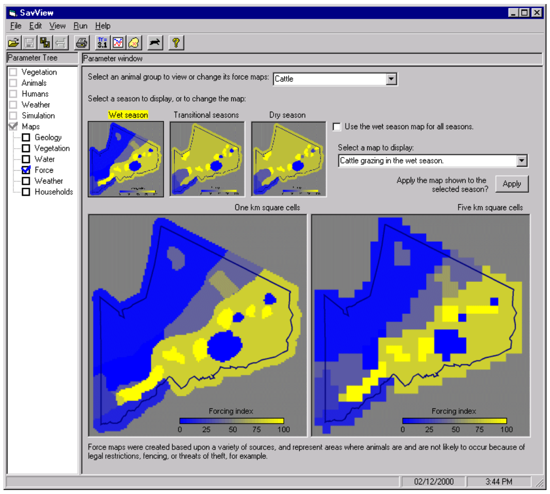
Restricting Animal Movements in Savanna

In general, in Savanna animals are distributed based upon forage quantity and quality, and physical relationships. There are many situations, however, where animal distributions are restricted for reasons not related to biology. For example, in Ngorongoro Conservation Area, Maasai are not allowed to graze animals in Ngorongoro Crater because of legal restrictions. Other restrictions might be due to fences or high likelihood of disease.



Select an animal group to view or change its force maps: Cattle

Select a season to display, or to change the map:

☐ Use the wet season map for all seasons.

Select a map to display: Cattle grazing in the wet season.

Apply the map shown to the selected season?

Force maps were created based upon a variety of sources, and represent areas where animals are and are not likely to occur because of legal restrictions, fencing, or threats of theft, for example.

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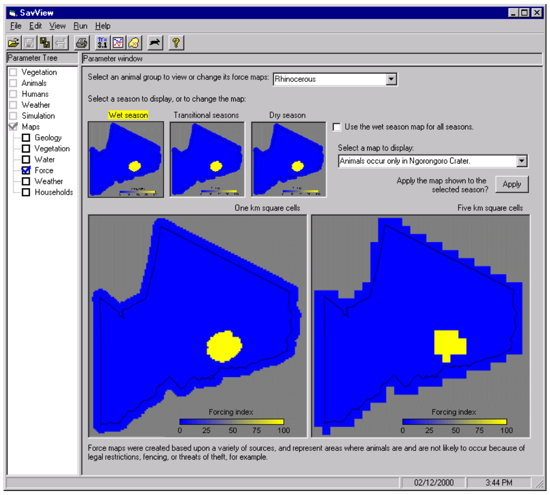
To include these restrictions in Savanna, *force maps* are used. Force maps contain scores from 0 to 100, reflecting how likely animals are to use an area. A grid cell with a score of 0 cannot be used by the animal in question. A grid cell with a score of 100 reflects no restriction on animals being placed in that cell.



Select an animal group to view or change its force maps: Rhinocerous

Select a season to display, or to change the map:

☐ Use the wet season map for all seasons.

Select a map to display: Animals occur only in Ngorongoro Crater.

Apply the map shown to the selected season?

Force maps were created based upon a variety of sources, and represent areas where animals are and are not likely to occur because of legal restrictions, fencing, or threats of theft, for example.

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Some animal groups, such as cattle, have different force maps for each of the seasons modeled. However, most animal groups have the same force map for each season.

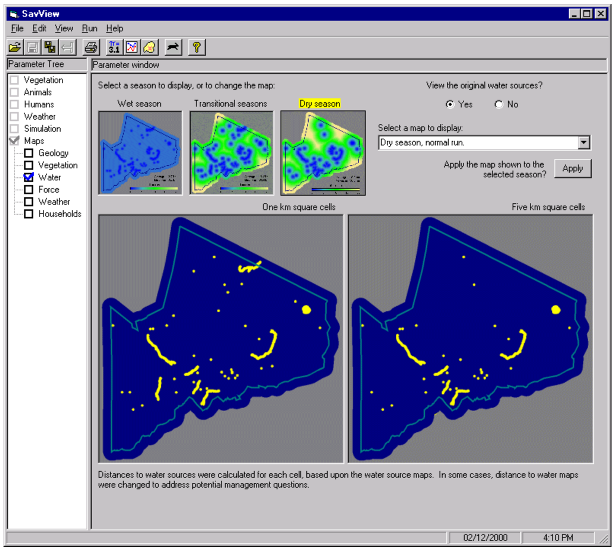
Exercise: Look at the force maps used for each of the 17 animal groups in NCA-Savanna.

Method: Use the methods listed on page 17 to open a set of parameters in SavView. With the parameter window shown, click on "Maps" and on "Force". Then select each animal group in turn, in the list at the top of the large window. As a group we will discuss why each of the maps looks as it does.

Notes: Disregard the other buttons and switches on the force map window for now. When we review the SavView tool in detail, we will discuss their use.

Distance to Water

Water quantities and movements are being modeled at the grid cell level throughout Savanna. In addition, at the landscape level, the distance to water is used to model the distribution of animals.



Select a season to display, or to change the map:

View the original water sources? ● Yes ○ No

Select a map to display: Dry season, normal run.

Apply the map shown to the selected season?

Distances to water sources were calculated for each cell, based upon the water source maps. In some cases, distance to water maps were changed to address potential management questions.

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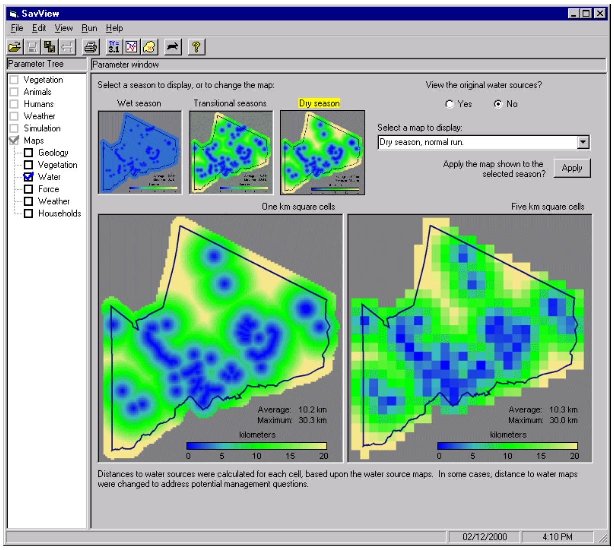
Water sources must be mapped to adapt Savanna to a site, but the water sources themselves are not used directly in Savanna. Instead we use a geographic information system to calculate the distance between each cell in the map and the closest water source.



Select a season to display, or to change the map:

View the original water sources? ○ Yes ● No

Select a map to display: Dry season, normal run.

Apply the map shown to the selected season?

One km square cells: Average: 10.2 km, Maximum: 30.3 km

Five km square cells: Average: 10.3 km, Maximum: 30.0 km

Distances to water sources were calculated for each cell, based upon the water source maps. In some cases, distance to water maps were changed to address potential management questions.

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Savanna can include brackish water sources if used by animal groups. Water types may be assigned water quality scores, and animal groups may be assigned which water quality types they will use.

Exercise: Look at the water maps used in NCA-Savanna.

Method: Use the methods listed on page 17 to open a set of parameters in SavView. With the parameter window shown, click on “Maps” and on “Water”. When shown, the distance to water maps will be displayed. Select “Yes” under the question “View the original water sources?” to see the original sites.

Notes: Disregard the other buttons and switches on the water map window for now. When we review the SavView tool in detail, we will discuss their use.

Although not used in NCA-Savanna, an important piece of information that Savanna can use is *water discharge*. If the amount of water being produced by wells are known, for example, Savanna can use the amount required by each animal in the animal groups to determine how many animals the site can support.

Disease Modeling in IMAS - MCF

As part of IMAS, we will be creating a Savanna submodel to simulation the effects of disease upon livestock and wildlife, for three diseases: malignant catarrhal fever, East Coast fever, and rinderpest. Because this submodel is still under development, it has not yet been merged with Savanna, and runs separately using Savanna output. When joined with Savanna there will be feedbacks between the main Savanna program and the disease model, with the number of animals dying in a given year affecting the next year’s population, for example. For now, those feedbacks do not take place.

The malignant catarrhal fever (MCF) portion of the submodel is essentially complete. MCF is shed by wildebeest calves while they are grazing on the plains of Ngorongoro, and can infect cattle, but not small livestock.

We used a risk-based mixing model to estimate MCF infection in cattle. From Savanna we have estimates of migratory wildebeest numbers and cattle for each week of each year. In the mixing model, mathematical functions are used to estimate how likely cattle are to come in contact with vegetation that has been grazed by wildebeest calves in the previous few hours. A portion of those cattle are considered to be infected. After the incubation period for the disease, almost all of these animals die.

Disease.prm
sample

```
  ...
.05         //noise       — The amount of noise (
.0,0.07,0.15,0.15,0.07,0.02,.0,.0,.0,.0,.0,.0  //e
.15         //p           — Proximity estimate (.
.25         //i           — Infectiousness estima
.70         //pv          — Prevelence estimate i
.0          //v           — Probability of risk m
1.0         //m           — Disease growth rate,
1.0         //r           — Number of animals in
  ...
```

p **- Proximity Index** The probability of exposure (0 to 1).

I **- Infectiousness** The agent’s capacity to cause infection (0 to 1).

***pv* - Prevelance** The proportion of animals in the target population that may already be exposed to the infectious agent (0 to 1).

***e* - Exposure** The fraction of time within each time step that infectious agent shed from one host animal will expose one target animal.

***v* - Mitigation** The probability of risk mitigation (0 to 1).

***m* - Growth Rate** The probability of disease progression within the target population.

***R* - Infection Threshold** The number of animals that are infected before the target population is considered to be infected.

***N* - Noise to Add** The number of animals estimated to be infected in each grid cell may be made more variable by adjusting this parameter, which can be represented by any positive integer.

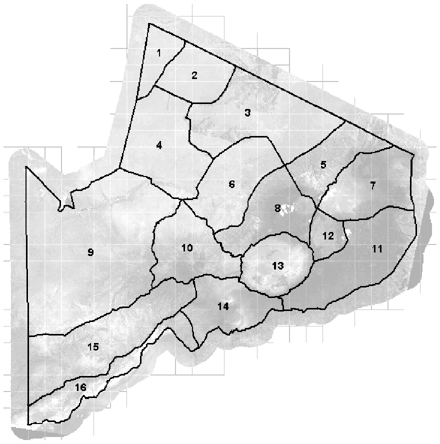
Exercise: We will review the MCF model output as a group. R. Howe and I developed the MCF model, joined by P. Pelissier and T. McCabe, and led by J. DeMartini.

Disease Modeling in IMAS - Rinderpest

Our model of rinderpest is not yet complete, but significant progress has been made. There are several ways that rinderpest modeling differs from MCF, and is generally more complex. In MCF, a single host (wildebeest) may transmit disease to a single target (cattle), and the cattle do not spread the disease amongst themselves. In rinderpest, cattle may infect wildebeest and other wildlife species, to varying degrees, which may in return infect cattle. In addition, cattle may infect other cattle, so we must account for movements of herds around Ngorongoro Conservation Area.

Our rinderpest model applies SEIR ("Susceptible, Exposed, Infected, and Removed") equations, which have been used successfully by team members in other work, to estimate the number of cattle that might serve as hosts for rinderpest; in essence, the growth rates of the disease within the susceptible cattle population are estimated. From there, risk-based mixing models of the type used to model MCF are used for each of the susceptible groups of wildlife, modeling the spread of rinderpest from cattle to wildlife. To limit the complexity of an already complex modeling effort, we will assume that reinfection of cattle by wildlife is not a significant effect within the system.

To ensure that cattle movements are included when modeling disease spread, we have estimated the movements herders make between 16 blocks within NCA, for five seasons (early wet to wet; wet to transitional; transitional to dry; dry to transitional;



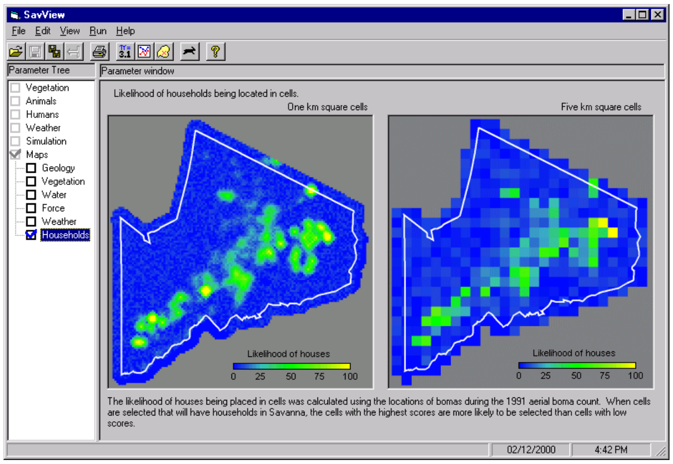
transitional to early wet). The likelihood of infection in each of the blocks will be determined, in part, by how much movement had occurred between that block and other blocks with infected animals. Using this technique, a rinderpest infection in a portion of NCA where herders are predominately sedentary will have less of an effect than in a block with a great deal of movement.

Notes: R. Howe and J. Mariner have developed the rinderpest submodel. T. McCabe and I mapped the movements of Maasai herders and their cattle, and I am modeling movements across NCA. We are led by J. DeMartini.

Households and Agriculture in Savanna

Households and agriculture are linked in Savanna, where each household may have some associated agriculture. There will be more realistic relationships between people, agriculture, livestock and wildlife when the full economic model is incorporated into Savanna. Until then, people affect animals by reducing the grazing areas available to the animals, because of agriculture.

The number of houses set for the model must be placed realistically on the site. To do this, a map reflecting the current density of houses is used. This map *is not* the distribution of houses and agriculture in the simulation, but how likely each grid cell is to contain houses. As households are distributed on the landscape during a simulation, cells with high scores (100) in the map are more likely to receive houses than those with low scores (0).



Likelihood of households being located in cells.

The likelihood of houses being placed in cells was calculated using the locations of bomas during the 1991 aerial boma count. When cells are selected that will have households in Savanna, the cells with the highest scores are more likely to be selected than cells with low scores.

The amount of agriculture is set for three household wealth values, poor, moderate, and wealthy. The proportion of households with each wealth value is set as well.

A human population growth rate may be set when doing modeling. If set, at the end of each month the population is changed according to the growth rate.

Exercise: Look at the likelihood of households map used in NCA-Savanna.

Method: Use the methods listed on page 17 to open a set of parameters in SavView. With the parameter window shown, click on "Maps" and on "Households".

Exercise: Look at AGRIC.PRM in the "parms" directory.

Method: Use Windows Explorer to move to the \savanna\sites\nca\parms directory, and double-click upon the file.

Notes: The household density map was created using results provided by K. Campbell from a 1991 aerial survey of bomas. Cell-based rules within a geographic information system were used to convert the points where bomas occurred into a density map. With that, the distribution of modeled households reflects where households were placed in 1991.

Household-level Economics

A rule-based model representing cash flow and dietary energy intake in households typical of Ngorongoro Conservation Area is being created by Phillip Thornton, of ILRI, and Kathy Galvin, of CSU. Like the disease submodel of Savanna that is under development, the socio-economic submodel is being developed separate from Savanna. Output files from Savanna are read into the socio-economic model, with the model responding to changes in the Savanna output, but not feeding back information. Eventually the submodel will be joined with Savanna, to allow feedbacks.

The socio-economic model being created will be based upon an original pastoralist model (NORAD) created by David Swift and Michael Coughenour. Both models use sets of relatively simple rules that govern how pastoralists (and more economically linked stakeholders in Kajiado, Kenya) respond to conditions. In general terms, the NORAD model calculated the food available to households, and calculated how much energy each household required. If there was a deficit, the difference was made-up through slaughtering animals, trade, famine relief, hunting, begging, bleeding, or human weight loss. Each of these behaviors was given a score, showing how likely households were to use a given behavior.

The new socio-economic model includes a target energy level for each household, as did NORAD, but it also includes more detail about cropping and the economic status of households. Households may gain wealth and security both through building food reserves, such as tropical livestock units, and through building cash. All significant sources of money coming into the household and being spent are recorded. For example, households may consider expanding their agricultural plot, if there is adequate labor available to tend it. From that agriculture, they will receive some benefit from maize, which will add to their food stores, and perhaps be sold if in surplus.

As stated by Thornton and Galvin an our recent annual report, once the model is finished and joined with Savanna, experiments can be conducted to answer questions such as:

- What will be the effects (socio-economic and ecological) if household maize cropping area increases?
- What are the likely impacts of a single drought, or of recurrent droughts in successive years?
- What are the likely impacts of changes in household targets for livestock numbers and cash?