCont	mate selection
[redacted]	[redacted]	PEST & VCE	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	PEST & VCE	genetic evaluation
[redacted]	[redacted]	OCSelect and GenCont	mate selection

R			
Breeding company / institute.user (breeding company or institute)	**Breeding company / institute.country**	**Software details.Name of software (abbreviation)**	**Software details.Type of software.Value**
[redacted]	[redacted]	ASREML	variance component estimation (heritability, correlations etc)
[redacted]	[redacted]	GENUP- Computer aided learning for quantitative genetics	model/simulate selective breeding program
[redacted]	[redacted]	BLUPF90	genetic evaluation
[redacted]	[redacted]	TGRM® Mate Selection Service (Total Genetic Resource Management)	mate selection
[redacted]	[redacted]	X'Aim	mate selection
[redacted]	[redacted]	GenMate	mate selection
[redacted]	[redacted]	WOMBAT—A tool for mixed model analyses in quantitative genetics by restricted maximum likelihood (REML)*	variance component estimation (heritability, correlations etc)

Appendix 2. Count of software types

Count of software types Query

Software details.Type of software.Value	Count Of Software details
pedigree analysis from genotype	3
trait recording relational database	15
genetic evaluation	22
mate selection	9
model/simulate selective breeding program	5
bioeconomic model	6
pedigree analysis from tag record	4
economic weights & selection indices	4
variance component estimation (heritability, correlations etc)	9
automation of data collection	8
economic model	3
general statistical or analysis tools	3
survival analysis	2
connectedness estimation	1
Crossbreeding design	1

Appendix 3. Count of species for which software is applied (where number of species is >1)

Count of species being used Query1		
Name of software (abbreviation)	**Type of software**	**CountOfSpecies/breed**
ADAM	model/simulate selective breeding program	2
AFGC mate selection program	mate selection	7
AKVAFORSK data collection software	automation of data collection	2
ASREML	variance component estimation (heritability, correlations etc)	7
CSIRO Oracle Database	trait recording relational database	2
DMU	genetic evaluation, variance component estimation (heritability, correlations etc)	4
EVA	mate selection	3
FAP (Family Assignment Program)	pedigree analysis from genotype, mate selection, pedigree analysis from tag record	2
Home made scripts	trait recording relational database	2
Image capture system - MediaCybernetics	automation of data collection	2
Interbull & Interbeef	genetic evaluation	2
LabVIEW	automation of data collection	2
Mixed99	genetic evaluation	3
MS-Excel own scripts	automation of data collection	2
OCSelect and GenCont	mate selection	3
Own models for selective breeding programs-MathCad	model/simulate selective breeding program	2
PEST & VCE	genetic evaluation, variance component estimation (heritability, correlations etc)	6
QU-GENE	model/simulate selective breeding program	2
R	bioeconomic model, general statistical or analysis tools	3
SAC-EGENES commercial databases in Edinburgh	trait recording relational database	5
SAS	genetic evaluation, variance component estimation (heritability, correlations etc)	3
SheepBreeder	trait recording relational database, genetic evaluation	3
SyGrow	bioeconomic model	2
TGRM® Mate Selection Service (Total Genetic Resource Management)	mate selection	3

Count of species being used Query1		
Name of software (abbreviation)	**Type of software**	**CountOfSpecies/breed**
Vitassign	pedigree analysis from genotype	3
Winwedge	automation of data collection	3

Appendix 4. Software used for aquaculture species

Software used for aquaculture species		
Species/breed.Species/breed	**Software details.Name of software (abbreviation)**	**Software details.Type of software.Value**
Abalone	CSIRO Oracle Database	trait recording relational database
Abalone	LabVIEW	automation of data collection
Abalone	R	general statistical or analysis tools
Abalone	R	bioeconomic model
Abalone	ASREML	variance component estimation (heritability, correlations etc)
Atlantic cod	PEST & VCE	genetic evaluation
Atlantic cod	AFGC mate selection program	mate selection
Atlantic cod	PEST & VCE	variance component estimation (heritability, correlations etc)
Carp	R	general statistical or analysis tools
Carp	R	bioeconomic model
Oysters	SAS	variance component estimation (heritability, correlations etc)
Oysters	ASREML	variance component estimation (heritability, correlations etc)
Oysters	Vitassign	pedigree analysis from genotype
Oysters	SAS	genetic evaluation
Oysters	Winwedge	automation of data collection
Oysters	PEST & VCE	genetic evaluation
Oysters	PEST & VCE	variance component estimation (heritability, correlations etc)
Salmon	AKVAFORSK data collection software	automation of data collection
Salmon	MS-Excel own scripts	automation of data collection
Salmon	Photofish	automation of data collection
Salmon	ASREML	variance component estimation (heritability, correlations etc)
Salmon	DMU	genetic evaluation
Salmon	DMU	variance component estimation (heritability, correlations etc)
Salmon	OCSelect and GenCont	mate selection
Salmon	SAC-EGENES commercial databases in Edinburgh	trait recording relational database
Salmon	Mixed99	genetic evaluation

Software used for aquaculture species		
Species/breed.Species/breed	**Software details.Name of software (abbreviation)**	**Software details.Type of software.Value**
Salmon	Image capture system - MediaCybernetics	automation of data collection
Salmon	Own models for selective breeding programs-MathCad	model/simulate selective breeding program
Salmon	FAP (Family Assignment Program)	mate selection
Salmon	AKVAFORSK Bioeconomic simulation software for selective breeding design	bioeconomic model
Salmon	EVA	mate selection
Salmon	FAP (Family Assignment Program)	pedigree analysis from tag record
Salmon	AFGC mate selection program	mate selection
Salmon	LabVIEW	automation of data collection
Salmon	FAP (Family Assignment Program)	pedigree analysis from genotype
Salmon	Analysis of complex survival data	genetic evaluation
Salmon	Analysis of complex survival data	survival analysis
Salmon	Formulation of economic weights	economic weights & selection indices
Salmon	PEST & VCE	genetic evaluation
Salmon	PEST & VCE	variance component estimation (heritability, correlations etc)
Salmon	CSIRO Oracle Database	trait recording relational database
Salmon	R	bioeconomic model
Salmon	Optimum contribution selection software	mate selection
Salmon	R	general statistical or analysis tools
Sea Bass	SAS	variance component estimation (heritability, correlations etc)
Sea Bass	AFGC mate selection program	mate selection
Sea Bass	Vitassign	pedigree analysis from genotype
Sea Bass	Winwedge	automation of data collection
Sea Bass	PEST & VCE	variance component estimation (heritability, correlations etc)
Sea Bass	PEST & VCE	genetic evaluation
Sea Bass	SAS	genetic evaluation
Sea Bream	ASREML	variance component estimation (heritability, correlations etc)

Software used for aquaculture species		
Species/breed.Species/breed	**Software details.Name of software (abbreviation)**	**Software details.Type of software.Value**
Sea Bream	AFGC mate selection program	mate selection
Shrimp	TGRM® Mate Selection Service (Total Genetic Resource Management)	mate selection
Shrimp	BLUPF90	genetic evaluation
Shrimp	SyAqua Relational Database- Oracle database	trait recording relational database
Shrimp	SyAqua Relational Database- Oracle database	pedigree analysis from genotype
Shrimp	SyAqua Relational Database- Oracle database	pedigree analysis from tag record
Shrimp	SyGrow	bioeconomic model
Shrimp	AFGC mate selection program	mate selection
Tilapia	AFGC mate selection program	mate selection
Trout	Mixed99	genetic evaluation
Trout	FAP (Family Assignment Program)	mate selection
Trout	EVA	mate selection
Trout	OCSelect and GenCont	mate selection
Trout	ADAM	model/simulate selective breeding program
Trout	AFGC mate selection program	mate selection
Trout	Vitassign	pedigree analysis from genotype
Trout	Winwedge	automation of data collection
Trout	PEST & VCE	variance component estimation (heritability, correlations etc)
Trout	PEST & VCE	genetic evaluation
Trout	SAC-EGENES commercial databases in Edinburgh	trait recording relational database
Trout	FAP (Family Assignment Program)	pedigree analysis from tag record
Trout	FAP (Family Assignment Program)	pedigree analysis from genotype
Trout	Image capture system - MediaCybernetics	automation of data collection
Trout	MS-Excel own scripts	automation of data collection
Trout	Home made scripts	trait recording relational database
Trout	SAS	genetic evaluation
Trout	AKVAFORSK data collection software	automation of data collection
Trout	DMU	variance component estimation

Software used for aquaculture species		
Species/breed.Species/breed	**Software details.Name of software (abbreviation)**	**Software details.Type of software.Value**
		(heritability, correlations etc)
Trout	DMU	genetic evaluation
Trout	Own models for selective breeding programs-MathCad	model/simulate selective breeding program
Trout	Vatjus-Micro Oy	automation of data collection
Trout	SAS	variance component estimation (heritability, correlations etc)
Trout	Finish spreadsheet	economic model
Trout	Biomark data collection tab with P3 software	automation of data collection
Trout	MTDFREML (Multiple Trait Derivative Free REML, Boldman and Van Vleck)	genetic evaluation
Trout	MTDFREML (Multiple Trait Derivative Free REML, Boldman and Van Vleck)	variance component estimation (heritability, correlations etc)
Trout	Pedigree viewer	pedigree analysis from tag record
Trout	MYSQL relational databases with MS Access interface	trait recording relational database
Trout	ASREML	variance component estimation (heritability, correlations etc)
Whitefish	Home made scripts	trait recording relational database
Whitefish	DMU	variance component estimation (heritability, correlations etc)
Whitefish	DMU	genetic evaluation
Whitefish	ASREML	variance component estimation (heritability, correlations etc)