SLAUGHTER QUALITY OF ATLANTIC SALMON (*SALMO SALAR*) USING COMPUTERIZED TOMOGRAPHY

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Motivation

- Current slaughter quality evaluation:
  - ✓Costly, time consuming and laborious
  - ✓Based on relatives
  - ✓Measurement error

Reliable genetic evaluation of slaughter quality in Atlantic salmon using individual CT-phenotypes of breeding candidates.

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Data: manual dissection and CT data

Manual dissection N=3044

- Harvest weight, gutted weight, fillet weight, body length
- Fat precentage with NIR
- Pigmentation, wounds, gaping, melanin spots, fillet deformity

- Alternative methods for measuring fat and pigmentation assessed

CT scanning, dead fish N=2012

- Virtual cuts

- Phenotypes from CT scans created using 3D image analysis of the different x-ray absorption properties of different tissues

CT scanning, live fish N=1425

- Feasibility

- Similar phenotypes as in dead fish scanning

- Additionally: proportion cuts

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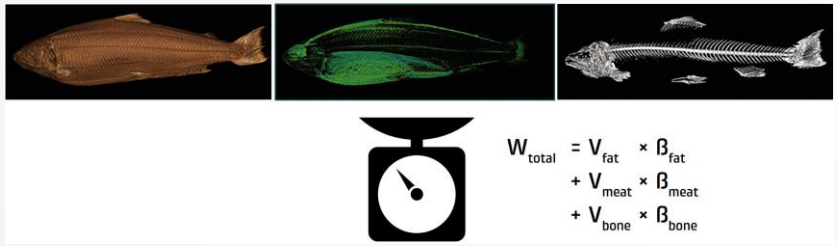
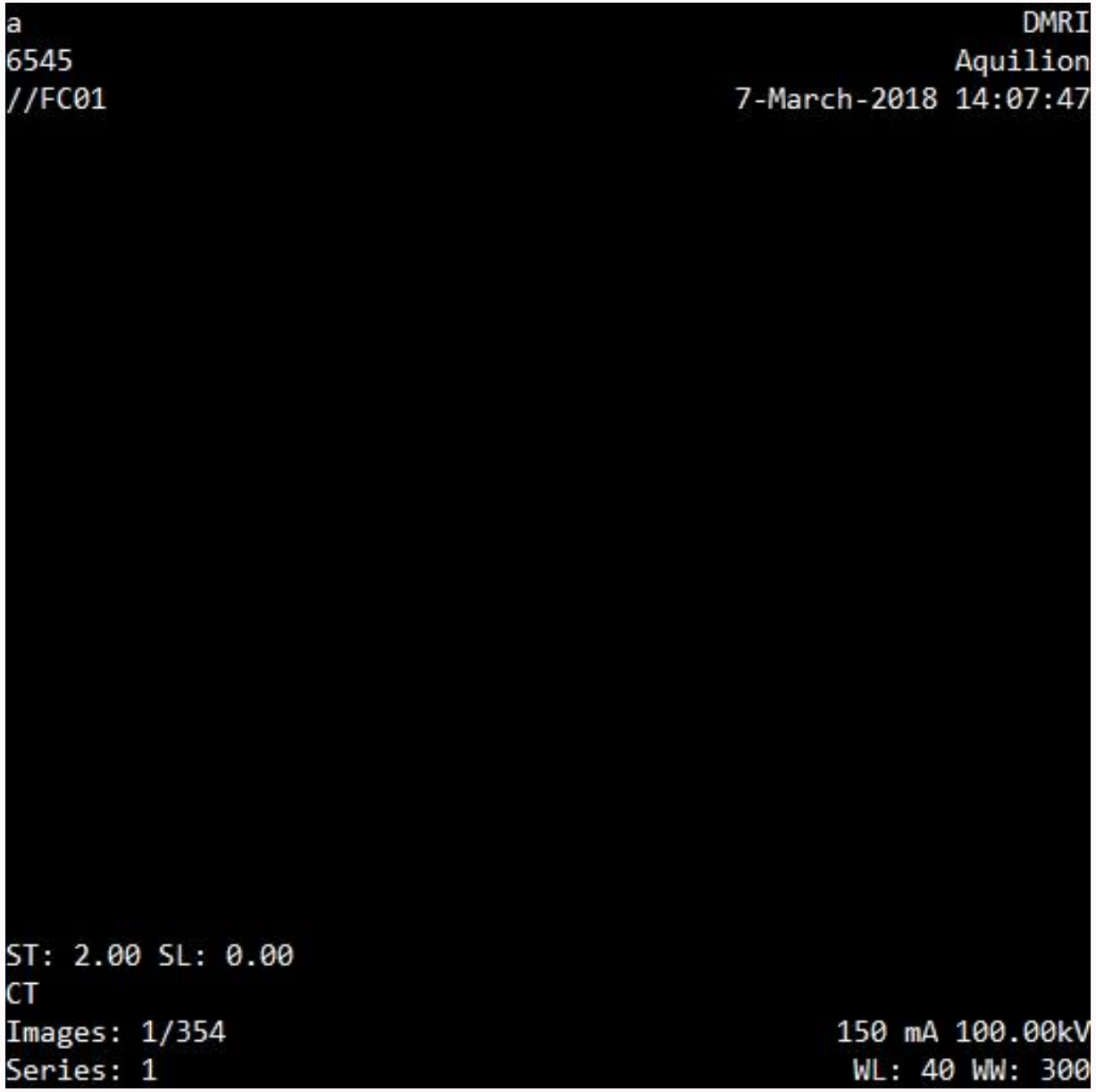
CT scanning

- Three salmon scanned at a time
- Toshiba Aquilion 16
- 2 mm slice thickness





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Genetic parameters

Variable	h2	c2
Manual slaughter		
MHWT	0.26 (0.07)	0.05 (0.03)
MGWT	0.29 (0.08)	0.04 (0.03)
MFWT	0.28 (0.08)	0.06 (0.03)
MFAT (%)	0.33 (0.08)	0.04 (0.03)
CT scanning		
FWT_CT	0.22 (0.08)	0.04 (0.03)
FFAT_CT (g)	0.35 (0.10)	0.03 (0.03)
FFAT_CT (%)	0.48 (0.06)	-
INTFAT_CT	0.21 (0.04)	0.07 (0.04)

Variable	h2	c2
Live fish CT		
FWT_CT	0.31 (0.09)	0.07 (0.03)
FFAT_CT (g)	0.35 (0.09)	0.06 (0.03)
FFAT_CT (%)	0.34 (0.08)	0.02 (0.03)
INTFAT_CT	0.35 (0.08)	0.04 (0.03)
Live fish CT: proportions		
LOINMEAT	0.24 (0.10)	0.10 (0.04)
LOINFAT (g)	0.42 (0.10)	0.04 (0.04)
LOINFAT (%)	0.47 (0.08)	-
NQC_MEAT	0.25 (0.10)	0.07 (0.04)

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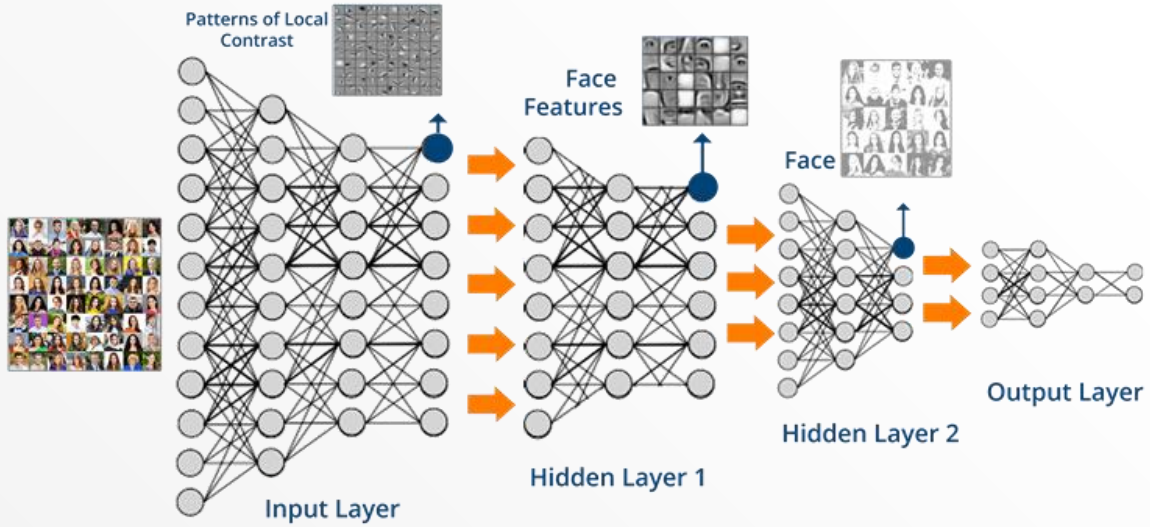
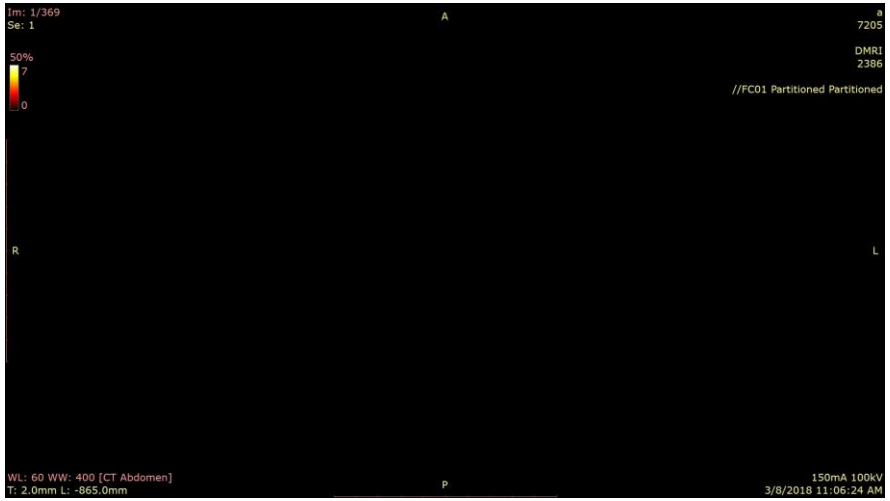
Variable	MHWT (g)	MFWT (g)	FAT (%)	FWT_CT	FFAT_CT (g)	FFAT_CT (%)	INTFAT_CT
MHWT (g)		0.89 (0.02)	0.35 (0.09)	-	0.92 (0.02)	0.61 (0.07)	0.69 (0.06)
MFWT (g)	0.90 (0.00)		0.65 (0.06)	1.0 (0.00)	0.95 (0.01)	0.68 (0.06)	0.72 (0.05)
FAT (%)	0.37 (0.02)	0.43 (0.02)		0.64 (0.08)	0.85 (0.04)	0.91 (0.03)	0.21 (0.12)
FWT_CT	-	0.94 (0.00)	0.52 (0.02)		0.90 (0.02)	0.56 (0.08)	0.56 (0.08)
FFAT_CT (g)	0.91 (0.00)	0.88 (0.01)	0.65 (0.02)	0.92 (0.02)		0.87 (0.03)	0.39 (0.10)
FFAT_CT (%)	0.57 (0.02)	0.57 (0.02)	0.67 (0.02)	0.55 (0.02)	0.82 (0.01)		0.11 (0.11)
INTFAT_CT	0.80 (0.01)	0.75 (0.01)	0.39 (0.03)	0.77 (0.01)	0.66 (0.02)	0.35 (0.03)	

Other results:

- Melanin spots
- The Q-point NIR system
- SORS





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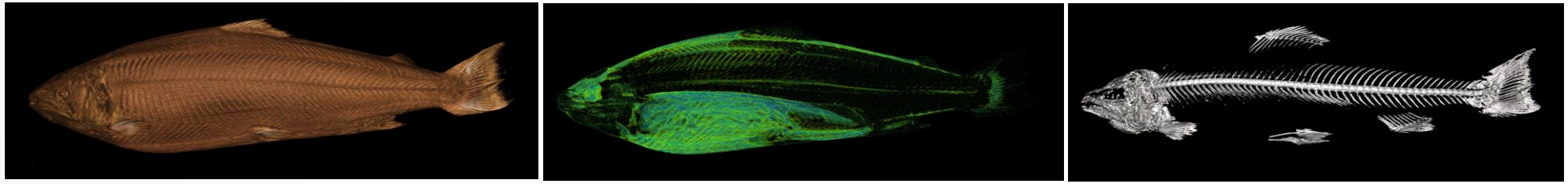
Conclusions

CT scanning and derived virtual cuts reliably describe the slaughter quality of the fish relative to carcass composition and fat content

CT scanning can be performed on live fish



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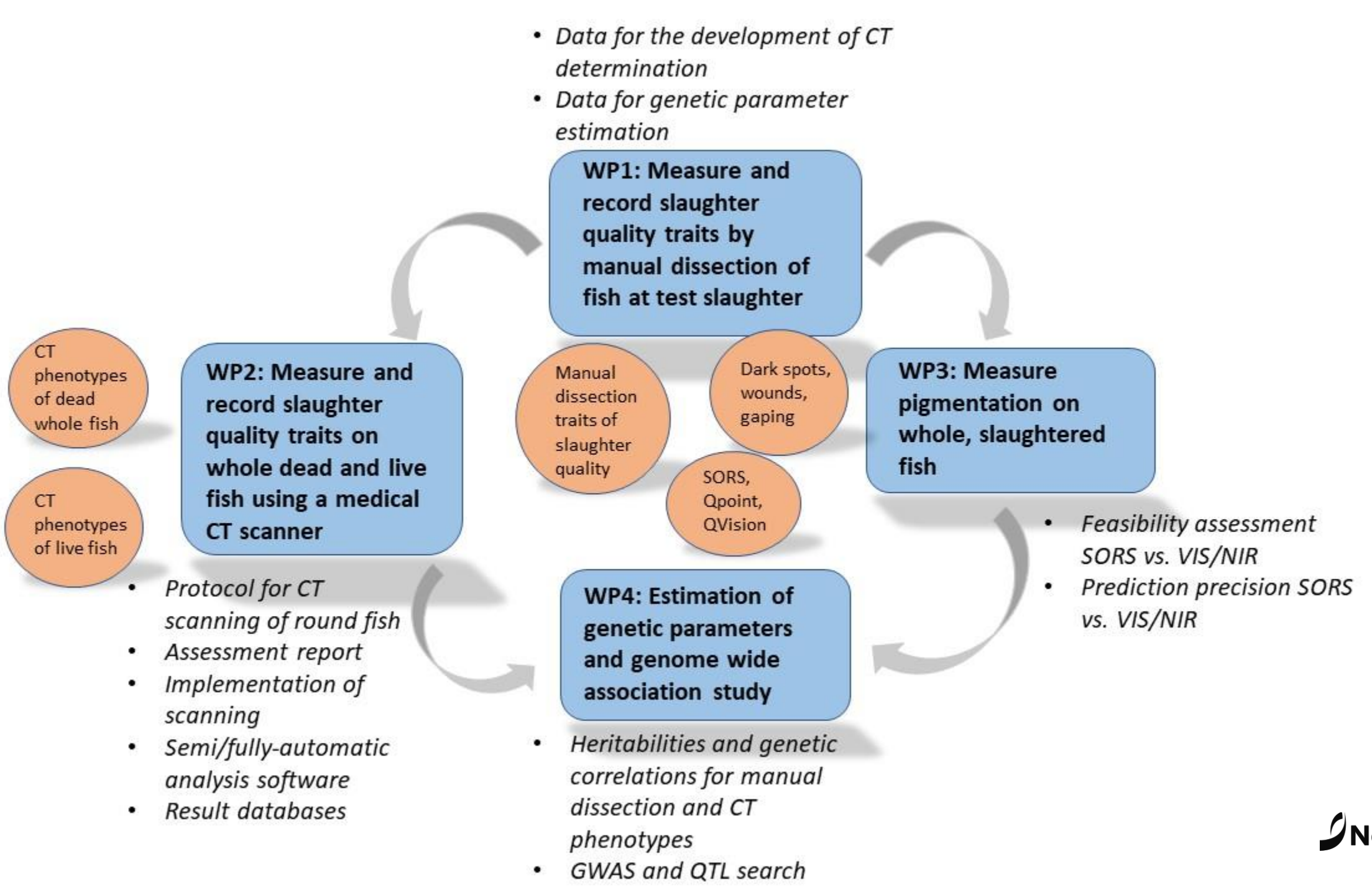
• Data for the development of CT determination
• Data for genetic parameter estimation
WP1: Measure and record slaughter quality traits by manual dissection of fish at test slaughter
Manual dissection traits of slaughter quality
Dark spots, wounds, gaping
SORS, Qpoint, QVision
CT phenotypes of dead whole fish
CT phenotypes of live fish
WP2: Measure and record slaughter quality traits on whole dead and live fish using a medical CT scanner
WP3: Measure pigmentation on whole, slaughtered fish
• Protocol for CT scanning of round fish
• Assessment report
• Implementation of scanning
• Semi/fully-automatic analysis software
• Result databases
WP4: Estimation of genetic parameters and genome wide association study
• Heritabilities and genetic correlations for manual dissection and CT phenotypes
• GWAS and QTL search
• Feasibility assessment SORS vs. VIS/NIR
• Prediction precision SORS vs. VIS/NIR

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