Landing Strips: model development for estimating body surface area of farmed Atlantic salmon (*Salmo salar*).

Catherine Frederick[a,*], Damian C. Brady[b], and Ian Bricknell[a]
[a]School of Marine Sciences, The University of Maine, Orono, Maine 04469, USA
[b]School of Marine Science, The University of Maine, Walpole, Maine 04573, USA
*Corresponding author: catherine.frederick@maine.edu +1(502) 619-2618

1. INTRODUCTION

Although relatively difficult to measure, utilizing body surface area (BSA; cm^2) in applied research can prove insightful. For example, sea lice impact (*Lepeophtheirus salmonis* and *Caligus* spp.) is still an active area of scientific research in salmonid culture. A standardized unit of density is lice g^{-1} and used to assess the physiological health of the host (Wagner et al. 2003). Density standardized to BSA (lice cm-2) is a more robust metric and better reflects parasitized space (Abé et al., 2015; Caltran and Silan, 1996; Halliday et al., 2014; Tucker et al., 2002). BSA can also be a proxy of host density in model simulations, as Rogers et al. (2013) had done with farmed Atlantic salmon (*Salmo salar*).

A paucity of literature on BSA of major aquaculture species is evident after a thorough review. Few relevant publications actually describe mathematical models capable of estimating individual BSA. Articles describe BSA models of carp species (Ling et al., 2008), but most concentrate on Atlantic salmon. Reported methodologies in model development for BSA of Atlantic salmon raised skepticism. For example, Tucker et al. 2002 assume linearity between allometric estimators (Osse and van den Boogaart, 1995) and O'Shea et al. (2006) informs their model with as few as 8 samples. In response, the authors offer an updated mathematical BSA model derived from a year 1 juvenile Atlantic salmon population.

2. MATERIALS AND METHODS

2.1 Fish source

Hatchery-reared Atlantic salmon *Salmo salar* L., originated from the ARS-USDA National Cold Water Marine Aquaculture Center (NCWMAC) in Franklin, Maine. Monthly subsamples from a single-year class cohort were collected from June 2013-May

2014. An administered dose of MS-222 (200 mg L^{-1}) was used to euthanize fish. Euthanasia practices were in accordance to and approved by The University of Maine's Institutional Animal Care and Use Committee (IACUC).

2.2 Measurement protocol

A total of 960 Atlantic salmon were measured for BSA (length: 128 - 477 mm, mass: 21.83-1115.84 g). Fork length (mm) and mass (g) were measured using scale and ruler and condition factor (K) was calculated with Fulton's equation (Froese, 2006)

$$K = 100\ (W/L^3)$$

Where W= whole body mass (g) and L = fork length (cm). Total BSA was measured by methods described in O'Shea et al. (2006). Tracings were scanned into a computer and ImageJ (NIH, public domain) measured BSA; fins were doubled to account for the total fin surface area.

2.3 Model development

The construction of a linear model used fork length (mm), mass (g), and condition factor (K) as predictors of BSA. A total of 844 juveniles were used in model construction with the R program (RStudio Team, 2015). The method of backwards-stepwise regression was applied to construct and analyze linear models. A residual QQ-Plot was compared against simulated normal, logarithmic, and lepto- and platy- kurtic residual plots. A Shapiro-Wilks statistical analysis was also employed to determine normality.

Non-linear models were constructed using MatLab software (The Mathworks, 2015). Least squares regression was replaced with Tukey bisquare weights in model construction. Tukey’s bisquare is a method of robust least squares that minimizes the influence of extreme values. Points further from the line than would be expected by random chance have zero weight (Huggins, 1993).

The coefficient of determination (R2) and the square root of the variance of residuals (RMSE) identified the best-fit model. Measurements of 116 individuals with known BSA validated the best-fit model. A two-tailed paired-t-test of estimated and true BSA values determined if means were statistically similar.

2.4 A comparison of previously published models

Individuals used in validating the new model were also compared to estimations from four published models. The mathematical models previously published were:

1. $BSA = 9.5864W^{0.629}$ (Jaworski and Wolm, 1992)
2. $BSA = 86.144 + 0.613W$ (Tucker et al., 2002)
3. $BSA = 12.045W^{0.613}$ (Glover et al., 2004)
4. $BSA = 14.93^{0.59}$(O'Shea et al., 2006)

A repeated measures ANOVA comparing estimated and true BSA values determined if means were statistically similar. Tukey's HSD Post hoc analysis determined which pair-wise means differed.

3. Results

3.1 Model development

Morphometric data were not normally distributed (Shapiro-Wilks; p-value = 0.00) and matched best with leptokurtic data simulations. However, the large sample size is sufficiently robust to approximate normality under the central limit theorem. Parameter estimates of BSA regressed against mass, length, and condition factors are in Table 1. The best regression model for BSA based on highest R^2 was $BSA=13.9W^{0.61}$ ($R^2 = 0.97$, RMSE = 21.5). BSA estimations from $13.9W^{0.61}$ were statistically equal to corresponding true BSAs of sampled fish (N = 116; $\alpha = 0.05$, $p = 0.97$).

3.2 A comparison of previously published models

The repeated measures ANOVA showed that at least two pairs of means were significantly different ($p < 0.001$). Figure 2 is a summary of TukeyHSD results with 95% confidence intervals. In brief summary: *Post hoc* analysis revealed that means between true BSA and estimations from the developed model, $13.9W^{0.61}$, were equal. Estimations from $13.9W^{0.61}$ have a similar distribution as those generated by the O'Shea et al. (2006) model ($p = 0.97$) and both have means equal to the true BSA ($p = 0.99$). Estimated values from the model described in (Glover et al., 2004) are also equal to true BSA ($p = 0.12$). All other comparisons were significantly different ($p < 0.001$). Figure 1 demonstrates how well the new model fits the dataset compared to previous models. A box-plot of true and estimated BSAs also shows that the 1992 and 2002 models could underestimate true BSA; the 2004 model is only slightly less matched than the 2006 and presented model (Figure 3).

4. Discussion

The mass-power function as an estimator of BSA best fit the data set for juvenile Atlantic salmon. A power function of body mass was also suggested as a proxy for BSA in other fishes (Ling et al., 2008; Niimi, 1975), amphibians (Chen et al., 2014), and birds (Perez et al., 2014; Silva et al., 2009). Estimated values produced by the O'Shea et al. (2006) and current models were found to be equal to true BSA ($p = 0.99$). Those values obtained from the Hamre et al. model, cited by Glover et al. (2004), were also equal to true BSA, but the probability that the null is true is much weaker ($p = 0.12$). It is with confidence that the new model is best at capturing true BSA of Atlantic salmon with known body mass (g) than previous models.

The exception is that outputs from $BSA=13.9W^{0.61}$ and O'Shea et al. (2006) are equal to one another (p=0.97). A total of 8 fish ranging in mass between 18.8-539 g designed the O'Shea et al. (2006) BSA formula. The strength of the model $BSA=13.9W^{0.61}$ is the extraordinary sample size used for model development (N=844) and validation (N=119). The range of juvenile fish used in for the latest model was also extensive (length: 128-477 mm, mass: 21.8-1,115.8 g) compared to O'Shea et al. (2006)'s fish (length: 131-188 mm, mass: 18.8-539 g). Although the O'Shea model does remarkably well, use of previous models poses the risk of BSA underestimation (Figure 3).

An interesting trend emerges when regressions, including $BSA=13.9W^{0.61}$, are plotted on a scatter chart of true BSA (cm2) and fish mass (g). In Figure 1, model fit seems to improve with each year of publication. The exception is Tucker et al. (2002) because their model assumes a linear relationship between parameters that are allometric in nature (Osse and van den Boogaart, 1995). The authors speculate that methods in BSA measurement could improve the fit of a mathematical model. Rapid progression in aquaculture may also weaken the fit of an older model when applied to current salmon stocks

Domestication has changed the biology of the farmed fish in the last 30 years. In New Brunswick and Maine, Atlantic salmon are heavier and more robust today than in the 1980's (Chang and Page, 2014). Body weight has a high heritability trait (Tsai et al., 2015) that correlates with appetite, energy allocation, and feed conversion ratios (Neely et al., 2008; Thodesen et al., 1999). As a result, domesticated salmon grow larger and faster than wild types (Harvey et al., 2016) and continue to improve over generations of breeding (Gjedrem, 2000). Improvements in diet composition and quality further enhance weight gain in Atlantic salmon (Oliva-Teles, 2012). Weight gain correlates positively with condition factor and is greater in farmed fish (Acharya, 2011; Glover et al., 2009). Since condition factor is a parameter descriptive of girth it is also indicative of BSA.

Mariculture continues to evolve with rapid advancements in breeding and culture techniques. Breeding programs continue targeting genes that affect salmon growth. Amendments to mathematical models should occur on occasion to avoid outdatedness. It is with confidence that the model presented can estimate BSA of farmed Atlantic salmon juveniles with improved accuracy. The authors hope that it will prove useful among the applied sciences.

Acknowledgements

This work was carried out as part of a PhD dissertation funded by the National Oceanographic and Atmospheric Climate Administration’s SEAGRANT program. The authors would like to thank the National Cold Water Marine Aquaculture Center (USDA-ARS) in Franklin, ME, USA for providing the source of fish. The authors would also like to thank Katie Liberman, Corrine Mooring, David Noyes, and the remaining undergraduate staff for their assistance in measuring body surface areas.

References

Abé, H., Ohtsuka, Y., Ohba, S., 2015. Water mites (Acari: Hydrachnidiae) parasitic on aquatic hemipterans in Japan, with reference to host preferences and selection sites. Int. J. Acarol. 41, 494–506.

Acharya, D., 2011. Fillet Quality and Yield of Farmed Atlantic Salmon (Salmo salar L): variation between families, gender differences, and the importance of maturation. Norwegian University of Life Sciences.

Caltran, H., Silan, P., 1996. Gill filaments of Liza ramada, a biotope for ectoparasites: surface area acquisition using image analysis and growth models. J. Fish Biol. 49, 1267–1279.

Chang, B.D., Page, F.H., 2014. Historical and spatial trends in selected aspects of the finfish aquaculture industry in southwestern New Brunswick, Bay of Fundy, 1978-2012. St. Andrews, NB, Canada.

Chen, G., Liu, J., Dai, Q., Jiang, J., 2014. Body surface area prediction in Odorrana grahami. Asian Herpetol. Res. 5, 54–59.

Froese, R., 2006. Cube law, condition factor and weight-length relationships: History, meta-analysis and recommendations. J. Appl. Ichthyol. 22, 241–253.

Gjedrem, T., 2000. Genetic improvement of cold-water fish species. Aquac. Res. 31, 25–33.

Glover, K.A., Hamre, L.A., Skaala, Nilsen, F., 2004. A comparison of sea louse (Lepeophtheirus salmonis) infection levels in farmed and wild Atlantic salmon (Salmo salar L.) stocks. Aquaculture 232, 41–52.

Glover, K.A., Otterå, H., Olsen, R.E., Slinde, E., Taranger, G.L., Skaala, Ø., 2009. A comparison of farmed, wild and hybrid Atlantic salmon (Salmo salar L.) reared under farming conditions. Aquaculture 286, 203–210.

Halliday, W., Paterson, J., LD, P., SJ, C., Blouin-Demers, G., 2014. Testosterone, body size, and sexual signals predict parasite load in Yarrow’s spiny lizards (Sceloporus jarrovii). Can. J. Zool. 92, 1075–1082.

Harvey, A.C., Solberg, M.F., Troianous, E., Carvalho, G.R., Taylor, M.I., Creer, S., Dyrhovden, L., Matre, I.H., Glover, K.A., 2016. Plasticity in growth of farmed and wild Atlantic salmon: is the increased growth caused by evolutionary adaptations in to the commercial diet? Bmc Evol. Biol. 16, 264–272.

Huggins, R.M., 1993. A Robust Approach to the Analysis of Repeated Measures. Biometrics 49, 715–720.

Jaworski, A., Wolm, J., 1992. Distribution and structure of the population of sea lice, Lepeophtheirus salmonis Krøyer, on Atlantic salmon, Salmo salar L ., under typical rearing conditions. Aquac. Fish. Manag. 577–589.

Ling, F., Wang, J.G., Li, A.H., Zhang, J.Y., Li, M., Gu, Z.M., Gong, X.N., 2008. Determination of the surface area of common carp, Cyprinus carpio L. J. Appl. Ichthyol. 24, 690–693.

Neely, K.G., Myers, J.M., Hard, J.J., Shearer, K.D., 2008. Comparison of growth, feed intake, and nutrient efficiency in a selected strain of coho salmon (Oncorhynchus kisutch) and its source stock. Aquaculture 283, 134–140.

Niimi, a J., 1975. Relationship of body surface area to weight in fishes. Can. J. Zool. 53, 1192–4.

O’Shea, B., Mordue-Luntz, A.J., Fryer, R.J., Pert, C.C., Bricknell, I.R., 2006.

Determination of the surface area of a fish. J. Fish Dis. 29, 437–440.

Oliva-Teles, A., 2012. Nutrition and health of aquaculture fish. J. Fish Dis. 35, 83–108.

Osse, J.W.M., van den Boogaart, J.G.M., 1995. Fish larvae, development, allometric growth, and the aquatic environment. ICES Mar. Sci. Symp. Copenhagen 201 21–34.

Perez, C.R., Moye, J.K., Pritsos, C. a, 2014. Estimating the surface area of birds: using the homing pigeon (Columba livia) as a model. Biol. Open 3, 486–8.

Rogers, L.A., Peacock, S.J., McKenzie, P., DeDominicis, S., Jones, S.R.M., Chandler, P., Foreman, M.G.G., Revie, C.W., Krkošek, M., 2013. Modeling Parasite Dynamics on Farmed Salmon for Precautionary Conservation Management of Wild Salmon. PLoS One 8.

Silva, E., Júnior, T., Júnior, R., Lopes, M., FA, 2009. Desenvolvimento e validação de um modelo matemático para o cálculo da área superficial de frangos de corte. Eng. Agríc 1–7.

Team RStudio, 2015. RStudio: Integrated Development for R.

The Mathworks, I., 2015. MATLAB and Statistics Toolbox Release 2015b.

Thodesen, J., Grisdale-Helland, B., Helland, S.J., Gjerde, B., 1999. Feed intake, growth and feed utilization of offspring from wild and selected Atlantic salmon (Salmo salar). Aquaculture 180, 237–246.

Tsai, H.Y., Hamilton, A., Guy, D.R., Tinch, A.E., Bishop, S.C., Houston, R.D., 2015. The genetic architecture of growth and fillet traits in farmed Atlantic salmon (Salmo salar). BMC Genet. 16, 51.

Tucker, C.S., Tucker, C.S., Sommerville, C., Wootten, R., 2002. Does size really matter ?

Effects of fish surface area on settlement and initial survival of Lepeophtheirus salmonis , an ectoparasite of Atlantic salmon Salmo salar. Dis. Aquat. Organ. 49

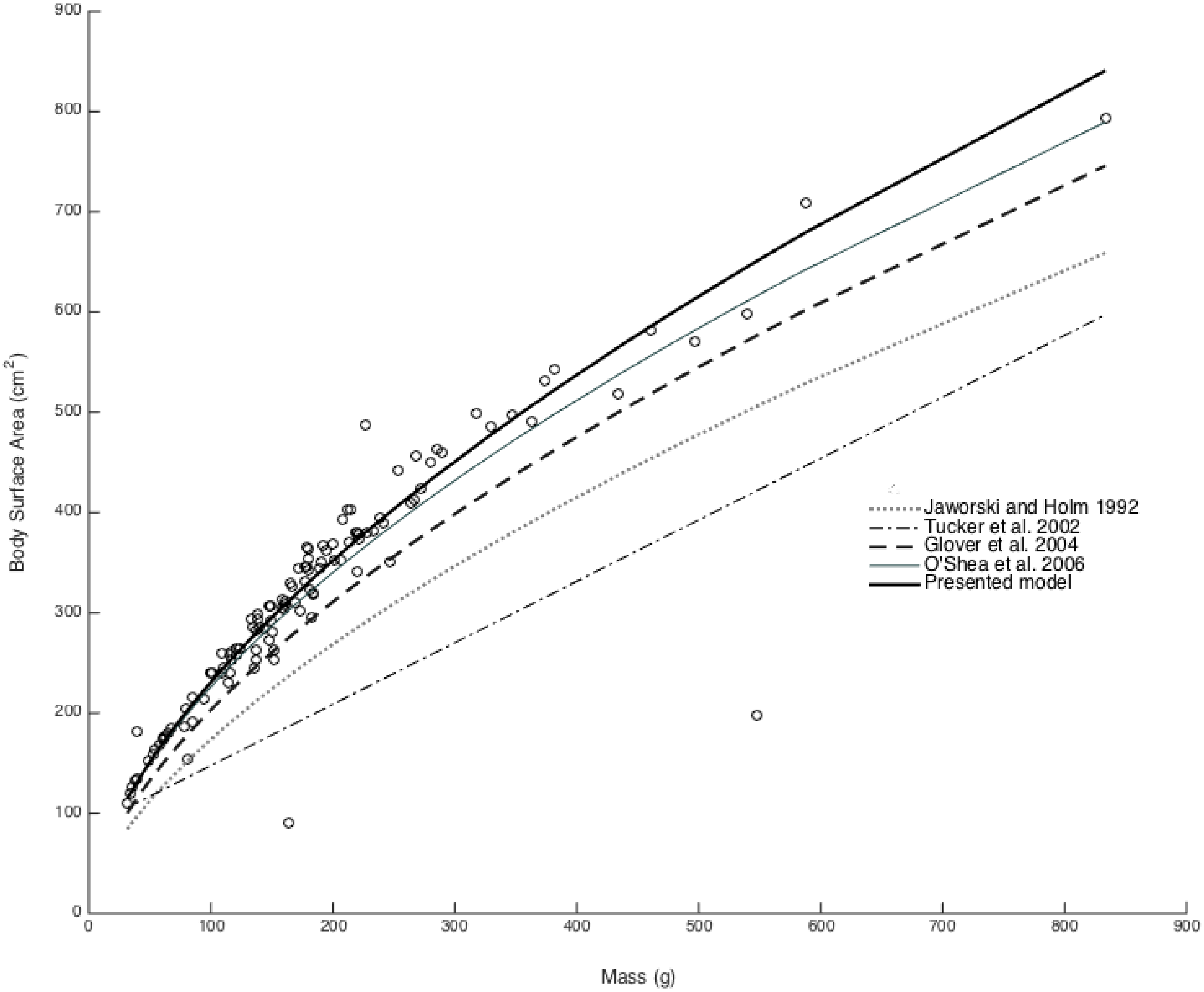

Figure 1: True body surface area (cm^2) of 116 juvenile Atlantic salmon plotted against their corresponding mass (g). Regression lines from previously published models are plotted against data points, including the current model: BSA=$13.9W^{0.61}$, whose R^2 value is 0.97 (thick black line).

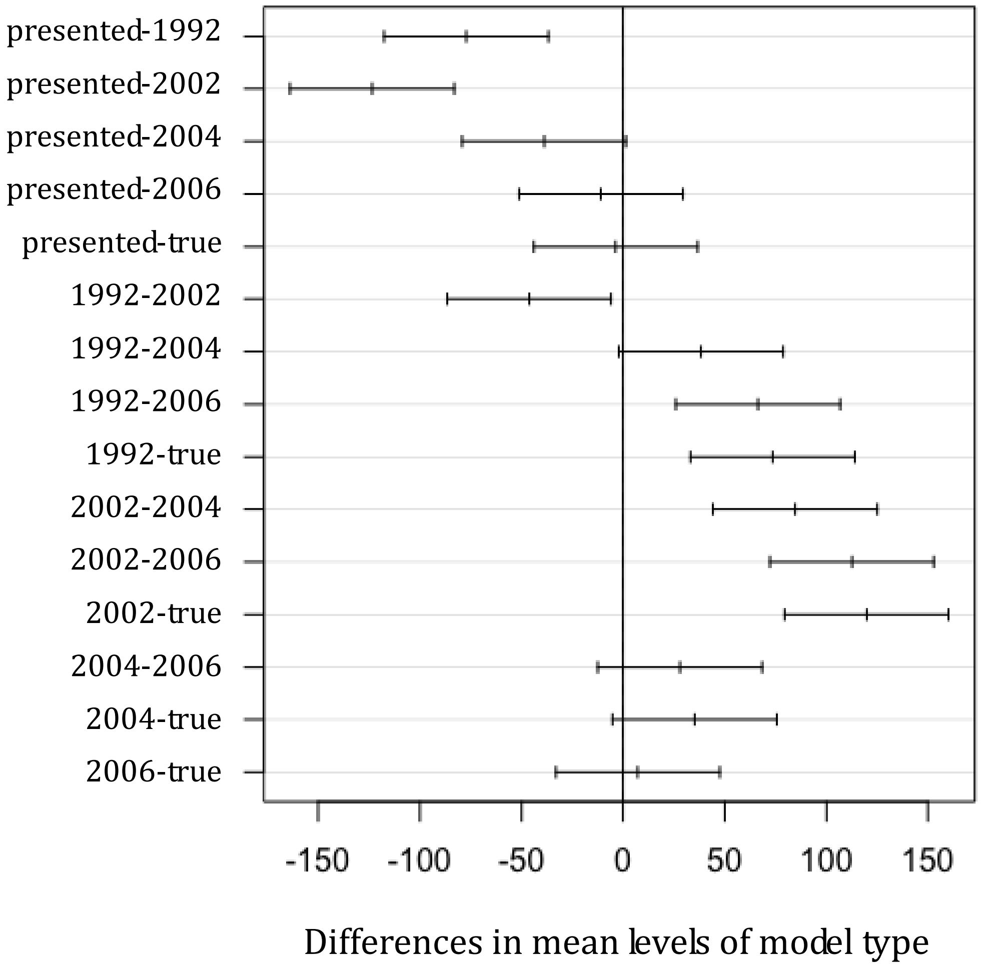

Figure 2: Test statistics of TukeyHSD for 116 individual juvenile Atlantic salmon. Each line represents the 95% confidence interval on the differences between means of the Jaworksi and Holm 1992, Tucker et al. 2002, Glover et al. 2004, O'Shea et al. 2006, the presented model, and true BSA. A comparison without "0" in the confidence interval is indicative of significant differences.

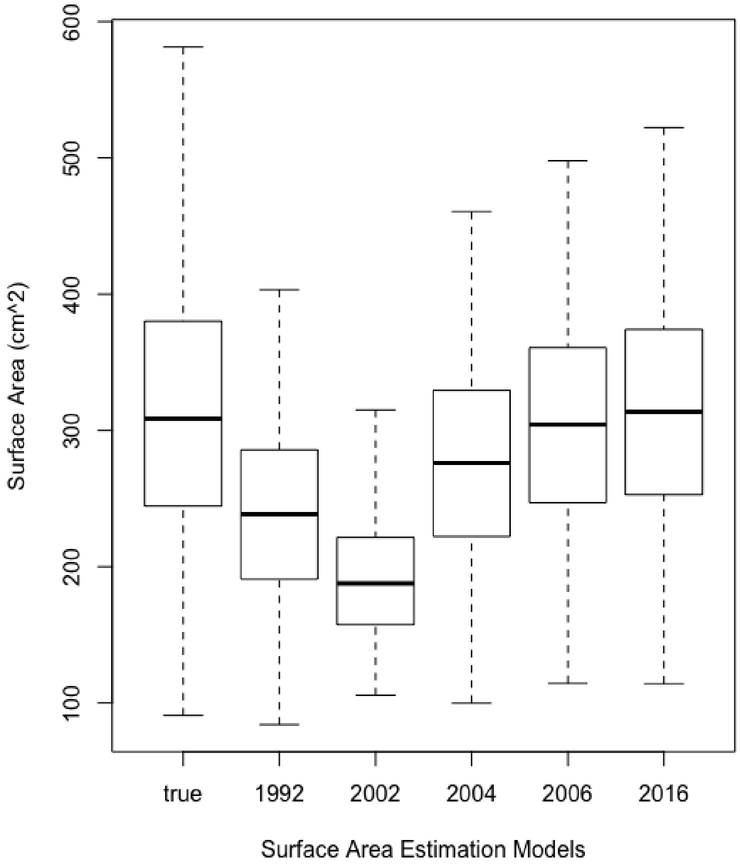

Figure 3: Surface area estimation comparison of the Jaworski and Holm 1992, Tucker et al. 2002, Glover et al. 2004, O'Shea et al. 2006, and Frederick et al. 2016 mathematical models to the true surface area of 116 juvenile Atlantic salmon. Median values of the 2016, 2006, and 2004 models are matched closely to the median values of the true surface area. The 2004, 2006, and 2016 model was statistically similar to the true surface area in a *post hoc* analysis (p=0.12, 0.99, 0.99, respectively).

Table 1: Formulae estimating total surface area as a function of mass (g), fork length (mm), and condition factor (K) for juvenile Atlantic salmon. Data collected from 844 individuals were used to construct the mathematical models. The power model $SA = 13.9W^{0.61}$ is the best fit for the sample's data ($R^2 = 0.97$) and was also statistically similar to true surface area values, as determined by a two-tailed paired t-test (N= 119; p=0.97).

Model	Formulae	R^2	RMSE	Coefficient confidence intervals	
				a	b
Exponential	$SA = 328.3e^{0.0K}$	0.31	112.2	(320.7, 335.8)	(-0.02, 0.02)
	$SA = 325.7e^{0.35L}$	0.94	31.42	(323.4, 328.0)	(0.35, 0.36)
	$SA = 341.9e^{0.37W}$	0.90	39.19	(339.3, 344.6)	(0.36, 0.37)
Power	$SA = 329.3K^{0.03}$	.31	112.4	(321.2 337.4)	(-0.10, 0.15)
	$SA = 0.59L^{1.93}$	0.94	31.36	(0.52, 0.65)	(1.90, 2.00)
	$SA = 13.9W^{0.61}$	0.97	21.54	(13.4, 14.4)	(0.60, 0.61)
Linear	$SA = 132.3 + 1.08W$	0.95	29.88	(128.7, 136.0)	(1.06, 1.09)