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FRIEDRICH-LOEFFLER-INSTITUT
FLI
Bundesforschungsinstitut für Tiergesundheit
Federal Research Institute for Animal Health

A Software Pipeline for Animal Genetic Evaluation

QS@breeding

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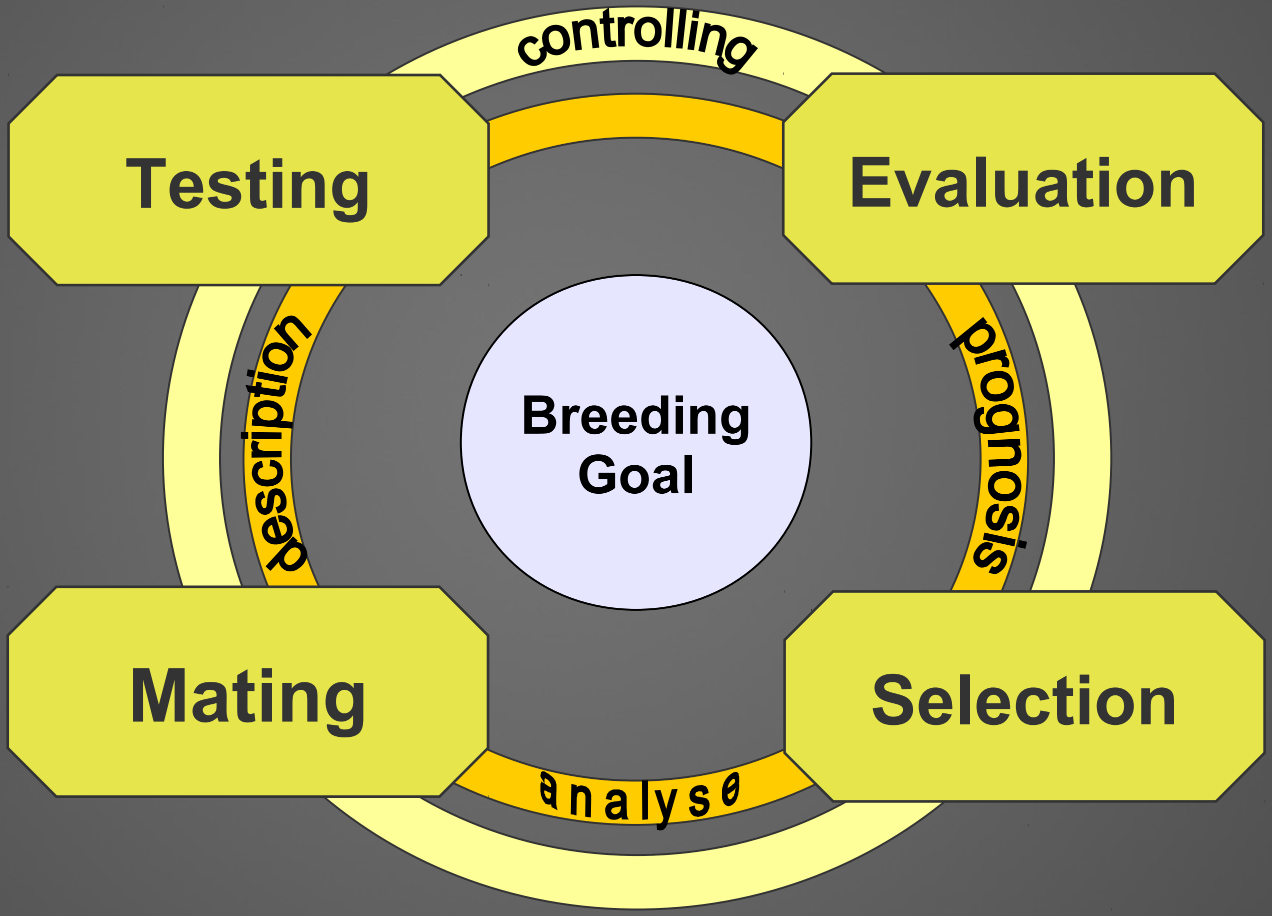
How to set up a breeding program

- Population and its structure
- Breeding goal
- Testing
- Genetic evaluation
- Publish results
- Selection

A Breeding Program



controlling

Testing

Evaluation

description

Breeding Goal

prognosis

Mating

Selection

analyse

Genetic Evaluation

- Genetic improvement
  - Defining breeding objectives
  - Identifying future parents
- BLUP
- Software assistances

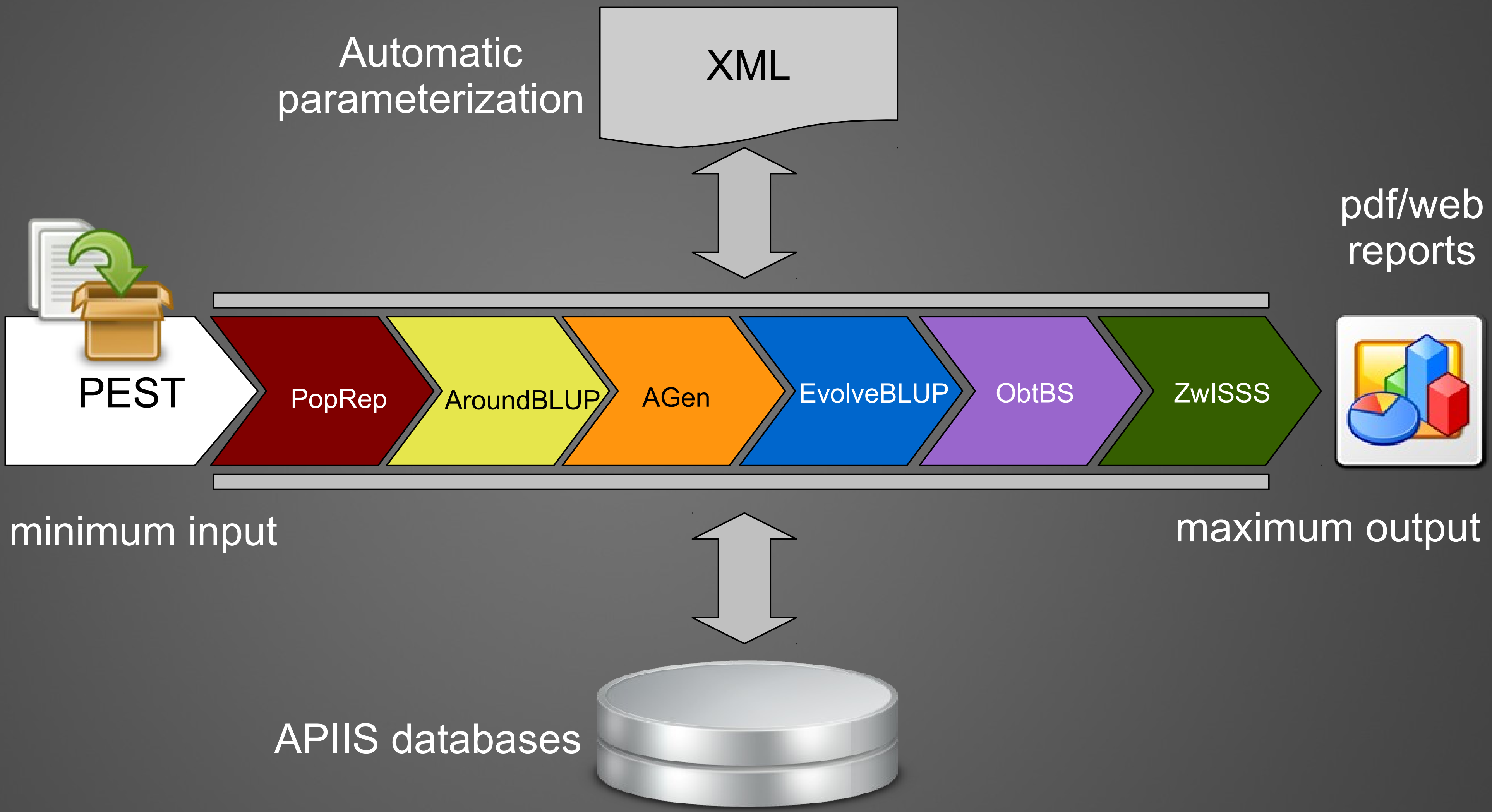
Chain of processing

- Data collection: pedigree, measurements
- Analysis of data
- Analysis of BLUE and BLUP
- Aggregate genotypes
- BLUP over time
- Breeding values
- ...

Packages developed previously

- **APIIS**: Setting up integrated animal databases
- **PEST**: Computing breeding values
- **PopRep**: Checking pedigree & creating pop reports
- **AGen**: Computing aggregate genotypes
- **AfterBLUP**: Analyzing BLUE & BLUP
- **EvolveBLUP**: Monitoring BLUP over time
- **ZwISSS**: Publishing breeding values
- **OptBS**: Optimizing the structure of breeding programs

What is our solution?



Automatic parameterization

XML

pdf/web reports

PEST

PopRep

AroundBLUP

AGen

EvolveBLUP

ObtBS

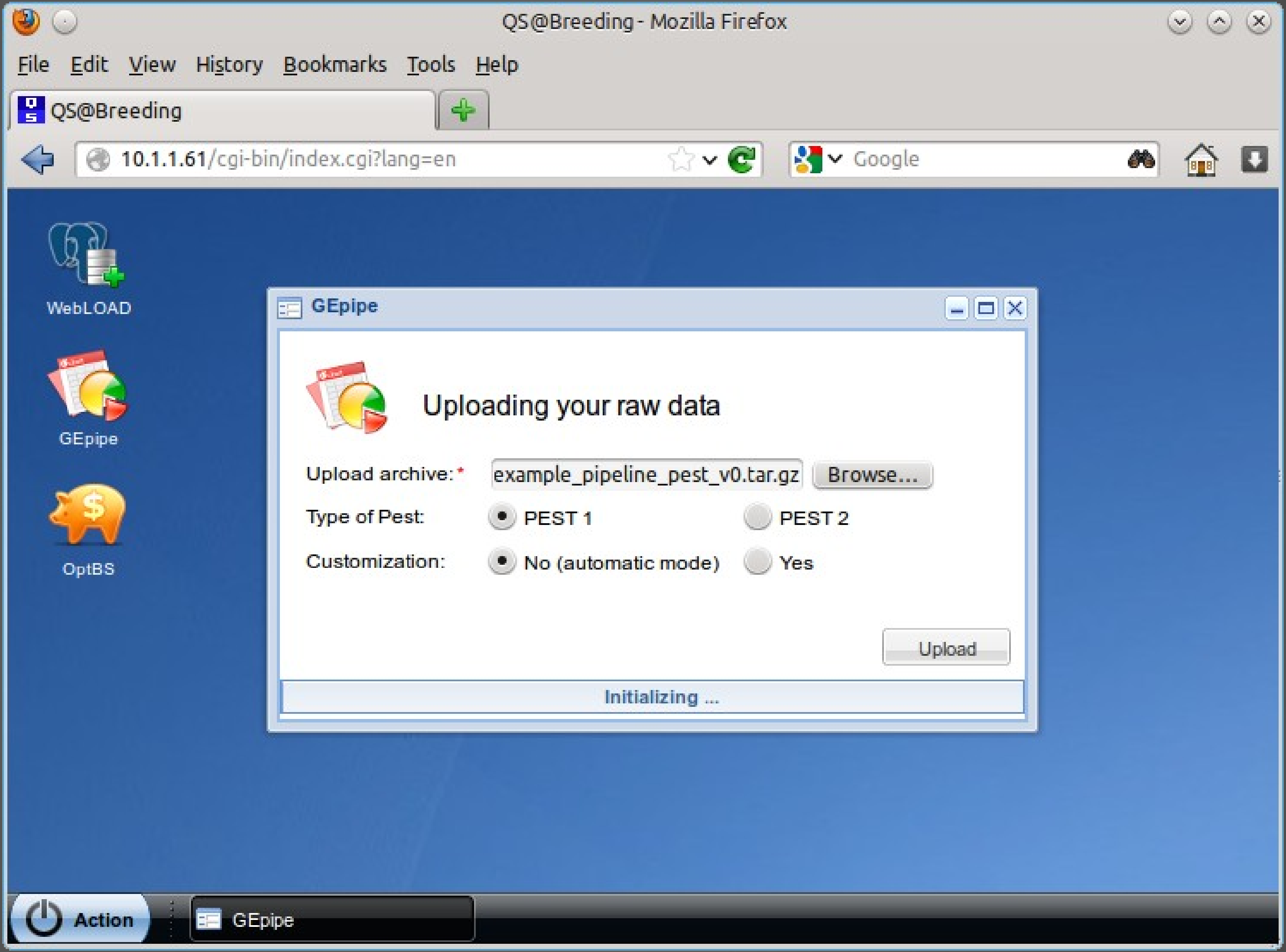
ZwISSS

minimum input

maximum output

APIIS databases

Start by uploading PEST data



Uploading your raw data

Upload archive:* example_pipeline_pest_v0.tar.gz

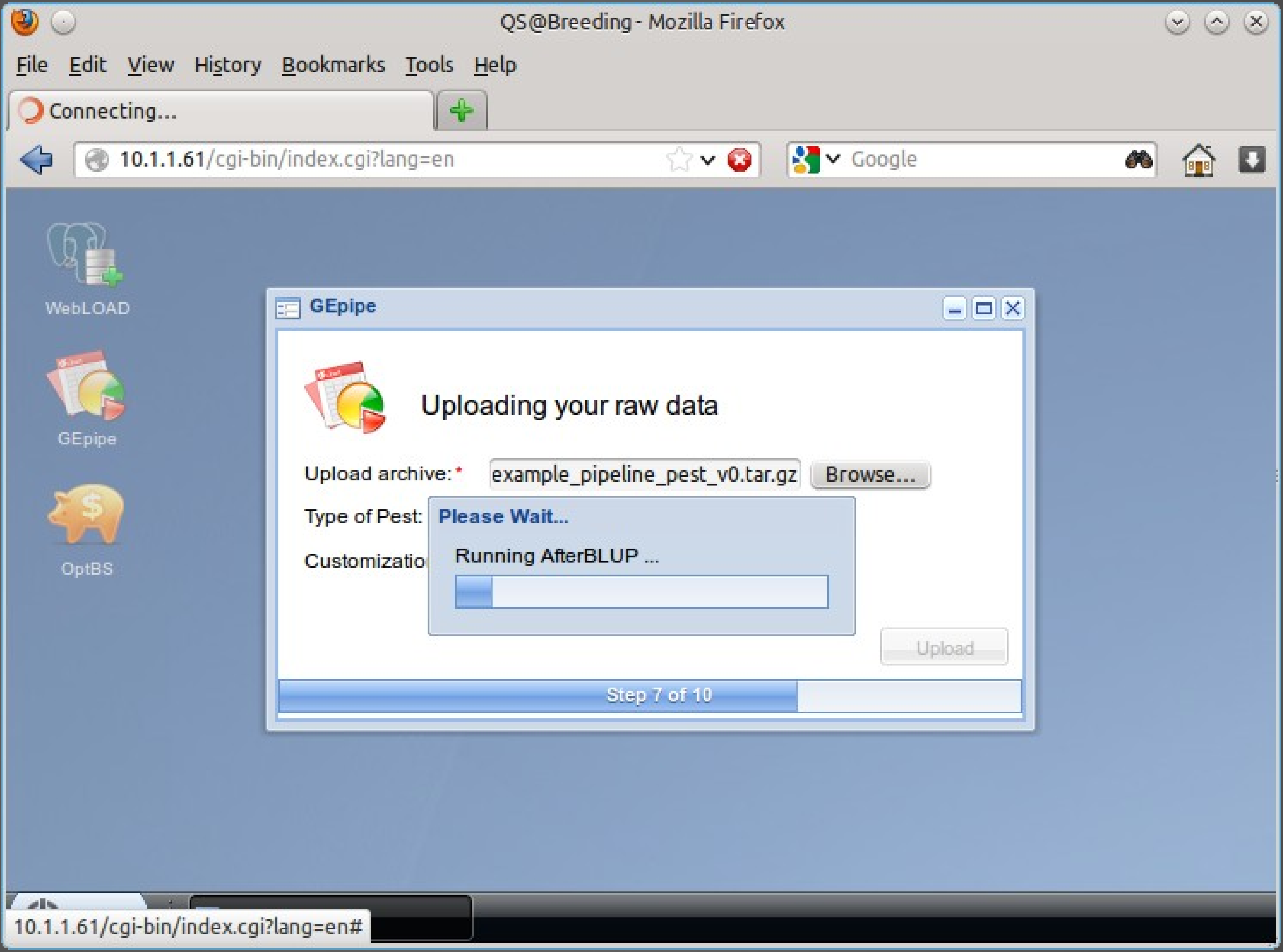
Type of Pest: ● PEST 1 ○ PEST 2

Customization: ● No (automatic mode) ○ Yes

Initializing ...

GEPipe A Software Pipeline for Animal Genetic Evaluation

Run sub-systems automatically



Uploading your raw data

Upload archive:* example_pipeline_pest_v0.tar.gz

Type of Pest:

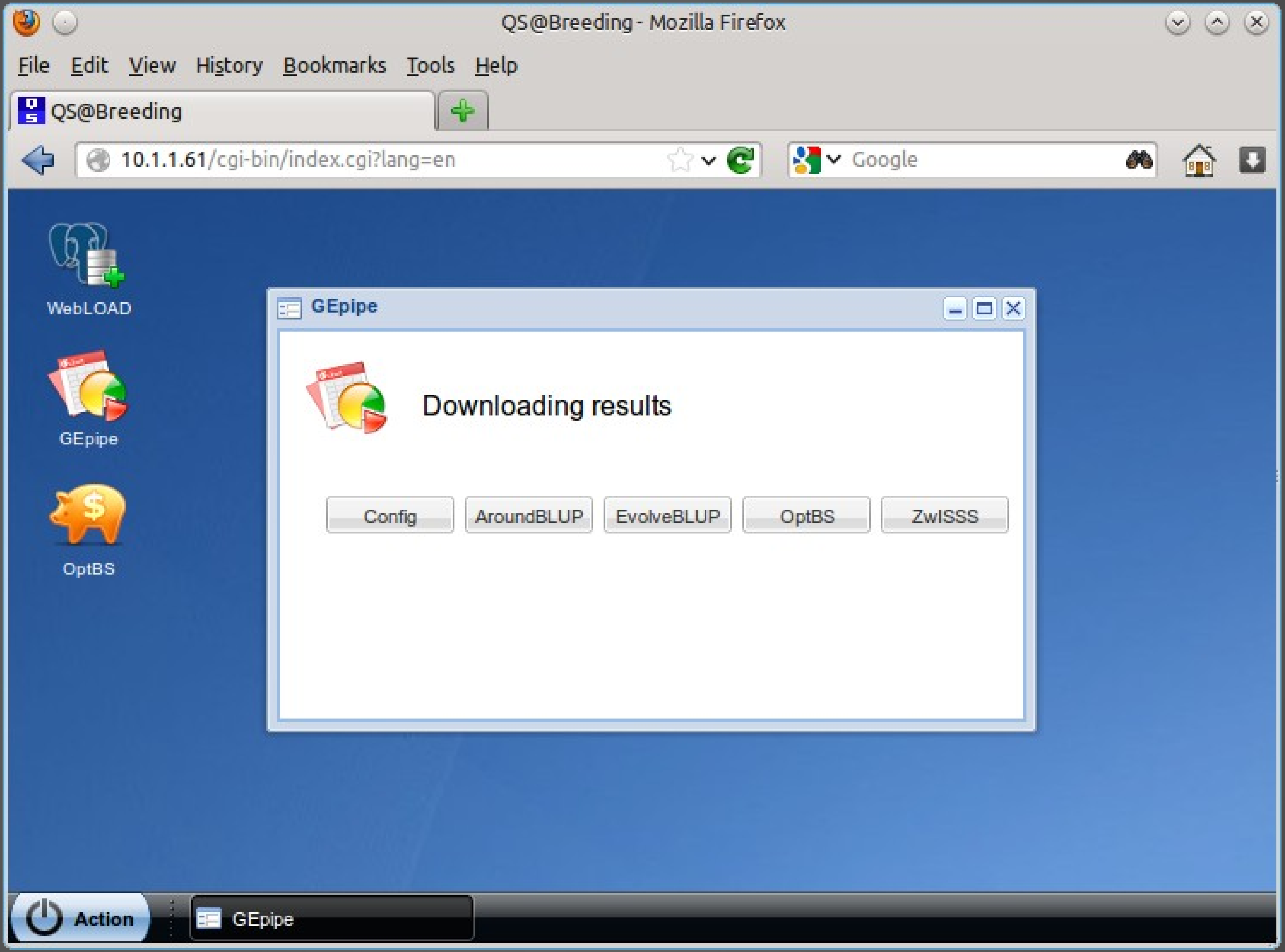
Customizatio

Please Wait...

Running AfterBLUP ...

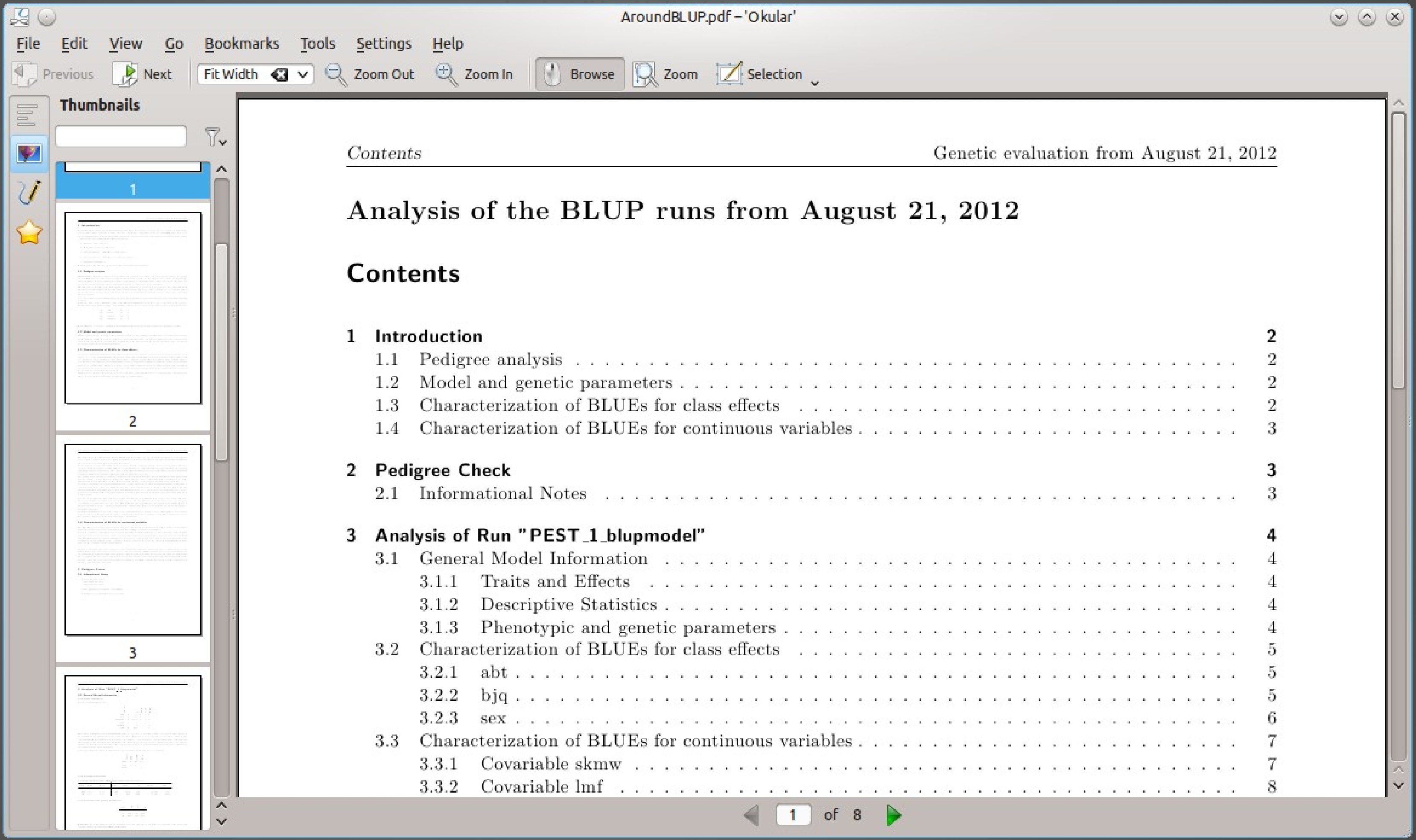
Step 7 of 10

Provide complete documentation



Downloading results

AroundBLUP results



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Analysis of the BLUP runs from August 21, 2012

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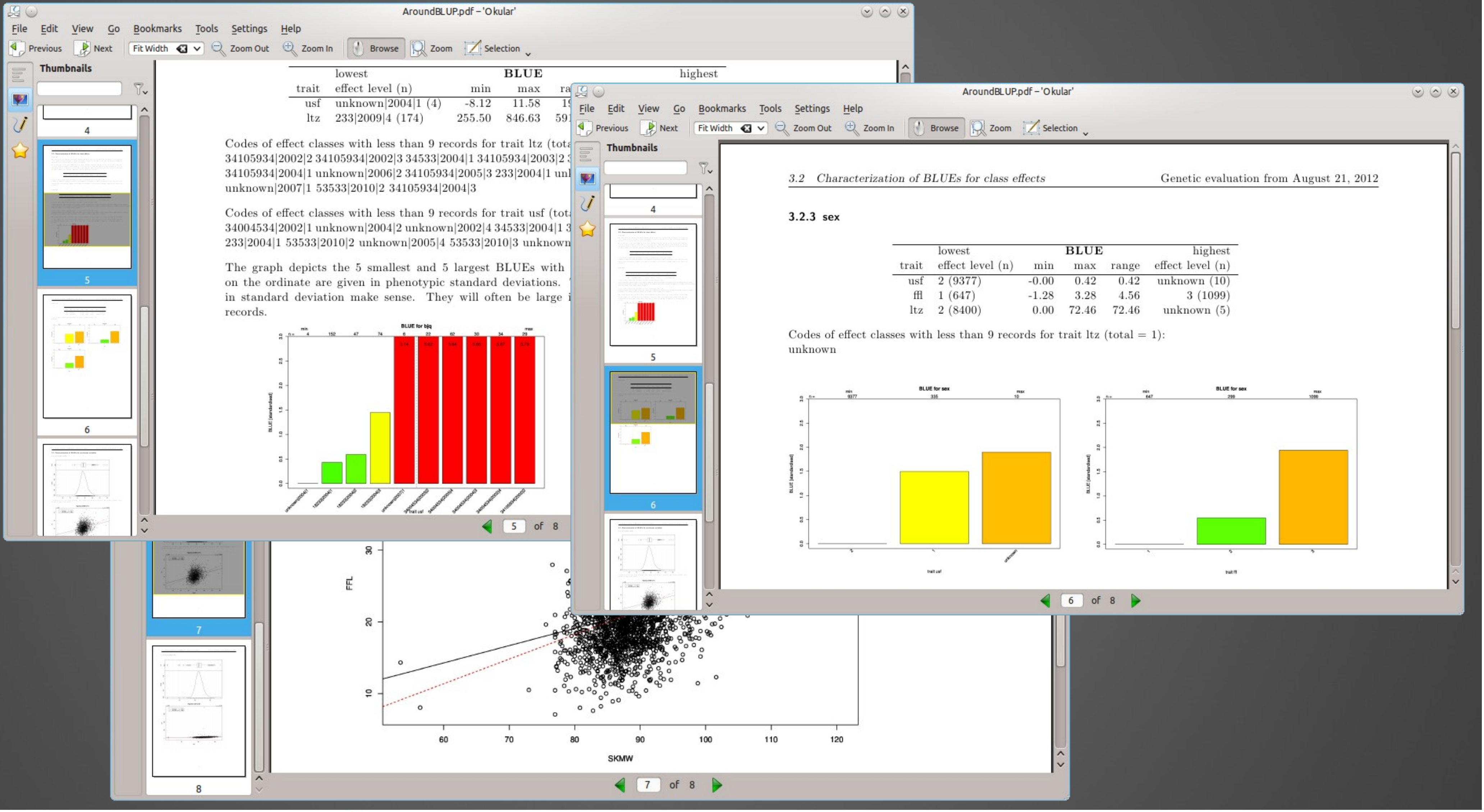
AroundBLUP results



	lowest	BLUE		
trait	effect level (n)	min	max	ra
usf	unknown|2004|1 (4)	-8.12	11.58	19
ltz	233|2009|4 (174)	255.50	846.63	591

Codes of effect classes with less than 9 records for trait ltz (tota
34105934|2002|2 34105934|2002|3 34533|2004|1 34105934|2003|2
34105934|2004|1 unknown|2006|2 34105934|2005|3 233|2004|1 unl
unknown|2007|1 53533|2010|2 34105934|2004|3

Codes of effect classes with less than 9 records for trait usf (tota
34004534|2002|1 unknown|2004|2 unknown|2002|4 34533|2004|1 3
233|2004|1 53533|2010|2 unknown|2005|4 53533|2010|3 unknown

The graph depicts the 5 smallest and 5 largest BLUEs with
on the ordinate are given in phenotypic standard deviations.
in standard deviation make sense. They will often be large i
records.

3.2 Characterization of BLUEs for class effects Genetic evaluation from August 21, 2012

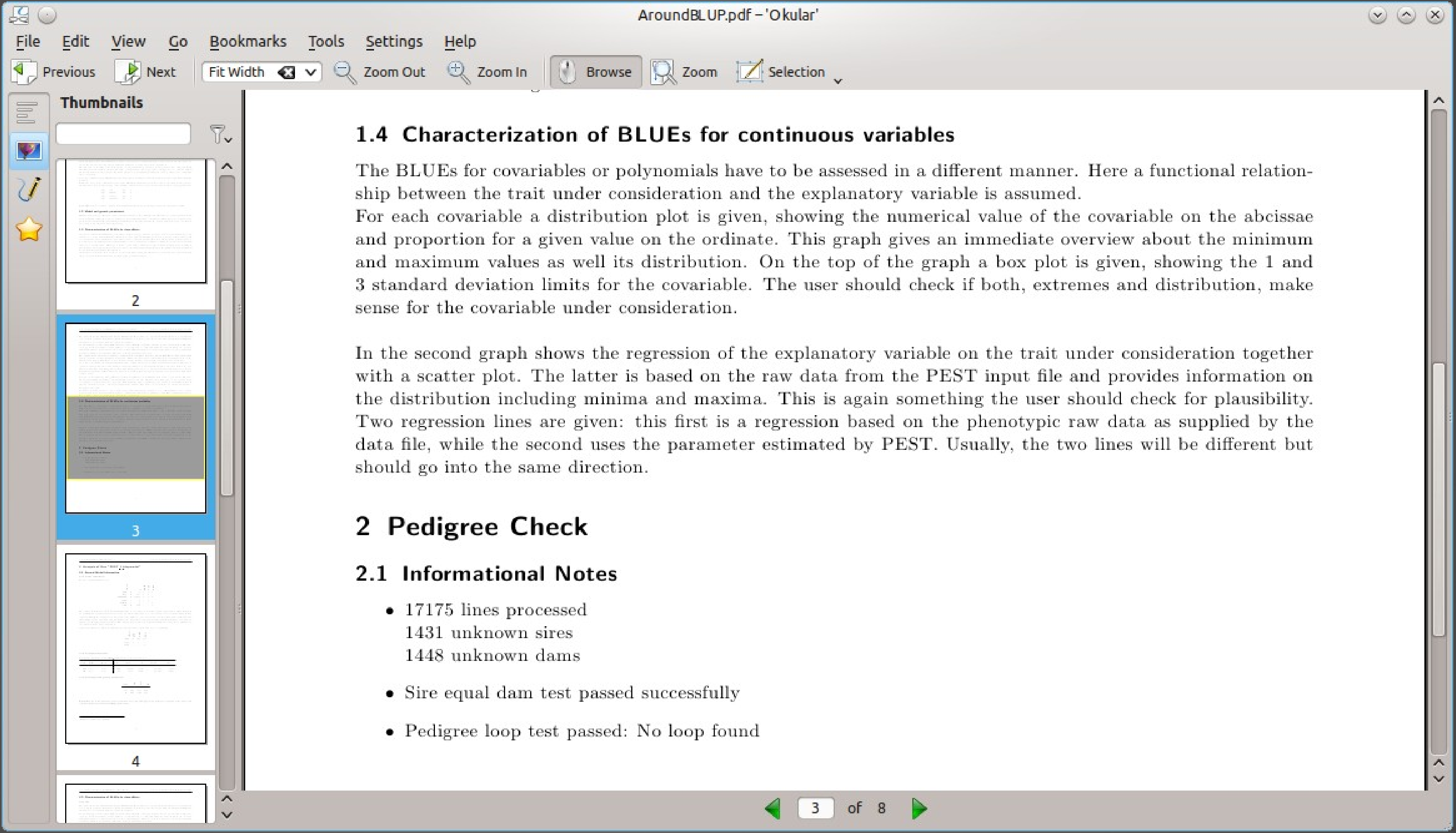
3.2.3 sex

	lowest	BLUE			highest
trait	effect level (n)	min	max	range	effect level (n)
usf	2 (9377)	-0.00	0.42	0.42	unknown (10)
ffl	1 (647)	-1.28	3.28	4.56	3 (1099)
ltz	2 (8400)	0.00	72.46	72.46	unknown (5)

Codes of effect classes with less than 9 records for trait ltz (total = 1):
unknown

GEPipe A Software Pipeline for Animal Genetic Evaluation

PopRep results



1.4 Characterization of BLUEs for continuous variables

The BLUEs for covariables or polynomials have to be assessed in a different manner. Here a functional relationship between the trait under consideration and the explanatory variable is assumed.
For each covariable a distribution plot is given, showing the numerical value of the covariable on the abcissae and proportion for a given value on the ordinate. This graph gives an immediate overview about the minimum and maximum values as well its distribution. On the top of the graph a box plot is given, showing the 1 and 3 standard deviation limits for the covariable. The user should check if both, extremes and distribution, make sense for the covariable under consideration.

In the second graph shows the regression of the explanatory variable on the trait under consideration together with a scatter plot. The latter is based on the raw data from the PEST input file and provides information on the distribution including minima and maxima. This is again something the user should check for plausibility. Two regression lines are given: this first is a regression based on the phenotypic raw data as supplied by the data file, while the second uses the parameter estimated by PEST. Usually, the two lines will be different but should go into the same direction.

2 Pedigree Check

2.1 Informational Notes

- 17175 lines processed
  1431 unknown sires
  1448 unknown dams
- Sire equal dam test passed successfully
- Pedigree loop test passed: No loop found

EvolveBLUP results

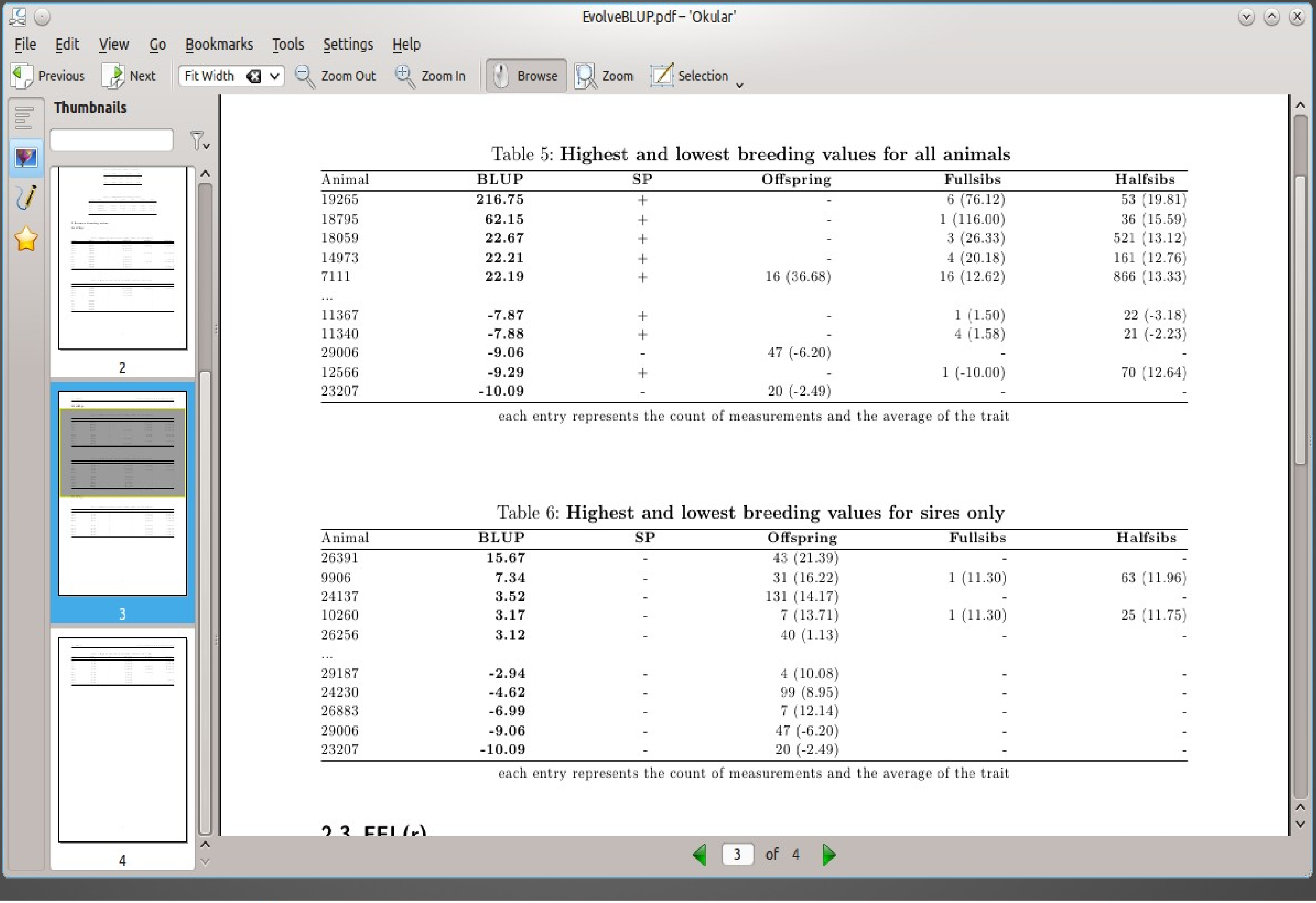


Table 5: **Highest and lowest breeding values for all animals**

Animal	BLUP	SP	Offspring	Fullsibs	Halfsibs
19265	**216.75**	+	-	6 (76.12)	53 (19.81)
18795	**62.15**	+	-	1 (116.00)	36 (15.59)
18059	**22.67**	+	-	3 (26.33)	521 (13.12)
14973	**22.21**	+	-	4 (20.18)	161 (12.76)
7111	**22.19**	+	16 (36.68)	16 (12.62)	866 (13.33)
...					
11367	**-7.87**	+	-	1 (1.50)	22 (-3.18)
11340	**-7.88**	+	-	4 (1.58)	21 (-2.23)
29006	**-9.06**	-	47 (-6.20)	-	-
12566	**-9.29**	+	-	1 (-10.00)	70 (12.64)
23207	**-10.09**	-	20 (-2.49)	-	-

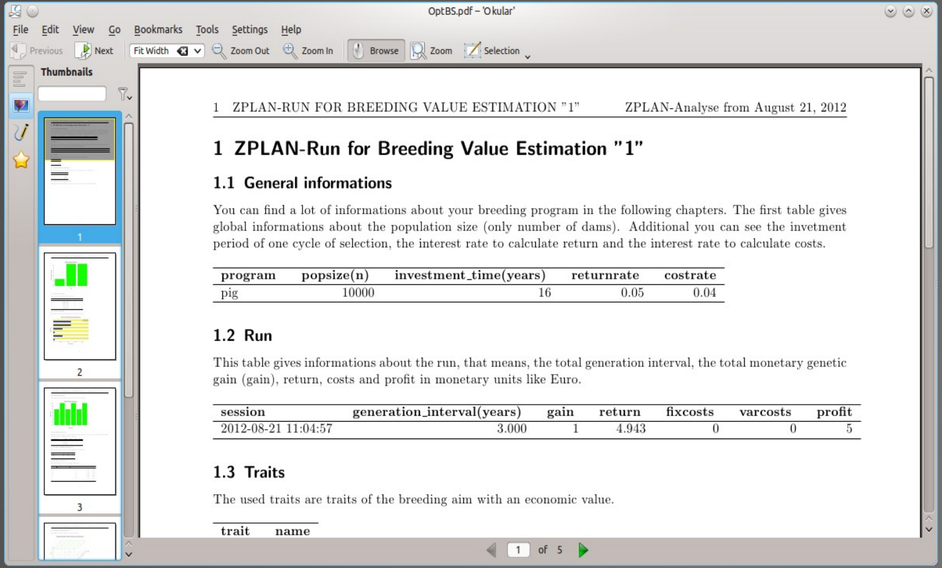
each entry represents the count of measurements and the average of the trait

Table 6: **Highest and lowest breeding values for sires only**

Animal	BLUP	SP	Offspring	Fullsibs	Halfsibs
26391	**15.67**	-	43 (21.39)	-	-
9906	**7.34**	-	31 (16.22)	1 (11.30)	63 (11.96)
24137	**3.52**	-	131 (14.17)	-	-
10260	**3.17**	-	7 (13.71)	1 (11.30)	25 (11.75)
26256	**3.12**	-	40 (1.13)	-	-
...					
29187	**-2.94**	-	4 (10.08)	-	-
24230	**-4.62**	-	99 (8.95)	-	-
26883	**-6.99**	-	7 (12.14)	-	-
29006	**-9.06**	-	47 (-6.20)	-	-
23207	**-10.09**	-	20 (-2.49)	-	-

each entry represents the count of measurements and the average of the trait

OptBS results



1 ZPLAN-RUN FOR BREEDING VALUE ESTIMATION "1" ZPLAN-Analyse from August 21, 2012

1 ZPLAN-Run for Breeding Value Estimation "1"

1.1 General informations

You can find a lot of informations about your breeding program in the following chapters. The first table gives global informations about the population size (only number of dams). Additional you can see the invetment period of one cycle of selection, the interest rate to calculate return and the interest rate to calculate costs.

program	popsize(n)	investment_time(years)	returnrate	costrate
pig	10000	16	0.05	0.04

1.2 Run

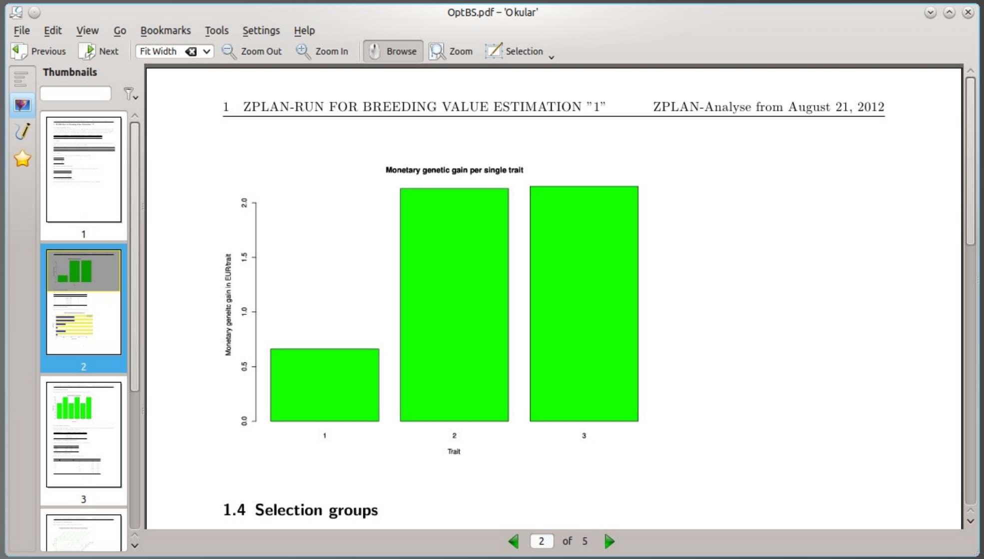
This table gives informations about the run, that means, the total generation interval, the total monetary genetic gain (gain), return, costs and profit in monetary units like Euro.

session	generation_interval(years)	gain	return	fixcosts	varcosts	profit
2012-08-21 11:04:57	3.000	1	4.943	0	0	5

1.3 Traits

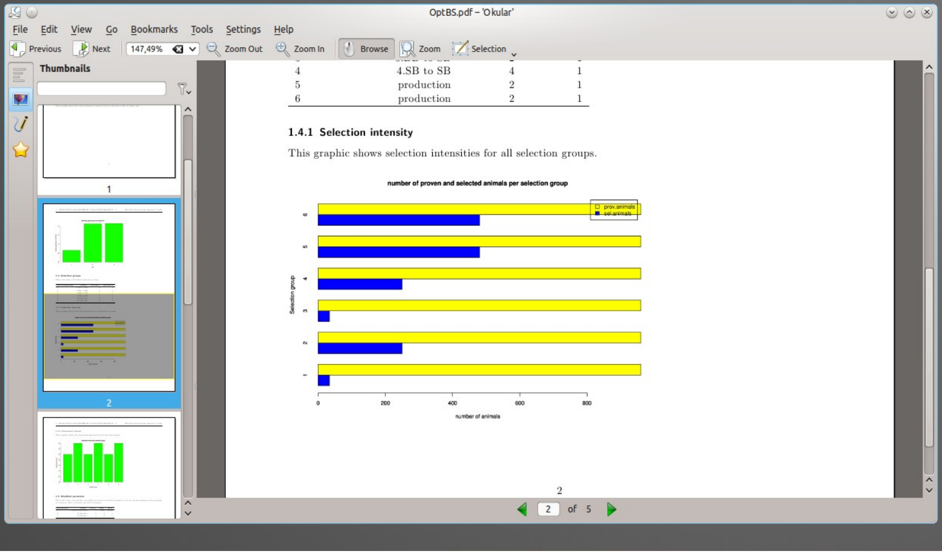
The used traits are traits of the breeding aim with an economic value.

trait	name



1 ZPLAN-RUN FOR BREEDING VALUE ESTIMATION "1" ZPLAN-Analyse from August 21, 2012

1.4 Selection groups

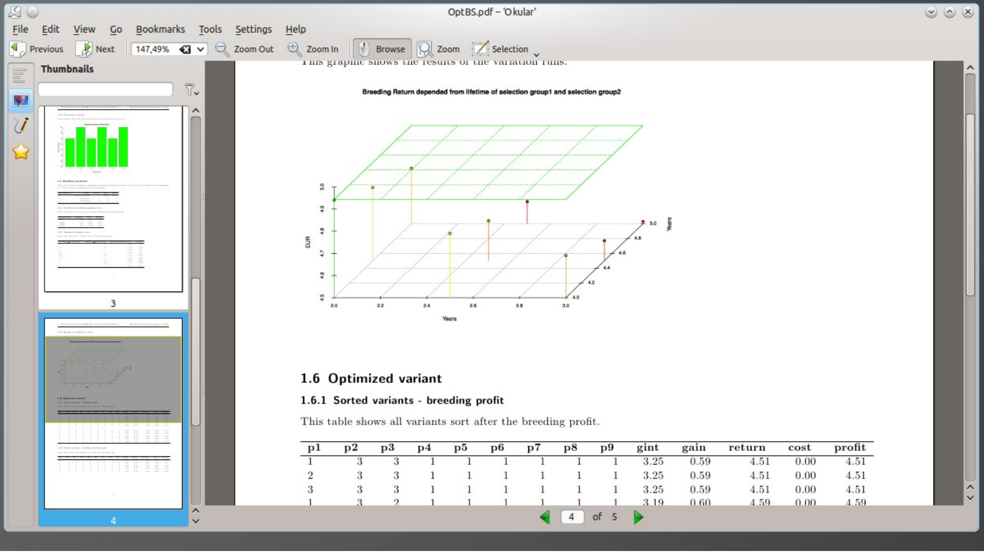


4	4.SB to SB	4	1
5	production	2	1
6	production	2	1

1.4.1 Selection intensity

This graphic shows selection intensities for all selection groups.

2



This graphic shows the results of the variation runs.

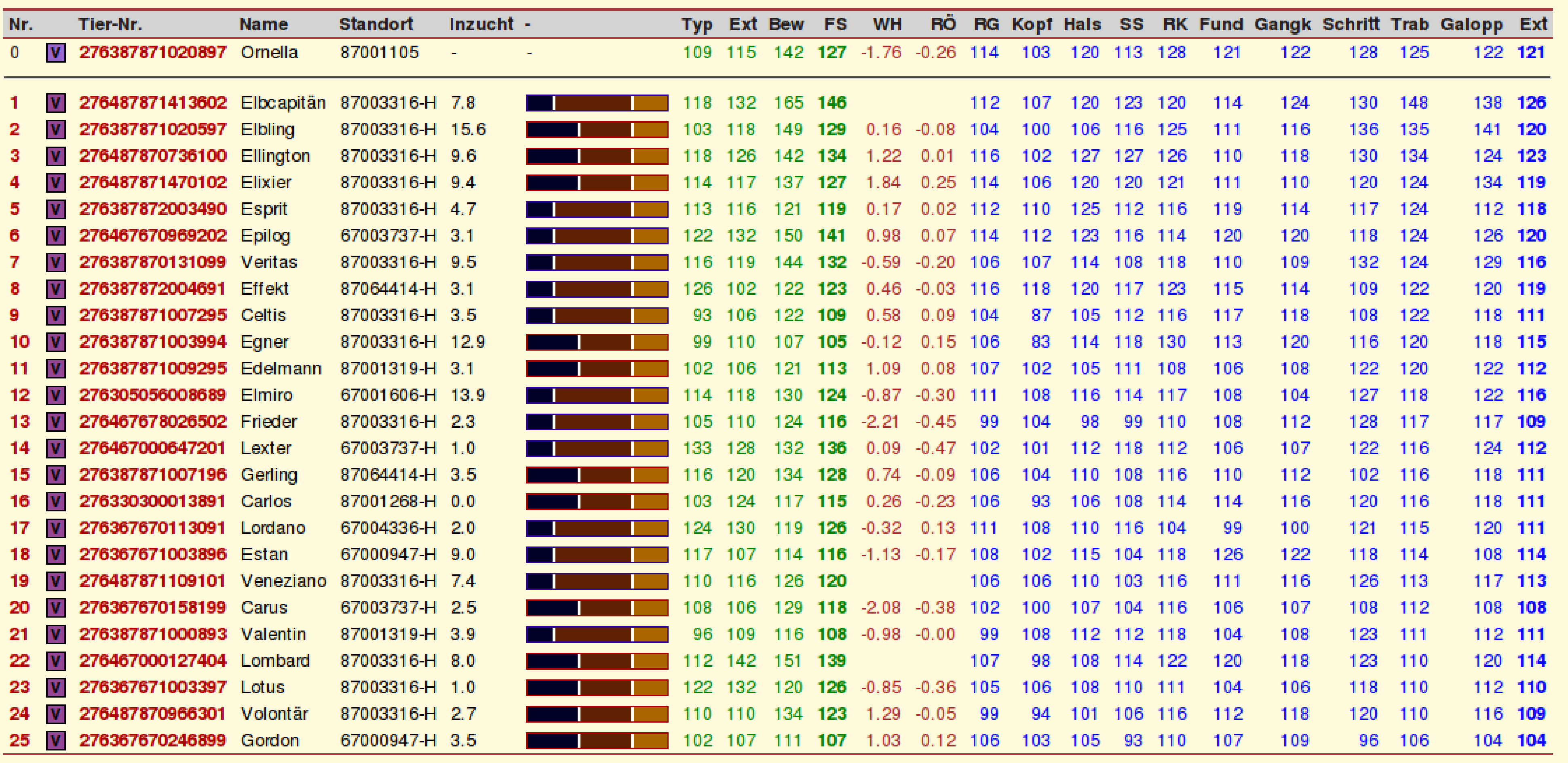
1.6 Optimized variant

1.6.1 Sorted variants - breeding profit

This table shows all variants sort after the breeding profit.

p1	p2	p3	p4	p5	p6	p7	p8	p9	gint	gain	return	cost	profit
1	3	3	1	1	1	1	1	1	3.25	0.59	4.51	0.00	4.51
2	3	3	1	1	1	1	1	1	3.25	0.59	4.51	0.00	4.51
3	3	3	1	1	1	1	1	1	3.25	0.59	4.51	0.00	4.51
1	3	2	1	1	1	1	1	1	3.19	0.60	4.59	0.00	4.59

ZwISSS results



Nr.		Tier-Nr.	Name	Standort	Inzucht	-	Typ	Ext	Bew	FS	WH	RÖ	RG	Kopf	Hals	SS	RK	Fund	Gangk	Schritt	Trab	Galopp	Ext
0	V	**276387871020897**	Ornella	87001105	-	-	109	115	142	**127**	-1.76	-0.26	114	103	120	113	128	121	122	128	125	122	**121**
1	V	**276487871413602**	Elbcapitän	87003316-H	7.8		118	132	165	**146**			112	107	120	123	120	114	124	130	148	138	**126**
2	V	**276387871020597**	Elbling	87003316-H	15.6		103	118	149	**129**	0.16	-0.08	104	100	106	116	125	111	116	136	135	141	**120**
3	V	**276487870736100**	Ellington	87003316-H	9.6		118	126	142	**134**	1.22	0.01	116	102	127	127	126	110	118	130	134	124	**123**
4	V	**276487871470102**	Elixier	87003316-H	9.4		114	117	137	**127**	1.84	0.25	114	106	120	120	121	111	110	120	124	134	**119**
5	V	**276387872003490**	Esprit	87003316-H	4.7		113	116	121	**119**	0.17	0.02	112	110	125	112	116	119	114	117	124	112	**118**
6	V	**276467670969202**	Epilog	67003737-H	3.1		122	132	150	**141**	0.98	0.07	114	112	123	116	114	120	120	118	124	126	**120**
7	V	**276387870131099**	Veritas	87003316-H	9.5		116	119	144	**132**	-0.59	-0.20	106	107	114	108	118	110	109	132	124	129	**116**
8	V	**276387872004691**	Effekt	87064414-H	3.1		126	102	122	**123**	0.46	-0.03	116	118	120	117	123	115	114	109	122	120	**119**
9	V	**276387871007295**	Celtis	87003316-H	3.5		93	106	122	**109**	0.58	0.09	104	87	105	112	116	117	118	108	122	118	**111**
10	V	**276387871003994**	Egner	87003316-H	12.9		99	110	107	**105**	-0.12	0.15	106	83	114	118	130	113	120	116	120	118	**115**
11	V	**276387871009295**	Edelmann	87001319-H	3.1		102	106	121	**113**	1.09	0.08	107	102	105	111	108	106	108	122	120	122	**112**
12	V	**276305056008689**	Elmiro	67001606-H	13.9		114	118	130	**124**	-0.87	-0.30	111	108	116	114	117	108	104	127	118	122	**116**
13	V	**276467678026502**	Frieder	87003316-H	2.3		105	110	124	**116**	-2.21	-0.45	99	104	98	99	110	108	112	128	117	117	**109**
14	V	**276467000647201**	Lexter	67003737-H	1.0		133	128	132	**136**	0.09	-0.47	102	101	112	118	112	106	107	122	116	124	**112**
15	V	**276387871007196**	Gerling	87064414-H	3.5		116	120	134	**128**	0.74	-0.09	106	104	110	108	116	110	112	102	116	118	**111**
16	V	**276330300013891**	Carlos	87001268-H	0.0		103	124	117	**115**	0.26	-0.23	106	93	106	108	114	114	116	120	116	118	**111**
17	V	**276367670113091**	Lordano	67004336-H	2.0		124	130	119	**126**	-0.32	0.13	111	108	110	116	104	99	100	121	115	120	**111**
18	V	**276367671003896**	Estan	67000947-H	9.0		117	107	114	**116**	-1.13	-0.17	108	102	115	104	118	126	122	118	114	108	**114**
19	V	**276487871109101**	Veneziano	87003316-H	7.4		110	116	126	**120**			106	106	110	103	116	111	116	126	113	117	**113**
20	V	**276367670158199**	Carus	67003737-H	2.5		108	106	129	**118**	-2.08	-0.38	102	100	107	104	116	106	107	108	112	108	**108**
21	V	**276387871000893**	Valentin	87001319-H	3.9		96	109	116	**108**	-0.98	-0.00	99	108	112	112	118	104	108	123	111	112	**111**
22	V	**276467000127404**	Lombard	87003316-H	8.0		112	142	151	**139**			107	98	108	114	122	120	118	123	110	120	**114**
23	V	**276367671003397**	Lotus	87003316-H	1.0		122	132	120	**126**	-0.85	-0.36	105	106	108	110	111	104	106	118	110	112	**110**
24	V	**276487870966301**	Volontär	87003316-H	2.7		110	110	134	**123**	1.29	-0.05	99	94	101	106	116	112	118	120	110	116	**109**
25	V	**276367670246899**	Gordon	67000947-H	3.5		102	107	111	**107**	1.03	0.12	106	103	105	93	110	107	109	96	106	104	**104**

Conclusions

- Our software is a web-based software pipeline.
- It requires less human effort to run (automatic parameterization) all sub-systems.
- It helps breeders and breeding organizations to improve their breeding programs.
- It has been tested with sample datasets.
- The software will be released under GPL.

Acknowledgements

Project Partners

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