

## File S2. Derivation of MGMS

In developing the multi-gear mean standardization (MGMS), our goal was to find a way to standardize data that would 1) maintain patterns of relative abundance among species within a sample/observation, 2) maintain patterns of relative abundance among sites within a species, and 3) put data into a new relative scale that would be common across gears. We began with the idea of converting catch per unit effort (CPUE) data to relative abundance by dividing the mean catch of each species  $i$  in each sample  $j$  ( $c_{ij}$ ) per effort ( $e$ ) of each species in each sample by the total catch (TC) per effort of all  $i$  species in sample  $j$  ( $\frac{TC_j}{e}$ ):

$$(1) \quad \frac{c_{ij}/e}{TC_j/e}$$

Obviously, relative abundance (equation 1) can be converted back to CPUE by multiplying by  $\frac{TC_j}{e}$ . To preserve both the relative abundance patterns among species within a sample while simultaneously preserving the relative abundance patterns among sites within a species, we decided to standardize  $\frac{TC_j}{e}$  by dividing total catch per effort of all species in each sample by mean of total catch per effort among all samples ( $\overline{TC}$ ), and then multiplying relative abundance by the resulting quotient to create the mean standardized catch of species  $i$  in sample  $j$  ( $MSC_{ij}$ ):

$$(2) \quad MSC_{ij} = \frac{c_{ij}/e}{TC_j/e} \cdot \frac{TC_j/e}{\overline{TC}}$$

Which reduces to:

$$(3) \quad MSC_{ij} = \frac{c_{ij}/e}{\overline{TC}}$$

Table S1. Base model conditions for catchability and coefficient of variation used to sample the 18 species abundance distributions.

<b>Species</b>	<b>Electrofishing q</b>	<b>Mini-fyke q</b>	<b>Electrofishing CV</b>	<b>Mini-fyke CV</b>
<b>1</b>	0.35	0.0005	15%	25%
<b>2</b>	0.35	0.0005	15%	25%
<b>4</b>	0.35	0.0005	15%	25%
<b>5</b>	0.35	0.0005	15%	25%
<b>6</b>	0.35	0.0005	15%	25%
<b>7</b>	0.035	0.0035	15%	25%
<b>8</b>	0.035	0.0035	15%	25%
<b>9</b>	0.035	0.0035	15%	25%
<b>10</b>	0.035	0.0035	15%	25%
<b>11</b>	0.035	0.0035	15%	25%
<b>12</b>	0.035	0.0035	15%	25%
<b>13</b>	0.0001	0.035	15%	25%
<b>14</b>	0.0001	0.035	15%	25%
<b>15</b>	0.0001	0.035	15%	25%
<b>16</b>	0.0001	0.035	15%	25%
<b>17</b>	0.0001	0.035	15%	25%
<b>18</b>	0.0001	0.035	15%	25%

Table S2. Mean correlation coefficient ( $r \pm 1$  STD) from sensitivity analyses for transformations.

Standardization	Base Model	SQRT	LOG <sub>10</sub> + 1	<b>Mean</b>
MGMS	0.93 ( $\pm$ 0.05)	0.93 ( $\pm$ 0.05)	0.93 ( $\pm$ 0.06)	<b>0.93</b>
Relative abundance	0.81 ( $\pm$ 0.14)	0.83 ( $\pm$ 0.13)	0.83 ( $\pm$ 0.13)	<b>0.82</b>
SpeciesMax	0.90 ( $\pm$ 0.07)	0.88 ( $\pm$ 0.08)	0.89 ( $\pm$ 0.08)	<b>0.89</b>
sCPUE	0.87 ( $\pm$ 0.10)	0.92 ( $\pm$ 0.06)	0.91 ( $\pm$ 0.06)	<b>0.90</b>
	Number of runs where $r < 0.5$			
MGMS	0	0	0	<b>0</b>
Relative abundance	41	24	29	<b>31</b>
SpeciesMax	0	2	1	<b>1</b>
sCPUE	5	0	0	<b>2</b>

Figure S1. Representative beta-distributions generated by the model.

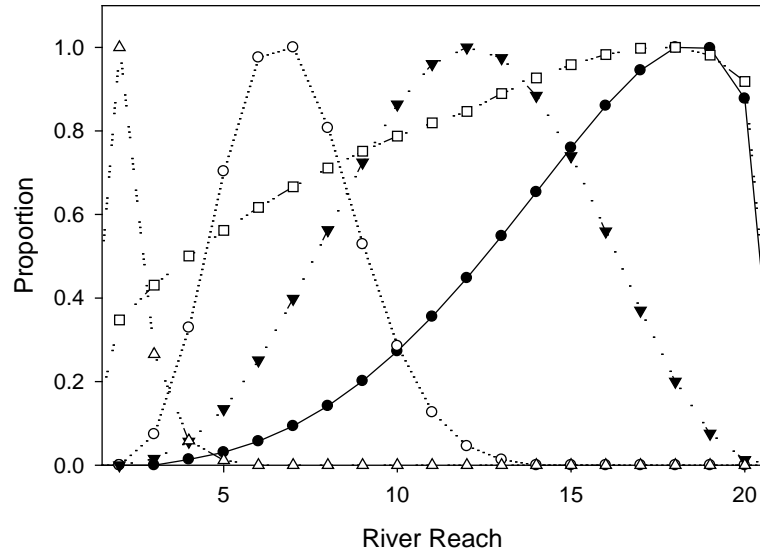


Figure S2. Gamma distribution for peak biomass of a species generated using the rangam function in SAS.

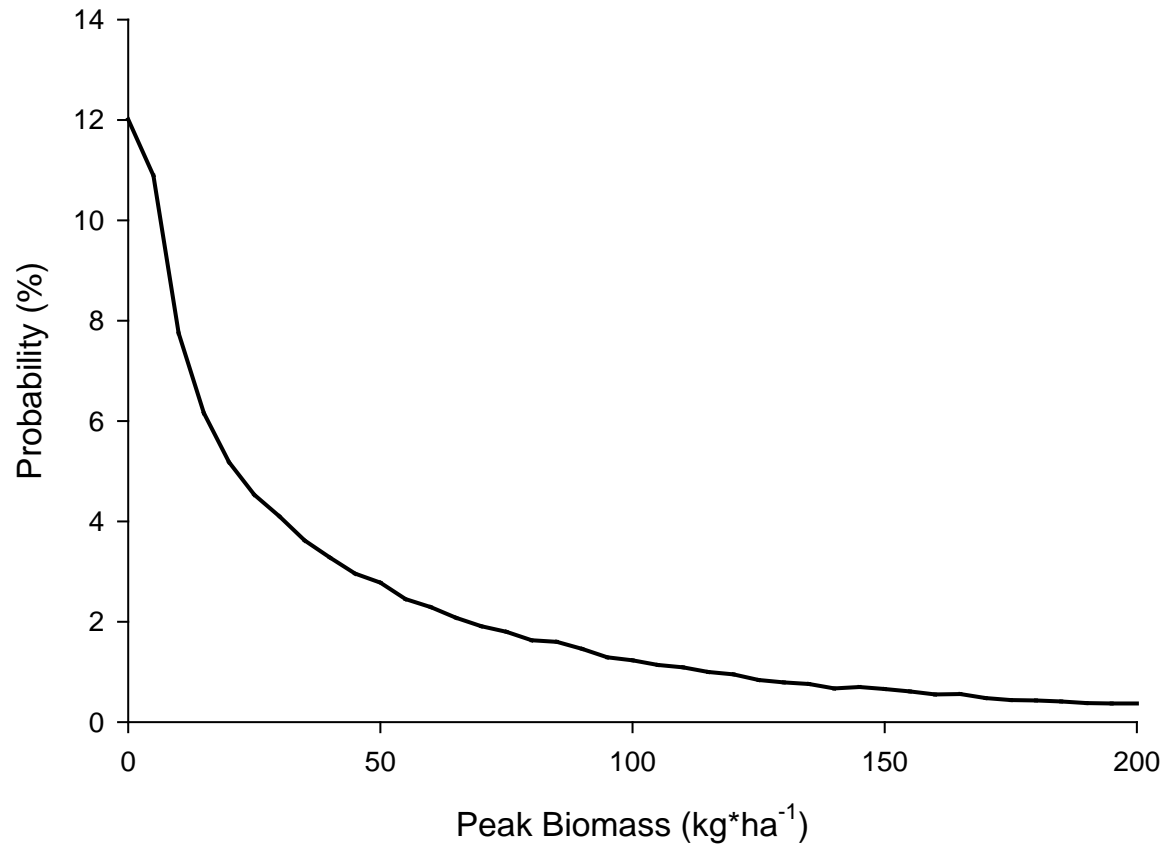


Figure S3. Representative MPUE distributions for species collected by A. electrofishing and B. mini-fyke netting from six reaches of the Upper Mississippi River System collected from 1994 – 2013 by the U.S. Army Corps’ of Engineers’ Upper Mississippi River Restoration Program, Long Term Resource Monitoring element.

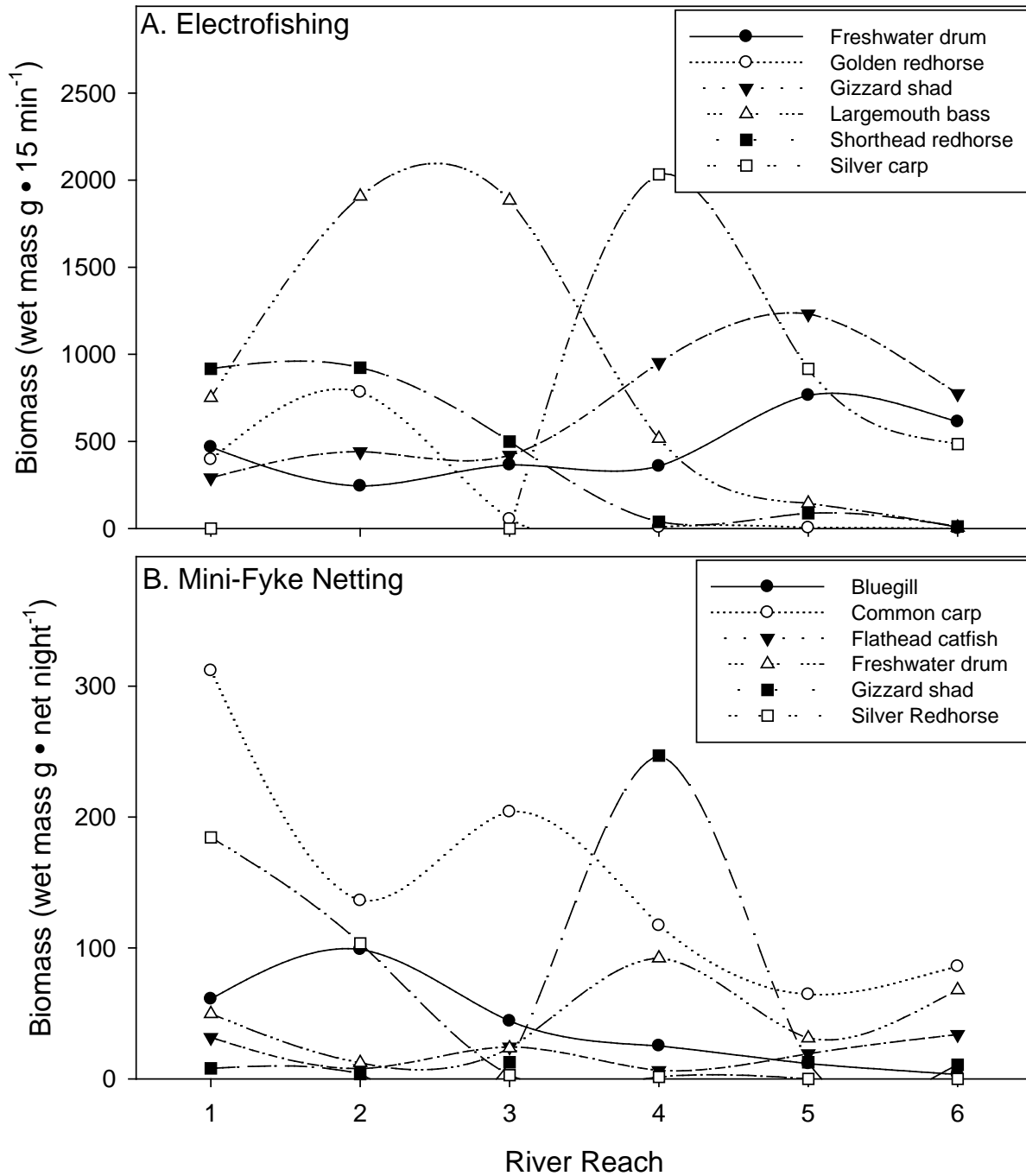


Figure S4. Distribution of the Pearson Correlation Coefficient for 1,000 iterations of each method, using base settings (A), square root transformed data (B), and log transformed data (C).

