ZPLAN+

A software to evaluate and optimise animal breeding programs

User’s Manual

vit Verden
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The development of the program has been supported by:
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Introduction

The program ZPLAN+ calculates breeding programs for complex animal breeding program tasks.
The software is available using the link: https://service.vit.de/zplanplus/ and is optimised for Mozilla/Firefox

Login

Insert your username and password. Please note that only one user is allowed to login per username.

Main page

On the main page new projects can be inserted or old projects edited. The basic structure for a new project is the development of a new breeding program.

Languages

Available languages are German and English. Your actual language will be taken from your own web-browser settings. You can manually change the language (button language next to your username).

Main task bar

On top of the website is a main task bar. The sub-pages breeding program (after selecting a breeding program) and main page are available on the left, on the right user preferences, language setting and logout buttons.

Main page: Top level menu to select breeding programs and breeds, to import XML and JSON files.

Breeding program: Start-menu for main sub-structures of the program. The user has access to all most important sub-pages

● Selection groups (Detailed and Lists)
● Logical Selection groups
● Index groups
Breeds
Pedigree matrix
Geneflow
Results
Optimisation (not available yet)

Import of breeding program- and breed files is only available on the main page. The program recognises automatically, if the import is a breeding program or a breed.

Welcome username: User editing, you can change your password here.
Language: select English or German
Logout: Exit ZPLAN+
?: Open This online help manual

Breeding programs

The page Breeding programs is used to define project-specific parameters:

- Interest rate to calculate discounted costs. Discount rate is always expressed per year and is a value between 0 and 1 (e.g. 0.04 = 4%).
- Interest rate to calculate discounted return. Interest rate is always expressed per year and is a value between 0 and 1 (e.g. 0.06 = 6%). These values represent discount rates as used in financial systems. They can be defined by the user in order to emphasis on a desired discount. It can be modeled a higher discount rate for return than for costs in order to calculate a more strict view on return than on costs.
- Time unit: Time frame all biological parameters refer to, e.g. one year in cattle, half a year in pigs. All biological input must be expressed in time units, if a sow reproduces each 6 months, its cycle of reproduction is .5 when based on one year or 1.0 when based on half a year. It is recommended to set the time unit first and adapt all biological parameters based on this time unit. All results are based on this time unit, not in years (Attention: Interest and discount rates are expressed per year, not per time units. The program automatically recalculates the rates). All age classes and the geneflow matrix as well as realisation vectors are based on time units.
  - Time unit: year
    - Age class 1 = up to one year
    - Age class 2 = one to two years
    - ...
  - Time unit: half year
    - Age class 1 = up to half of a year
    - Age class 2 = one half to one year
    - Age class 3 = one to one and a half years
    - ...

The discount rates are expressed per year, a value of .05 represents a rate of 5% per year. If a time unit less than one year is selected, the discount rate will automatically be re-calculated for the time unite, e.g. 1.05^{(1/2)} for half year or 1.05^{(1/12)} for months.

- Investment duration: Time of investment in time units as defined above. The breeding program will be calculated for results after some time of selection and investment.
Many parameters use this period, especially the calculation of gene flow, gene proportion and the discounting of breeding costs and return.

**It is strongly recommended to define breeds and traits within breed at first!!**

If breeds are already defined, they can be attached to a breeding program. To do this, select on the page 'Breeding programs: Breeds' a breed from the drop-down-list and add it by clicking the green cross button. To deselect breeds, click the red minus-button next to it. This page allows to select already defined breeds in other breeding programs or projects. Once a breed has been attached to a breeding program, more options become visible: Index source groups, selection groups and logical selection groups. The breeding program size is calculated as sum of size of all selection groups.

Export of breeding programs: There is a possibility to save data of a breeding program as a XML-file and to share it with others. With this option, already defined projects can be shared with other ZPLAN+ users. All information attached to a breeding program, as breeds, selection groups, index groups etc. will be exported to file. For an export click the button 'XML-Export' and a name and folder on your computer to save the file. If your browser is the Firefox-Browser (we recommend this) and no folder to save to will be asked, please change your settings in the browser options. For JSON-Export see below.
Breeds

The definition of breeds is mainly a definition of traits and costs. Fixed costs are defined per breed. These contain costs which are independent of the use of animals (e.g. selection groups) and will occur at the same amount for all animals in the breeding program. Fixed costs will be defined per animal. The number of animals with fixed costs can later be defined in each selection group separately.

Traits are defined per breed, different breeds may have different traits and/or parameters. All defined traits are inserted on this page including their genetic and phenotypic parameters. For each breed following parameters can be defined:

- Fixed breeding costs
  - Costs: Fixed breeding costs per animal
- Traits
  - Name
  - Economic value
  - Phenotypic standard deviation
  - Heritability
  - Repeatability
  - Litter effect
  - Herd effect
  - Additional random effect
  - Reproduction (yes/no)
  - Unit

Constraints:
There are some constraints in the parameters which measure the logical relationships. These are:

- Values which have a defined parameter space are not allowed to be inserted outside this space (e.g. Heritability only from 0 to 1)
- Repeatability must be equal or larger than heritability, if repeatability has a value of 0, the value for heritability will be inserted automatically.
- Sum of (Heritability + Litter effect + Herd effect + Additional random effect) must not be > 1.

Traits will be sorted by name in alphabetically order. If a special order is needed, just put characters in front of the trait names (e.g. aMilk, bFat, cProtein) in order to sort the names.

The checkbox 'reproduction' defines, if the trait is an F/C (fattening/carcass) trait or a reproduction trait. F/C-traits are realised once only, whereas reproduction traits can be realised several times. Activating the checkbox means the trait can be realised several times.

This has an influence on calculation of the realisation vector, further on standardised expressions. The reproductive trait will be realised in the same reproduction cycle as defined for each selection group separately.

If a trait is added on the page, it will automatically be added to each matrix below, where necessary correlations will be defined. Only upper triangle matrices are needed, the rest will
be added automatically. Only values within the defined parameter space (-1 to +1) will be allowed. Correlations matrices will automatically be checked for being positive definite, if necessary, matrices will be bended for internal use only.

Insert a genomic measured trait:
Once a trait has been defined as described above, it is possible to define the same trait as genomic measured trait. To insert it, click the green cross at the end of the descriptions for each polygenic trait. A new line will be opened, the name of the new definition will be given automatically. Four parameters will be needed:
- $q$: Proportion of genetic variance explained by markers
- $N$: number of animals in the reference population
- $k$: number of independent segregating QTLs
- $r(TI)$: Accuracy of the polygenic breeding value

The corresponding values for this trait (heritability, phenotypic standard deviation, random effects, genetic and phenotypic variances) will be calculated automatically using the formulas developed by Dekkers and Daetwyler.

In most cases the four necessary values are unknown, the only information available is the accuracy derived for a genomic breeding value. In this case, insert the derived accuracy as value for $q$, $N = 1$, $k = 0$ and $r(TI) = 1.0$. Then a selection index using the genomic measured trait as measured trait and the corresponding polygenic trait as desired trait gives exactly the accuracy given for $q$ in case for one trait as breeding goal.

**Clone**
This button will clone your breed. You will get an exact copy of it and there will be the possibility to change name and parameters. This has the advantage that for similar breeds equal information is not needed to be typed in two times.

**XML Export**
The button ‘XML Export’ will save all settings of this breed as external XML-file. It is similar to the export of complete breeding programs described above. All available information of this particular breed including costs, trait parameters etc. will be saved.
Selection groups

Defining selection groups is the most important step in the definition of the breeding program. It is very important to have an overview of potential selection groups, their relationship to each other and their structure to define the structure of a complex breeding program. Selection paths between separate groups are defined in their pedigree. A selection group can be defined as a group of animals of the same breed, sex and age, that are used to produce offspring and therefore are able to transmit their genes to the next generation. Each selection group can be defined to exist in different ages, different subgroups or transmit genes to a range of gene-receiving groups. The program is completely flexible for modeling complex breeding programs structures, but needs exactly defined parameters to model each selection group.

Definition of a selection group

Selection groups can be defined in two different views. The list view will be used to make a first definition of selection groups and to give an overview of already defined selection groups. Selection groups of the same sex, for example, can easily be compared to each other. Only a selection of parameters is available in the list view. These are the most important parameters, which are: Name, size, gender, breed, production, number of proven and selected, cycle of reproduction, productive lifetime, age at first reproduction, overall survival rate, accuracy of selection index, check box for use of accuracy, check box for realisation group. The check box for defining a selection group as realisation group is in the list view only available for female selection groups. Defining only female selection groups for realisation is a standardised procedure. ZPLAN+ offers the possibility to define male realisation, too. Normally only females realise genetic gain, because they produce offspring which will be sold (F/C traits) or produce reproductive traits (milk, fat,...) which can be sold. This covers most of all realisation in farm animals. In some cases, also male animals are able to realise genetic gain. This needs to be defined in the detailed view of each single selection group.

In the list view, it is possible to change to the detailed view of a selection group clicking the small yellow pen on the left side of each defined selection group.

In the detailed view following parameters can be defined:

- Name
- Gender: important for the pedigree matrix
- Breed: correct linkage of available traits and parameters
- Size: for cost calculation and relationship between realising selection groups, e.g. breeding and production.
- Number of proven and selected animals: for selection intensity
- Production unit: Using this check box, the selection group will not be available in the pedigree matrix as transmitter of genes, this group can only receive genes, this
selection group will not be shown on the results file as parent group and cannot contribute genetic gain.

- Variable costs: costs per animal in this specific selection group, contains normally sum of all costs to choose animals for testing, test animals and select them for breeding.
- Number of animals with fix costs: The number of animals that cause fix costs can be different from the number of animals causing variable costs. For example a testing station has a capacity of 100 animals, but only 50 animals will be tested each time. Then 100 places will cause fix costs, but only 50 will cause variable testing costs.
- Reproduction cycle: average time between two subsequent births in time units (defined on main page)
- Productive lifetime in time units
- Age at first reproduction in time units
- Probability to remain 1 and 2: value between 0 and 1. Insert a value here if the probability of an animal to be culled in the first two time units is different from the overall survival rate.
- Realisation group: This selection group will be used to calculate the realisation vector. Proportions of animals (breeding and production animals) are calculated from selection groups tagged as realisation group only. This checkbox is available for female selection groups only. If the selection group is female, the realisation vector is set up automatically for reproduction and fattening/carcass traits. It is possible to define individual realisation, using the checkboxes in the age class view. For male groups, realisation needs to be defined in the age-classes directly. If the youngest age class is marked for realisation, the reproduction and F/C realisation are set up exactly as for females automatically. Single age-classes can be marked separately for realisation. Then, no automatic calculation of the realisation vector is done. It is very important that the user will check the realisation vector on the geneflow page.
- Accuracy of selection index (if not calculated using index groups and selection index). This check box defines, if the reliability of selection will be used as defined in the selection group, or (if not selected), used as defined in the selection index used for this group. If the check box is not selected, a selection index must be defined. If the reliability is directly used, at the moment a selection index must also be defined, but the results will not be taken into account for calculating results. It is planned to omit this in future releases. The direct accuracy of selection will not be used for multi-stage selection. It is not possible to define the accuracy of selection directly in a multi-stage selection, because the increase of index information is needed to calculate the relationship of two selection groups.

**Pedigree**

If the selection group is not part of a logical selection group, the parental selection groups are shown.
**Cohorts**

After defining these parameters, the program calculates immediately and automatically the relative rate of each defined cohort. This is a group of animals at the same age. Depending on the productive lifetime, the number of cohorts will be shown here, age of the cohort, mean value (not used yet), survival rate and relative size. The survival rate per cohort is filled for each entry using the overall survival rate defined in the list view. It is possible to define individual survival rates for each cohort separately. If a unique value for all cohorts needs to be defined, a value for all cohorts can be defined at the bottom of the list.

**Age classes**

From the list of cohorts, a list of age classes will be calculated automatically and immediately. The age classes divide the cohorts, with their individual age, into equal groups in time units, e.g. years. It will be shown the gene contribution of each group of animals in time unit 1, 2, 3... This is needed to set up the geneflow matrix. For each calculated age class the realisation of this age class can individually be defined. If the first age class is selected, no other age class can be selected. Then it is assumed that the first age class will realise F/C traits and reproduction traits from all other age classes. If any of the age classes larger one will be selected for realisation, the realisation vector for F/C-trait will only be calculated from this selection. For reproduction traits this selection of age classes will not effect the normal procedure. It is possible to select age classes without any gene contribution for realisation, but the results will produce an error in setting up the realisation vector. If there is any individual selection of realising age classes it is strongly recommended to check the realisation vector shown on the geneflow page.

**Information on defining realisation:**

Realisation defines, which groups of animals are able to realise a defined performance of the breeding goal. In most cases female animals are able to realise performances, because in most cases desired traits are linked to female reproduction. Genetic gain of male selection groups can be realised through their female offspring.

To define a selection group as a realising group, the check box ‘realisation’ must be selected. Without any further settings, the corresponding age classes of this selection group will be recognised in a realisation vector. The youngest age class will realise F/C-trait, all others reproduction traits. In most cases it will not be necessary to define single age classes as realising classes.

In some cases, traits are not realised in the given scheme F/C or reproduction. For example in horse breeding, jumping animals realise prize money only at a specific age. Only for this case it is possible to define for each selection group single realising age classes. Each age class on the selection group page contains a checkbox. Using the checkboxes next to each age class will change entries only in the F/C realisation. The realisation vector can be adjusted in (de-) selecting single age classes. Either a selection group realises in the first age class (all others a not selectable any more) or in further age classes (the first is not selectable any more). Please be very careful in using this option, because the complete
results are based on the realisation vectors. If age classes are selected for realisation, all automatic options are overwritten. If you want to deselect realisation at all, please deselect also all checkboxes in the age classes, not only realisation at all.

Realisation of logical selection groups can also be defined. If single selection groups are part of a logical selection group, the realisation must be defined for the complete logical selection groups, because age classes and their gene proportion will be calculated based on the whole logical group. If only one selection group within a logical realises, all other groups must be deselected in their age classes.

It is very important to check the realisation vectors on the gene-flow page for correct realisation of age classes. If you are not sure how to use this feature properly, please refer to the simple checkbox ‘realisation’ and do not use the realisation within age classes at all. In most cases this feature will not be needed.

The proportion of realisation of different selection groups (e.g. female breeding animals and female production animals) will be calculated using the size of a selection group. If the size of SG1 is 2000 and the size of SG2 is 4000 (both marked a realising), their proportion in the realisation vector will be 1:2. A proportion between breeding and production animals will not be given directly, but always calculated from the size if each selection group directly.

After setting basic information of a selection group, additional fields become available. A breeding goal can be defined, as a selection of traits linked to the given breed. Note that there are only traits selectable, which belong to the selected breed. Index source groups can also be selected from a list of further defined index groups. The further definition of index groups has an advantage of defining very common groups only once (e.g. own performance). Later this information needs only to be selected for each information source which is an own performance. Breeding goal and information source will define the selection index and can be composed by simple clicking.

If only one selection group has been defined, it will not be possible to define a relationship. Relationship should always be defined, when all the definition of selection groups is finished. It is recommended to define relationships at the end of this step using breeding program -> Pedigree matrix.

Logical selection groups

In most breeding programs a group of (male) animals will be selected in several steps, or they will be used differently for producing breeding and production animals. In this case each group of selected animals needs to be defined as separate selection group, the groups descending from the same animals of equal sex will later be combined in logical selection groups (using breeding program -> logical selection group -> new). All predefined selection groups can be combined to one or more logical groups. Grouping selection groups is not compulsory.

- Possible elements: All selection groups, which are not yet part of another logical selection group. Is a selection group already defined as a member of a logical, only selection groups of the same sex can be added. Male and female selection groups
can form a logical selection groups, but only selection groups of the same gender can be grouped together.

The pedigree matrix defines in its column all defined single selection groups, in its row only logical selection groups and not combine single selection groups. The pedigree matrix allows to define more than two groups to transfer genes (from = columns) to another (to = rows). The table fields allow values lower than one to define fractions. The sum of genes transferred from a number of selection groups to one receiving groups must not exceed 1.0 per sex.

**Multiple-Stage selection**

Within a logical selection group predefined groups can be declared to be selected from an already existing selection group. For each selection group a list of younger selection groups of the logical group will be available as predecessor groups. The age of each selection group (age of first reproduction) is used to identify possible predecessor groups. Once a selection group is defined as previous stage of selection, it is assumed that the second stage selection group will be selected from the first stage and the preselected animals are not normally distributed. All selection index information sources of the first stage will automatically descent into the second selection stage, if not yet defined there. A correlation between the two indexes will be calculated and the selection intensity of the second stage recalculated according to the first selection step.

It is not possible, from a technical view, to define several selection steps without defining index groups for each selection group. You must define a selection index for each selection group, because the algorithm needs a covariance between two indexes. If only an accuracy is defined and no selection index, you get no results.

If two selection groups have exact the same index, the correlation between the indexes is one and there is no result given! For reasonable results, the amount of information increases significantly from one selection group to another. The larger the difference between two selection indexes the better your result. It does not make any sense to define two selection groups in a multiple selection step if there is no increase in information. Reasonable selection decisions can only be made if index information increases between two steps. The same argumentation is valid for the number of selected animals. If the number of proven and selected animals is equal, the selection intensity will be zero and no result can be given for a multiple stage selection. In the multiple-stage selection procedure the selection intensity is derived from a multidimensional integration, which finds zero values under a multidimensional normal distribution. If the proportion of selected animals is 1, or near 1, no zero values can be found and an error message will be displayed.

Please note that this procedure is extremely computing intensive and can take a lot of time. We experienced a calculation time of approximately 50 seconds for a 5-step selection.
Selection index

After definition of traits, parameters, index groups and selection groups, a selection index can be calculated for each selection group with a defined breeding goal. For each selection group a number of predefined index groups can be chosen (already combined with measured traits) and combined with breeding goal traits, defined in selection group. After clicking the button ‘selection index’ the index will be displayed with all used matrices (P, G and C), also the variance of index and breeding goal, b-values and the accuracy.
Index source groups

Index source groups define information sources for selection candidates. They are only used for calculating selection indexes. Based on the size of the group and its relationship to the selection candidate, other index groups and within the group the accuracy of selection will be defined. Index groups are defined by basic data which will define basic information of each index groups:

- Name of group
- Number of individuals within the group
- Number of repeated measures per individual
- Relationship between group and selection candidate
- Relationship between members of the group
- Breed of group

Next to the field for the relationship to the selection candidate, a drop down list will be available. This drop list provides 16 predefined relationships. Instead of inserting all relationships by hand, this list automatically defines all relationships between index groups and selection candidates, within and between index groups, if they are also predefined. If two index groups contain the same animals, e.g. progeny of a bull, measured two times in milk yield, once in BCS, there is a field to define two predefined groups as being equal, the relationship between them is set to one.

Selecting a specific breed for an index source group has several advantages. The previously defined traits for the selected breed will automatically be available as drop down list. All defined parameters (correlations, variances, ...) are used by default. In cross breeding schemes, crossbred animals can be information sources for purebred animals, using genetic parameters of crossbreds.

Based on the defined group, available traits (further defined for the selected breed) are listed on the right side. The trait combination measured on each index group can be defined by simple selection (clicking green cross or red minus). It is important that the trait will be listed below the drop down list. If a trait is still a part of the drop down list, it is not selected yet.

If there is more than one index group defined, the relationship between groups can be defined on the bottom of the page. For two predefined groups, the relationship will be inserted automatically. It is recommended to use predefined index source groups whenever it is possible. Then, especially using a large lists of different index source groups, the relationships between groups and selection candidates will always be correct. Otherwise wrong numbers typed in by the user will be likely to occur.

Index groups are linked to one breed, because the parameters used to calculate the selection index are also linked to one breed. If there is at least one trait linked to an index group, the breed can not be changed anymore. To change the breed, deselect all traits.
Names of index groups are only defined within a breed, it is possible to have equal index group names (e.g. own performance) within each breed. During an import of breeds or breeding programs, index groups will also be imported without changing their names. Additional random effects, as defined in the traits, will only be recognised, when selected by clicking the correct checkbox. Using a litter effect is needed in fullsib groups, but not in halvesib groups. When more than one index source group is used in a selection index, the entry for 'same trait - different group' will only use random effects, if they are used in both index source groups.
Pedigree matrix

On this page it is possible to define the relationships between all selection groups. Here will be defined, which selection group transmits genes and which receives genes. All single defined selection groups will be shown at the header of the matrix. Only single defined selection groups can transmit genes to the groups shown in the first column. If selection groups are combined in a logical selection group, only the logical group in total is able to receive genes. The program automatically spreads the genes into the correct age classes, independently of which single selection group. Selection groups can receive genes from more than one parental group. It is necessary to define the exact proportion of genes received from each parental group. The proportions within sex must have the sum of exact one, otherwise an error will be shown. For easier overview, first all male selection groups, then all female selection groups are listed in the matrix.
Geneflow

The button Breeding program -> geneflow will display the gene flow matrix, realisation vectors (F/C and reproduction). Selecting geneflow shows results of M-vectors for a given investment period and the generation interval for given path of selection. This page does not offer any possibilities to change settings, it is only information for the user. Please use this page to check your breeding program, control reproduction vectors, geneflow from one selection group to each other. The page gives a good overview of the age classes and which selection group contributes genes to their offspring.
Show results

Display of basic results. Note that genetic gain and return are displayed per animal, not per selection group. Following results will be shown for each selection path:

- Proven animals
- Selected animals
- Proportion (of proven and selected animals)
- Gene offspring proportion (relative number of genes contributed by this path)
- $\sigma$ (genotype): standard deviation of the desired breeding goal
- $\sigma$ (index): standard deviation of given index
- Accuracy: of given selection index
- Gen. interval: generation interval
- Selection intensity
- SDE (F/C): Standardised discounted expressions, with realisation vector for F/C-trends
- SDE (Repro.): Standardised discounted expressions, with realisation vector for reproduction traits (repeated measurements)
- Total Return: Monetary genetic gain calculated using economic values weighted with standardised discounted expressions
  ○ (...) clicking this field opens results for each traits
- mGG: Genetic gain of all traits calculated using economic values not weighted with standardised discounted expressions.
  ○ (...) clicking this field opens results for each traits. Shown here is natural genetic gain per trait and path, not weighted with any economic value (GG).

Common results

Results combined from all paths of selection. Shows an overall generation interval, combines genetic return for all breeding goal traits and (Sum:) Total return of the breeding program after the given investment period.

Breeding costs

This table contains a detailed overview of the given costs in the breeding program. On top of the list, all fixed costs per animal within breed are shown. The average fixed costs per breed will be divided by number of proven animals in the selection groups.

Average fixed costs will be calculated by dividing the total sum of fixed cost by the total number of animals. This is the sum of the field ‘size’ for all selection groups and is also displayed on the breeding program page.

Average variable costs is a weighted average calculated with the sum of variable cost per selection group divided by total number of animals (sum of size).
Profit is the difference between the sum of returns (Common results) and sum of costs (Breeding costs). The result is expressed in a monetary value per animal for the investment period and discounted with interest and discount rates.

**Calculation of average breeding costs and profit**

The calculation of average breeding costs is a sum of all breeding costs defined in the breeding program.

**Fixed costs:** Fixed costs per animal as defined on the ‘breed’ page multiplied with the number of animals with fixed costs per selection group, discounted with discount rate for costs (main page) and the mean generation interval of each selection group. Sumed up over all selection groups. Fixed costs will occur each year of the same amount for each animals with fixed costs, so a mean age of animals within selection group will be used for the discount time.

**Variable costs:** Variable costs are defined in each selection group. The first possibility is a sum of costs, which will be discounted with the discount rate for costs (main page) and the generation interval of the specific selection group. The second possibility is the definition of cost groups on the ‘breed’ page. These groups can be selected for all selection groups of the same breed. A sub-selection of groups is possible as well as all variable cost groups. The variable cost groups are defined per animal, the number of animals with variable costs can be defined, the number of proven animals is the default value. For discounting a time value can be defined, as default the mean generation interval of the specific selection group will be used.

The definition of overall variable cost groups for each breed allows to display structured economic results, where the sources for costs are separated within each breed. All sources of costs (fixed and variable) are added to the total costs of a breeding program. To calculate the average costs per animal in the breeding program, the sum of all costs will be divided by the total size of the breeding program. The costs that occur during testing and selection will be calculated to be covered by each animal in the complete breeding program. To calculate this number, the values defined as ‘size’ of each selection group within a breed are summed up to a total population size.

The genetic gain calculated as breeding profit is also expressed as discounted breeding profit per animal. That means, the breeding program causes breeding profit in all animals in the population, not only in selected animals or realising animals. Breeding profit generated in bulls, for example, will be realised in their female offspring and contributes to the overall breeding profit.

The discounted return is calculated as an overall return in each animal in the population, so breeding costs have to be re-calculated for each animal in the population, too. Due to this reason the total costs of the breeding program is divided by the whole population size. The larger the population size, the lower the costs per animal and the more likely is a positive profit of the breeding program system.
ZPLAN+ XML Import/Export

ZPLAN+ supports ex- and import of data using the XML format. This feature can be used to export breeding programs and exchange them between users or store them outside the database. It is recommended not to edit the XML-file, otherwise it cannot be imported anymore if the structure has been changed.

Data Export

Export of complete breeding programs can be done on the main breeding program page. On the right side a button with ‘XML Export’ is available. Using this will automatically save your whole breeding program including breeds, selection groups, index source groups. The XML-file will automatically be saved. If you can not define a folder to save the file, adjust your Firefox-Browser using 'Extras-Settings'. Export of breeds only is also possible. Open the breeds page of your project and click the button ‘XML Export’ and information of the breed (traits, parameters, correlations,...) will be saved. This helps to exchange complex breed information between users. Within your own username you do not have to import breeds, because all breeds defined are available for all projects- old an new ones.

Data Import

For Import, only one button is available at the main page. The program automatically recognises if the XML-file contains a breed or a complete breeding program. The breeding program or breed is identified by its name. If a breeding program or breed already exists, a ‘+’ is automatically added to avoid duplicate names.
ZPLAN+ JSON Import/Export

The new version of ZPLAN+ supports export and import of data using the JSON format.

Data Export

Opposite to the XML export the JSON exports provides just parts of the breeding program data: the breeding program and the lists selectionGroups and indexSourceGroups. The data will be exported as text and may be edited manually or by an external script or program.

Data Import

At the import, a breeding program is identified by its name. Therefore a breeding program can only be imported by a user which has the matching breeding program in his portfolio. The import creates not a new breeding program but replaces existing values given by the JSON data. Also values of matching selection groups and index source groups are changed if a matching group was found.

Conventions:

- Variable names and values are separated by colon (:).
- Variable names and string values must be set in double quotes (").
- Number and boolean values are set without quotes.
- Objects (structures) are set in brackets ().
- Identifier-value pairs are separated by comma (,).
- Arrays/lists are set in squared brackets ([ ]).

Data types

<table>
<thead>
<tr>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>boolean</td>
<td>Boolean expression [true</td>
</tr>
<tr>
<td>double</td>
<td>Floating point number (64bit IEEE 754)</td>
</tr>
<tr>
<td>long</td>
<td>Integer (64 bit)</td>
</tr>
<tr>
<td>String</td>
<td>Text/character</td>
</tr>
</tbody>
</table>

Breeding program:

```json
name : String
selectiongroups : SelectionGroup[]
indexSourceGroups : IndexSourceGroup[]
```

SelectionGroup:

```json
name : String
production : boolean
productiveLifetime : double
proven : double
```
realization : boolean
remain1 : double
remain2 : double
reproductionCycle : double
selected : double
size : long
useReliability : boolean
variableCosts : double

IndexSourceGroup:
name : String
numberOfIndividuals : Long
numberOfMeasures : Long

Example
{
   "name" : "Breeding program 1",
   "selectionGroups" :
   [
      // open array selectiongroups
      {
         // open 1.Selectiongroup
         "name" : "sg long",
         "production" : false,
         "productiveLifetime" : 8.0,
         "proven" : 100.0,
         "realization" : false,
         "remain1" : 1.0,
         "remain2" : 1.0,
         "reproductionCycle" : 1.0,
         "selected" : 10.0,
         "size" : 1000,
         "useReliability" : true,
         "variableCosts" : 12.34
      },
      // close 1. selectionGroup
      { ... } // 2. Selection group
   ],
   // close array selectiongroups
   "indexSourceGroups" :
   [
      // open Array indexSourceGroups
      {
         // open 1. IndexSourceGroup
         "name" : "EL_Prod",
         "numberOfIndividuals" : 1,
         "numberOfMeasures" : 1
      },
      // close IndexSourceGroup
      { ... } // 2. IndexSourceGroup
   ],
   // close Array indexSourceGroups
JSON

JSON (JavaScript Object Notation) is a lightweight data-interchange format. It is easy for humans to read and write. It is easy for machines to parse and generate. It is based on a subset of the JavaScript Programming Language, Standard ECMA-262 3rd Edition - December 1999. JSON is a text format that is completely language independent but uses conventions that are familiar to programmers of the C-family of languages, including C, C++, C#, Java, JavaScript, Perl, Python, and many others. These properties make JSON an ideal data-interchange language. ([http://json.org](http://json.org))

Links

- JSON.org
- Wikipedia
- Wikipedia (deutsch)
FAQ - Frequently Asked Questions

**General questions**

Q: Why were my changes not saved?
A: The program runs on a server. You open a client in your web browser. If you change something on your screen, the server will not notice until you tell him. Normally it works, when you press enter. Then a message will be sent to the server and your changes are saved in the database. Sometimes the communication between server and client is not so easy. I recommend to save your changes regularly using the 'save' button which is available on every page. Then you can be sure your changes were sent to the server and saved.

**Selection groups**

Q: Why do I get a message that the given survival rate is too small?
A: The survival rate calculates the number of animals in the next age class. If a selection group (100 animals) is defined of having a productive lifetime of 4 time units and a survival rate of 0.9, 25 of all animals are in age class 1, then 25*0.9 = 22.5 in age class 2, 22.5*0.9 = 20.25 in age class 3 and 20.25*0.9 = 18.225 in age class 4. The sum of all 4 age classes then is 25+22.5+20.25+18.225 = 85.975. To fill up to 100 animals the program adds new age classes, until the given number of 100 animals is reached in sum. In this example it add one age class with 14.025 animals and the calculated lifetime is 5.
If the survival rate is only 0.1, it will never be possible to add age classes to have a sum of 100 animals, try it by yourself. If there are more than 40 age classes needed to sum up to 100% the program stops with an error.

Q: Why can’t I change the breed of my selection group anymore?
A: Eventually you have already linked a trait a breeding goal to the selection group. Deselect all traits, then you should be able to chose a different breed.

**Index Source Groups**

Q: Which traits are available in the index source group page?
A: You may choose from traits that are neither already element of the traits (to measure) list of the current group nor element of a group that is marked as identical group of the current group.

Q: Which index source groups are selectable from the identical groups list.
A: The select box identical with contains groups which have the same candidate relationship as the current group and have disjoint traits.
Q: Why can’t the last trait be removed?
A: The last trait can’t be removed if the group is referenced by a selection index of a selection group. Remove the current index source group from the selection index data of that selection group and the trait will be removable.

Q: I change the number of animals in my index source group, but the accuracy of the selection index does not change
A: You likely have not linked the index source group to any selection group

Q: I change the number of measures per animal in my index source group, but the accuracy of the selection index does not change
A: You likely have not linked the index source group to any selection group, or the repeatability is zero (this has been fixed in version 1.0.0-beta-6)

Results

Q: Why is the accuracy on the results page equal to the result on the selection index page, but the standard deviation of index and breeding goal is different?
A: On the selection index page, the b-Values are calculated using $b=\text{inv}(P)*G*v$ with $v=$ economic values. These economic values are not discounted. On the Results-page the standard deviation of the index is shown using discounted economic values. The standard deviations are different but their relation is equal.

JSON Datatransfer

Q: What is JSON Data-Transfer for?
A: The JSON Data-Transfer may be used to export partial breeding program data to use it Eg. in an external calculation software. It is also possible to import breeding program data in JSON Format to ZPLAN.
Breeding programs are identified by their name. Due to the restrictions to the specified datatransfer format (breeding program data is not mapping a complete record) it’s only possible to update existing breeding programs of the current user.

Q: What is JSON
A: JSON (JavaScript Object Notation) is a lightweight data-interchange format. It is easy for humans to read and write. It is easy for machines to parse and generate. It is based on a subset of the JavaScript Programming Language, Standard ECMA-262 3rd Edition - December 1999. JSON is a text format that is completely language independent but uses conventions that are familiar to programmers of the C-family of languages, including C, C++, C#, Java, JavaScript, Perl, Python, and many others. These properties make JSON an ideal data-interchange language.
(http://json.org)