6.0 Quantitative Conceptual Model Development

This section provides a summary of the considerations, assumptions, and methodology used to develop a quantitative conceptual model of selenium cycling in the open waters of Great Salt Lake.

The simplified conceptual model for selenium cycling in the open waters of Great Salt Lake (refer to Figure 3-3) is composed of three primary components: (1) selenium in the upper food chain, (2) selenium in the lower food chain, and (3) selenium in the water and sediment. Due to the bioaccumulative nature of selenium, it is generally recognized to originate at the "bottom" of the conceptual model—that is, from selenium in the water and sediment (abiotic component)—and move "up" through the conceptual model through the lower food chain (food web component), and into the upper food chain (birds component). The development of the quantitative model is discussed first for the Abiotic and Food Web component of the model and then for the Birds component.

6.1 Mass Balance Model

6.1.1 Water Mass Balance

A modified mass balance approach was used to link measured and estimated Great Salt Lake concentrations of selenium in various media into a model that would be responsive to changing ambient conditions. The basic concept of the Mass Balance Model is to include all input and removal mechanisms to estimate a waterborne selenium concentration for the study area. Measured lake and influent selenium concentrations and loads were compiled as monthly geometric mean values, whenever possible. Modeled water column loads and concentrations step through time on a monthly average time step. The concept is to capture seasonal variability whenever possible. The model is meant to predict water column concentrations and therefore relies on both external loads (tributaries, atmospheric deposition) as well as internal loading (remineralization from seston and sediments).

The mass balance prediction for average water column loads can be depicted as:

EQUATION 1
Mass Balance for Average Water Column Load

$$\text{Se-lake}_{t1} = \text{Se-lake}_{t0} + (\text{Influent}_{t1}\ \text{Se} + \text{AtmDep}_{t1}\ \text{Se} + \text{Mineralized}_{t1}\ \text{Se}) - (\text{Volatilized}_{t1}\ \text{Se} + \text{Buried}_{t1}\ \text{Se} + \text{Brine shrimp harvest}_{t1}\ \text{Se})$$

Where:

- t0 and t1 are sequential months.
- Influent selenium sums the net load contributions from tributaries and estimated losses to the north lake for any given month as derived from Naftz et al. (2008).

- AtmDep selenium is an estimate, placeholder value for atmospheric deposition load directly onto the lake's surface, based on 0.5 multiplied by the Chesapeake Bay wet selenium deposition rate and all of the Chesapeake Bay dry deposition rate (annual rate divided by 12) (EPA, 1996). The assumption is that atmospheric deposition to the nonlake area of the watershed is captured in watershed runoff and is already included.
- Mineralized selenium load was estimated as shallow sedimentation rates minus permanent sediment burial rates. The difference between the two represents selenium that is sinking but not being permanently buried and is therefore being remineralized through any wide variety of sediment processes (diagenesis, resuspension, water column dissolution, etc.). It is recognized that net flux could be into or from the sediments for any given period of time.
- Volatilized selenium was estimated as the mean annual, lake-wide loss of volatile selenium provided by Johnson et al. (2008), divided by 12 to yield simple, monthly estimates. These values could be greatly improved through the estimation of monthly values based on temperature, volatile selenium concentrations in water, and wind speed measurements. Volatilization is strongly associated with such seasonally varying parameters as wind speed and temperature, which means that accurate modeling of this important variable (volatilization) must take those meteorological factors into account.
- Buried selenium was the estimated annual permanent sediment burial rate for the lake divided by 12 to produce monthly loss values.
- Brine shrimp harvest was estimated as the weight removed times the average cyst concentrations, following the methods of Johnson et al. (2008). Brine shrimp removal was allocated as an annual value that was equally divided among the months of third and fourth calendar quarters (the timing of actual harvest).

The components of the above mass balance equation were summed as loads and divided by lake volume to yield lakewide average selenium concentrations. Monthly average volumes were estimated using the elevation/volume relationship for the south lake of Baskin (2005) and the USGS Water Resources Division online record of lake elevation at the Saltair station (USGS 10010000 Great Salt Lake at Saltair Boat Harbor, Utah).

The technique of sequentially computing mass balances produced a relatively good match to measured values. At the end of the 15-month measurement period the predicted water column monthly total selenium concentrations were low by an average of 0.04 µg/L (7 percent). A remaining unmeasured total was noted in the reports of Johnson et al. (2008) and Naftz et al. (2008) as evidence for a significant, unmeasured load. In particular, lake water column concentrations during the 2006 through 2007 period were generally observed to rise during a relatively dry year of reduced stream loading. Future monitoring efforts should make an effort to include currently unmeasured but potentially significant contributors to load, such as atmospheric deposition (only estimated from literature values here) and groundwater.

6.1.2 Sediment

Sediments from shallow water depth—but away from shore and those underlying the deep brine layer—provided characterizations useful for tracking particle sedimentation and remineralization (Johnson et al., 2008) but were not used as measures of direct exposure to

invertebrates and birds. Instead, sediments in the immediate shore zone (shorebird wading depth) were assumed to provide direct exposure to brine fly larvae, other insects, and for incidental consumption by shorebirds. Dry-weight sediment concentrations of total selenium were corrected based on the salt content of the water in the wet sediment using the methodology described by Johnson et al. (2008) for deeper water sediments. Shore-zone sediment concentrations were assumed to vary directly with waterborne concentrations in the long term and were therefore modeled as a simple 1:1 relationship to water on a monthly basis. Surface sediment concentrations may be expected to lag in concentration response to changes in the overlying water but the duration of the lag is unknown.

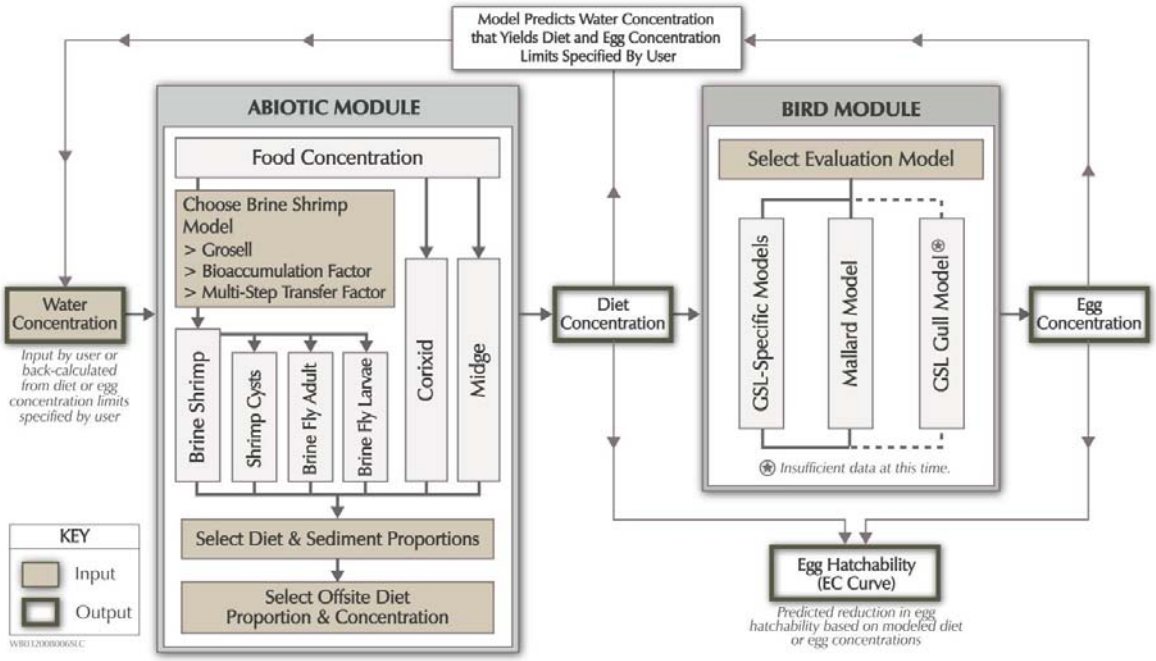
For this and all other modeled parameters, the mass balance model is designed to examine scenarios of possible future conditions that would be representative of a new, altered, steady-state condition. Data are insufficient to resolve the uncertainty in the dataset and resolve questions about long-term patterns of lake assimilation of selenium. The Science Panel recommended that additional monitoring be conducted to build and improve on the current model (potentially building a fully dynamic model) to allow for more accurate examination of scenarios for future conditions.

6.2 Bioaccumulation Model

A Bioaccumulation Model was developed to allow the user to estimate diet and egg selenium concentrations from an assumed waterborne selenium concentration. The model also allows the user to back-calculate a waterborne selenium concentration from an assumed diet or egg selenium concentration. Resulting waterborne, diet, and egg concentrations are listed and plotted upon egg and diet toxicity curves to illustrate potential effects of selenium on egg hatchability (Ohlendorf, 2003).

The Bioaccumulation Model is composed of a series of relationships that describe the transfer of selenium from water up through the food chain. The transfer factors and regression equations that represent these relationships were developed from data collected from Great Salt Lake as part of the research program. The user has the flexibility to select from numerous options to evaluate the sensitivity and results from alternative transfer relationships and bird diet combinations. Figure 6-1 illustrates inputs, outputs, and the general flow of logic of the Bioaccumulation Model.

FIGURE 6-1
Bioaccumulation Model Flow Chart



6.2.1 Bird Dietary Item Tissue Concentrations

The first part of the Bioaccumulation Model links measured biota tissue concentrations for the invertebrate food items to the water and sediment concentrations in which they were reared. The concept is that future, modeled tissue selenium concentrations could be estimated from modeled water and sediment values and knowledge of the existing relationships between invertebrate tissue selenium and concentrations in the ambient media. Measured brine fly tissue concentrations were taken from Cavitt (2007, 2008a) and Wurtsbaugh (2007), brine shrimp concentrations were compiled from the reports of Conover (2008a) and Marden (2007), and selenium concentrations in periphyton from biostromes were reported by Wurtsbaugh (2007). A limited number of other insect tissue selenium concentrations from 2006 were available from Conover et al. (2008a).

All invertebrate concentrations were summarized as monthly geometric means. None of the invertebrate species showed significant differences with spatial areas of the lake and the values used in the model are representative of lake-wide averages.

Brine fly selenium concentrations were examined for statistically significant relationships between fly tissue concentrations and periphyton algae or sediment concentrations, but there were few paired values and no statistically significant relationships. Selenium concentrations in brine flies (adults and larvae) and brine shrimp cysts were modeled with the assumption of a 1:1 relationship with changing brine shrimp concentrations (ultimately, modeled from waterborne concentrations). Periphyton algae (as measured on biostromes) were similarly assumed to vary in a 1:1 relationship with waterborne total selenium concentrations. Thus, insect food items for birds were assumed to vary directly and positively with changing lake water concentrations on a monthly basis.

In contrast, brine shrimp selenium concentrations could be quantitatively related to dissolved selenium in water and total seston (water column particulates) selenium concentrations using several modeling approaches (Figures 6-2 and 6-3). First, brine shrimp tissue concentrations were modeled based on a simple modification of Grosell's laboratory results (Grosell, 2007a, 2007b) for feeding experiments with Great Salt Lake brine shrimp fed *Dunaliella viridis*, the dominant Great Salt Lake algal food used by brine shrimp (listed as Grosell model in the Bioaccumulation Model). The modeled brine shrimp tissue concentrations were computed based on monthly estimates of dissolved selenium in water and the selenium concentrations in seston (surrogate measure for food). Grosell's Scenario 1 (based on waterborne concentrations less than 2.5 µg Se/L) was used for these estimates. Second, adult brine shrimp concentrations were based on the lake-derived Bioaccumulation Factor (listed as BAF model in the Bioaccumulation Model) of 6,720 as the ratio of brine shrimp tissue selenium concentrations to total concentrations of selenium in water. The third estimating method (listed as Multi Step – Transfer Factor [MS-TF] model in the Bioaccumulation Model) was to estimate seston from dissolved waterborne concentrations of selenium (K_d of 1,579) and brine shrimp from seston (Transfer Factor of 5.022). All methods tended to overestimate the measured brine shrimp selenium concentrations, with the monthly average differences being 1.3, 0.67, and 0.36 mg Se/kg dw for the Grosell, BAF, and MS-TF methods, respectively, over all months of measurement. Figure 6-2 shows a comparison of the monthly predictions versus measured average values.

In a comparative presentation of water, brine fly, and brine shrimp concentrations as documented from 17 studies of saline lakes and ponds, brine shrimp concentrations showed a probable "background" value of less than 2 mg Se/kg but ranged up to 110 mg Se/kg dw (J. Skorupa, personal communication). The lowest waterborne concentrations (below 5 µg Se/L) tended to have the highest water-to-brine-shrimp transfer factors (up to 3,400). The transfer factors at Great Salt Lake (6,720) are almost twice those ratios but representative of lower water column concentrations (those observed at Great Salt Lake are near the lowest in the comparative study). Site-specific conditions at Great Salt Lake may contribute to unusually elevated bioavailability and transfer of selenium to brine shrimp as compared to other lakes and ponds.

FIGURE 6-2
Measured vs. Modeled Brine Shrimp
Monthly Geometric Means

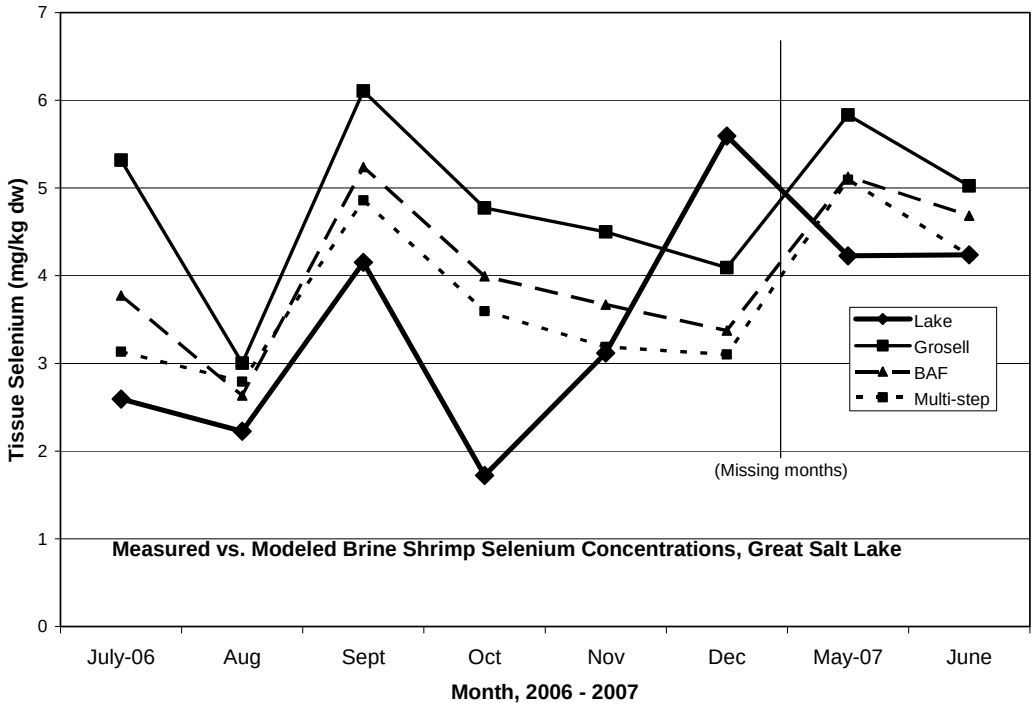


Figure 6-2 shows measured brine shrimp monthly geometric mean selenium concentrations versus modeled tissue levels predicted from Grosell's equations, a BAF factor from water, or an MS-TF from water to seston to shrimp.

6.3 Birds

Data from sampling and analysis of invertebrates (previously described) and birds at Great Salt Lake in 2006 and 2007 were used to develop selenium transfer relationships through the food web to birds and their eggs. Weighting factors (proportional composition of the diet) were developed based on food-habit studies conducted in 2006 by Conover et al. (2008a) and Cavitt (2008a) and additional samples collected in 2007 (Cavitt, 2008b; Conover et al., 2008a, 2008b, 2008c). Where site-specific data did not exist for Great Salt Lake (for example, assumed background selenium concentrations), data from other studies was used.

Detailed dietary, home range, and measured selenium accumulation data for gulls, stilts, and avocets (Cavitt 2008a; Conover et al., 2006) were used to develop regression equations and transfer and weighting factors for the Great Salt Lake food chain. Transfer factors were based on available measured selenium concentrations from Great Salt Lake biological studies.

Species-specific diet data were used to model selenium accumulation for each bird species (that is, the California gull [*Larus californicus*], black-necked stilt [*Himantopus mexicanus*], American avocet [*Recurvirostra americana*], eared grebe [*Podiceps nigricollis*], and common goldeneye [*Bucephala clangula*]). The percent of onsite foraging for each species was

determined from published foraging ranges and site-specific information, such as where on Great Salt Lake they tended to nest (for the breeding species).

The analytical techniques used in the models are based on a series of linear and log-linear relationships and transfer factors among environmental variables. In each case, assumptions are made about the underlying distribution of the data and the appropriateness of the relationship in explaining covariance of the variables. As is to be expected from environmental sampling data, there is much unexplained variation in the predictions, even in cases of statistically significant relationships. However, the basic assumption of the models is that the predictive relationships are all descriptive of underlying causal relationships.

Water, sediment, and invertebrate selenium concentrations for the avian portion of the model are taken from the abiotic/invertebrate portion of the model, which was previously discussed. The avian model uses the results of the abiotic/invertebrate model to estimate selenium transfer through the food web to gull and shorebird blood, liver, and eggs, and to grebe and goldeneye blood and liver.

After evaluating the model using all species and data, the Science Panel determined the reproductive endpoints were the most sensitive. Confounding variables and insufficient data did not allow a determination to be made regarding the effect of selenium and mercury on the body condition of eared grebes and common goldeneyes. The Science Panel discontinued further development of a model using eared grebes and common goldeneyes and this portion of the model was removed from the Bioaccumulation Model. Further discussion of the eared grebe and common goldeneye portion of the model is not included herein.

Modeling from diet to blood and liver selenium concentration remains in the model but is not used to estimate reproductive endpoints. In addition, since the model is for the open waters of Great Salt Lake, it was decided that diets would be 100 percent brine shrimp for gulls and that shorebird diets would be 100 percent brine fly larvae; however, the model still allows users to input varying composition of diet for gulls and shorebirds, insofar as concentrations in those dietary items are available. The brine fly selenium concentrations (adult and larvae) are based on a ratio of brine shrimp to brine fly selenium concentrations as discussed above.

A gull regression model was attempted to relate gull diet and egg selenium concentrations. However, a gull model could not be developed because of the small number of co-located gull diet and egg samples collected and the possibility that there is only a weak association between gull colonies and brine shrimp that were sampled. Regression models were developed from Great Salt Lake shorebird data and laboratory toxicological studies on mallards. The Shorebird Regression Model is site-specific; therefore, the Science Panel recommends its use for shorebirds. The gull transfer factor is site-specific; therefore, the Science Panel recommends its use for gulls.

6.3.1 Statistics

Simple regressions were used in developing equations based on measured parameters (from studies previously described) to be used for predicting future selenium concentrations in birds or their eggs. The model uses primarily the mean and 95 percent lower and upper

confidence intervals on the mean. ANOVA was used to measure the quality of the models (Zar, 1974; SAS Institute, 1996). All means are geometric means unless otherwise noted. Measured selenium concentrations were log-transformed due to the positive skewing of selenium data. Comparisons between measured selenium (see summary statistics in Section 5) and modeled selenium were made via ANOVA or the Student's *t*-test of log-transformed values (Zar, 1974; SAS Institute, 1996).

6.3.2 Avian Model

When there were enough data, regression was used to describe associations between diet and egg selenium concentrations, based on available measured selenium values from Great Salt Lake biological sampling (that is, from invertebrate to egg). The upper food chain was modeled using results of gull studies conducted by Conover et al. (2008a), and shorebird studies conducted by Cavitt (2008a, 2008b). Colocated water, sediment, and invertebrate samples were used to estimate selenium concentrations at the six sites where gulls and shorebirds were sampled during 2006, and the geometric mean of these was used to estimate the lakewide concentrations.

Weighting Factors

Selenium accumulation was weighted in three ways: (1) proportional composition of the diet for each species was based on food habits as determined from studies at Great Salt Lake that identified the proportions of the various dietary items in a species' diets; (2) home ranges or colony locations were determined from studies at Great Salt Lake or estimated from other studies and used to determine the proportion of onsite foraging for various species; and (3) an estimate of percent of offsite (or "background") food consumed was used.

The following diets described are listed in order of those found most often to least often for each species. In mixed diets, the proportions are approximated because there was generally a range of composition (proportions) among birds of that species. The demonstration model uses the first diet for each species; however, the model allows manipulation of the proportions of dietary items for all species.

Three shorebird diets were found in field studies at Great Salt Lake (Cavitt, 2007a):

1. 100 percent brine fly
2. 66 percent midge, 20 percent brine fly, 14 percent corixid
3. 40 percent midge, 36 percent brine fly, 24 percent corixid

Four gull diets were found in field studies at Great Salt Lake (Conover et al., 2006):

1. 100 percent brine shrimp
2. 100 percent brine fly
3. 100 percent corixid
4. 60 percent brine shrimp, 35 percent corixid, and 5 percent midge larvae

For eared grebes, four diets were found:

1. 100 percent brine shrimp
2. 100 percent brine fly
3. 60 percent brine shrimp, 40 percent brine fly

4. 60 percent brine shrimp, 30 percent brine fly, 10 percent corixid

Common goldeneyes fed on a variety of food items in Great Salt Lake but the proportions in individual birds collected are not known. Sixty-five percent of the goldeneyes collected contained brine fly larvae, five percent contained brine shrimp, 30 percent contained brine shrimp cysts, 40 percent contained wetland seeds, and 25 percent contained freshwater invertebrates. The following diets are in order of the percent of goldeneyes collected with the food item observed in their digestive tract, not the proportion in their diets:

1. 100 percent brine fly larvae
2. 100 percent wetland plant seeds
3. 100 percent brine shrimp cysts
4. 100 percent freshwater invertebrates
5. 100 percent brine shrimp

Transfer Factors

Simple numerical transfer factors were used for all steps that did not have a significant regression relationship or for which available data did not allow for the use of a regression equation. The transfer factors were based on spatially and temporally paired invertebrate and bird samples collected during 2006 (Equations 2, 3, and 4).

EQUATION 2
Transfer Factor for Diet Selenium to Blood Selenium

$$\text{Blood [Se]} = (\text{GM Blood [Se]} / \text{GM Diet [Se]})$$

EQUATION 3
Transfer Factor for Diet Selenium to Liver Selenium

$$\text{Liver [Se]} = (\text{GM Liver [Se]} / \text{GM Diet [Se]})$$

EQUATION 4
Transfer Factor for Diet selenium to Egg Selenium

$$\text{Egg [Se]} = (\text{GM Egg [Se]} / \text{GM Diet [Se]})$$

Diet Calculation

Selenium concentrations that were based on invertebrate samples colocated with bird or egg samples were used to determine weighting factors or regression equations from diet to tissue or diet to egg selenium. Dietary concentrations then used in the model were attained from the abiotic/invertebrate to biotic model as described above. Proportions of dietary items were then entered in the model and a diet was then estimated (Equation 5).

EQUATION 5
Diets for all Birds and Models were calculated from Abiotic/Invertebrate to Biotic Model Results

$$\text{Diet [Se]} = \text{Food Item [Se]} \times \text{proportion food item(s) in the diet}$$

In addition to the diet, birds eating invertebrates such as brine flies that live in the sediment are expected to incidentally ingest some sediment. The model calculates 0.05 fraction

sediment in addition to the diet proportion. The sediment concentration is calculated in the abiotic/invertebrate model and the percent of sediment ingested can be manipulated in the model.

6.3.3 Reproductive Effects

A general model for estimating egg selenium concentration from dietary concentration was developed from mallard feeding studies summarized by Ohlendorf (2003) and on which the threshold values are based (see Section 3.2.3). These data showed a significant positive relationship ($r^2 = 0.89$, $F_{1,17} = 128$, P less than 0.01) between diet and egg selenium concentrations in mallards. This regression equation (Equation 6) was compared to specific models (one for American avocets [Equation 7] and one for California gulls [Equation 8]) developed from colocated diet and egg samples collected from Great Salt Lake. The general model based on feeding studies where birds were exposed to a constant dietary selenium concentration under standardized conditions has the steepest slope. The specific models for avocets and gulls are based on only a few samples. The avocet model initially had only four paired samples collected as part of this program.

EQUATION 6
General Equation (Diet Selenium to Egg Selenium) Derived from Mallard Feeding Studies

$$\text{Egg Se } (\mu g/g \text{ dw}) = 0.787 + 3.267 \times \text{Diet Se } (\mu g/g \text{ dw})$$

EQUATION 7
American Avocet Diet-to-Egg Selenium Equation Based on Co-located Diet and Egg Samples from Great Salt Lake

$$\text{Avocet Egg Se } (\mu g/g \text{ dw}) = -1.34 + 2.52 \times \text{Diet Se } (\mu g/g \text{ dw})$$

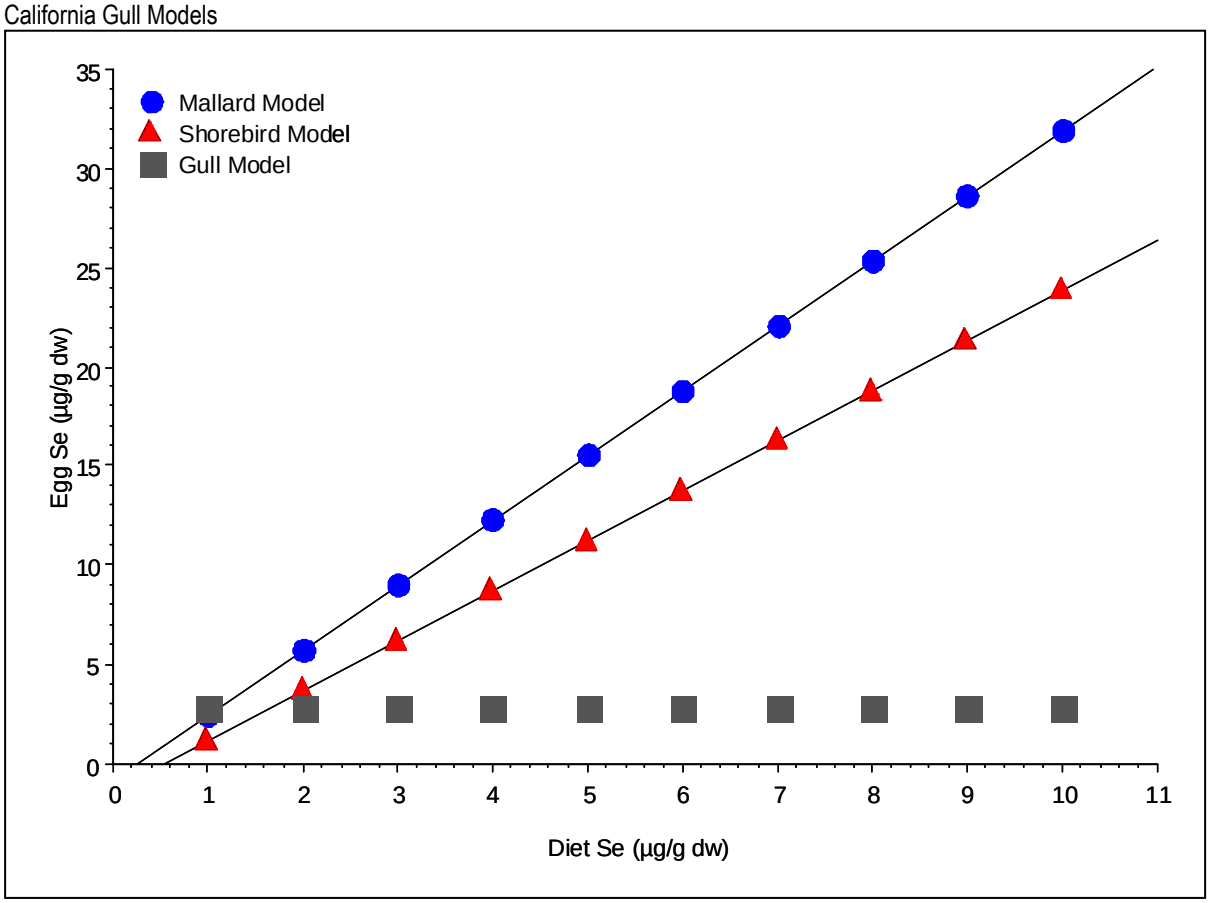
EQUATION 8
California Gull Diet-to-Egg Selenium Equation Based on Co-located Diet and Egg Samples from Great Salt Lake

$$\text{Gull Egg Se } (\mu g/g \text{ dw}) = -2.83 + 0.003 \times \text{Diet Se } (\mu g/g \text{ dw})$$

It is likely that birds primarily feed on invertebrates near their nests and that there is an association between selenium concentrations in invertebrates that are associated with a colony location and the birds in that colony. In other species, invertebrates collected from near the nest sites had similar selenium concentrations to invertebrates being fed to the young in the nest (Santolo, 2007). The avocet model (Equation 7) primarily uses food items (invertebrates) that are associated ($r^2 = 0.79$, $F_{1,3} = 7.3$, $P = 0.11$) with sediment from each location and show a similar slope to the generalized model (Figure 6-3). However, this was not the case with gulls because they do not feed on static resources at a colony but reflect a more dynamic relationship with Great Salt Lake water and therefore have only a weak association with the colony locations. The gull model (Equation 8) is based on brine shrimp for three locations and invertebrates from the Neponset Reservoir location, and it does not show a significant relationship ($r^2 = 0.001$, $F_{1,3} = 0.001$, $P = 0.9757$). This is possibly because even though the brine shrimp were collected from the locations where the gull eggs were collected, they are not tightly associated with the locations. Thus, the Science Panel concluded that the gull regression model should not be used or included in the Bioaccumulation Model until further data is collected that improves the relationship. When

the slopes of these models are compared, the general and shorebird models show similar slopes (Figure 6-3). The shorebird model is site-specific to Great Salt Lake; therefore the Science Panel recommends that it be used instead of the generalized mallard model for shorebirds. It should be noted that the Shorebird Model does overpredict egg selenium concentrations if used for gulls. The Shorebird Model should not be used for gulls.

FIGURE 6-3
Comparison of General Diet-to-Egg Selenium (Based on Mallard Studies) and Specific American Avocet and California Gull Models



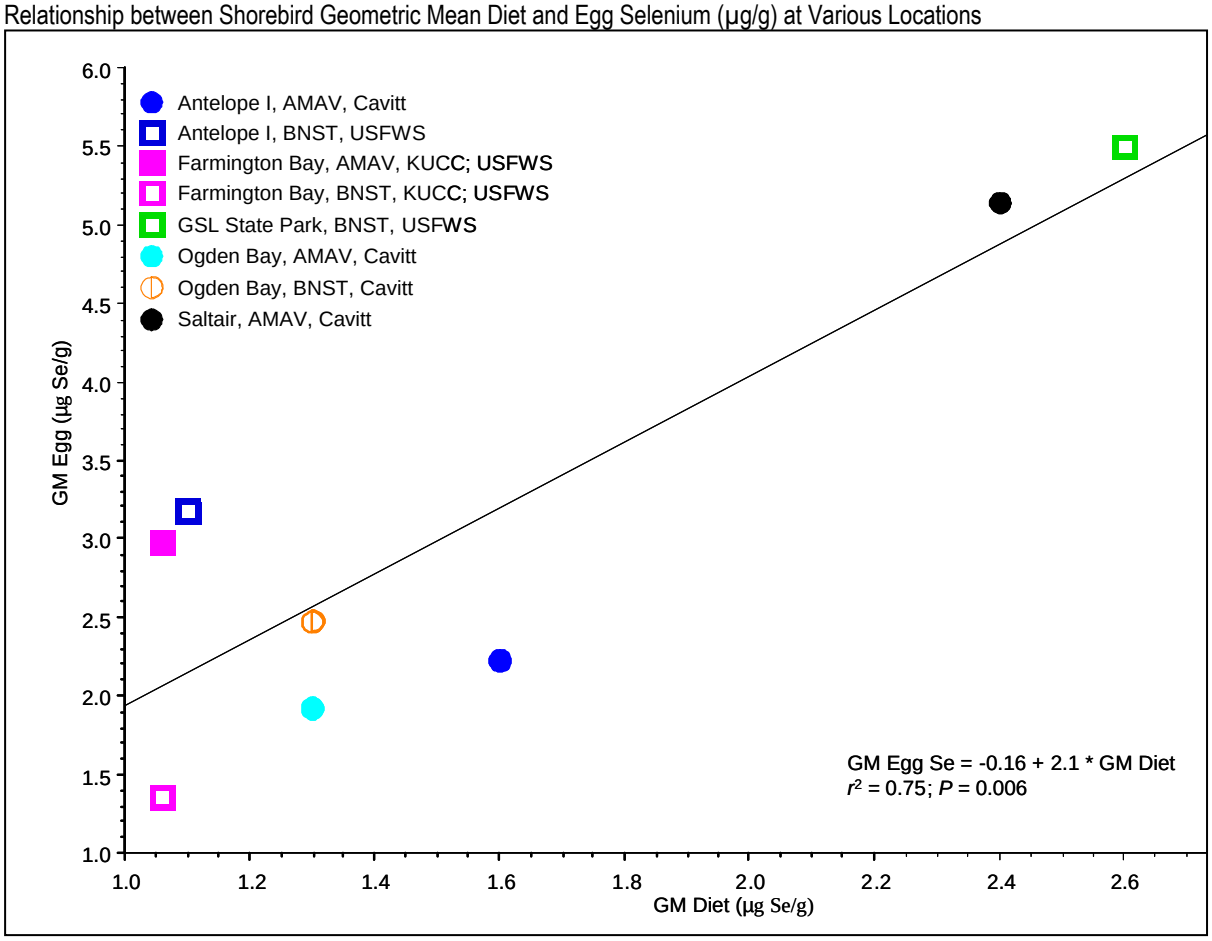
To increase the number of data points used in the shorebird diet-to-egg selenium regression model, spatially colocated samples collected from Great Salt Lake by the U.S. Fish and Wildlife Service (USFWS) and from Farmington Bay by EP&T (for Kennecott Utah Copper Corporation [KUCC]) were used. Assumptions that the egg and diet data were spatially co-located were made. Table 6-1 shows the data that was added to the sample results of diet and eggs collected for the project (Cavitt, 2007a).

TABLE 6-1
Additional Data Used in Shorebird Regression Model

Location	Species	GM Se (µg/g)	Mean (µg/g)	Collected by
Antelope Island	Brine fly adults and larvae	1.1	1.1	USFWS
Farmington Bay	Brine fly adults and corixids	1.1	1.1	USFWS
GSL State Park	Brine shrimp	2.6	2.7	USFWS
Antelope Island	Black-necked stilt eggs	3.2	3.2	USFWS
Farmington Bay	Black-necked stilt eggs	1.4	1.4	KUCC
Farmington Bay	American avocet eggs	2.9	3.3	KUCC
GSL State Park	Black-necked stilt eggs	5.5	5.6	USFWS

There was only a single invertebrate sample collected at Saltair so it was not used. Diet samples were collected in 1995 and 2005 from Farmington Bay and shorebird eggs were collected in 1995. The assumption was made that diet concentrations did not change significantly. Diet and eggs from Antelope Island were collected in 1996. Invertebrates and bird eggs were collected from Great Salt Lake State Park in 1997.

FIGURE 6-4
Relationship between Shorebird Geometric Mean Diet and Egg Selenium (µg/g) at Various Locations



The Shorebird Model (Equation 9) was selected by the Science Panel over the Mallard Model as the preferred bioaccumulation model because it is site-specific, shorebirds are less sensitive than mallards (using the Mallard Model for shorebirds would significantly overpredict egg concentrations), and the form of selenium used in the mallard studies creates a more conservative transfer factor than is observed on Great Salt Lake. The Gull Transfer Factor Model was selected by the Science Panel over the Shorebird and Mallard Models for use with gulls because it is site-specific and gulls appear to be less sensitive than shorebirds or mallards (using the Shorebird or Mallard Models for gulls significantly overpredicts egg concentrations for gulls). It should be noted that the Science Panel has more confidence in the shorebird relationships due to the colocated diet and egg samples collected for shorebirds. Preference should be given to the shorebird component of the Bioaccumulation Model until more is known about gull diet/egg relationships. The Shorebird Model and Gull Transfer Factor Model were combined into one option called the GSL-specific Model in the Bioaccumulation Model. Both the GSL-specific and Mallard Models are included in the Bioaccumulation Model for comparison. In addition, future co-located sampling should continue to improve this model.

EQUATION 9
Shorebird Diet-to-Egg Selenium Equation Based on Co-located Diet and Egg Samples from Great Salt Lake

$$\text{Shorebird Egg Se } (\mu g/g \text{ dw}) = -0.16 + 2.1 \times \text{Diet Se } (\mu g/g \text{ dw})$$

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