Predicting the effectiveness of Chronic Wasting Disease

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Introduction

Chronic Wasting Disease abbreviated as CWD is a transmissible neurological disease that affects cervids such as deer, elk, and moose causing severe impacts on these wildlife populations. The disease, part of a family of diseases known as transmissible spongiform encephalopathies (TSEs), is caused by misfolded proteins known as prions, leading to brain damage and ultimately death in infected animals. It is a fatal disease with no known cure, vaccine, nor environmental decontamination methods that affects the brain and lymphatic system causing neurodegeneration and eventually death. In the USA, it was first discovered in the 1960s, within a government research facility in Colorado, in a captive mule deer. Today CWD has been found in 31 states, 4 providences of Canada, Norway, South Korea, Finland, and Sweden [1]. CWD is the only TSE found in free ranging animals and has been in the spotlight for the last 50 years due to shown lasting negative effects on populations that were thought not possible [3]. Symptoms include loss of coordination, lethargy, drooling, gradual weight loss despite eating, loss of fear of humans, increased thirst and urination, and lowered head with blank stare. The disease can take 1.5 to 3 years to incubate but only 1 year to progress. The disease is originally known to be transmittable by direct contact between the cervids, however, there is an indirect transmission aspect through the depositing of prions in the natural environment through bodily fluids and waste that is part of the disease progression through the deer population [1]. Management culling efforts originally done as generalized mass reduction of the deer population (generalized culling) and recently more direct localized reduction (localized culling) because how generalized has not been proven to work the best due to an increase in prevalence in spite of generalized culling efforts , are the tools that organizations like the Minnesota Department of Natural Resources (MN DNR) have available for management of the disease [2]. The spread of CWD presents a significant challenge for wildlife management and conservation efforts, particularly in regions where hunting and wildlife tourism are critical components of the local economy. Effective management strategies are essential to control the spread of CWD and to maintain healthy wildlife populations.

Problem Statement

Management efforts to control the growth and spread of CWD in deer have been hampered by disagreements with access to land and the efficacy of different types of culling. Our project's goal is to use a spatially explicit model individualized based model (IBM) that simulates deer movements, deer features, the spread of CWD, and hunting and culling, to match output data to as close to reality as possible. This model, being an IBM and spatially explicit, has the benefit that ecologists getting to link individual behavior to population dynamics and the predictions that come with certain changes with individuals with the bonus that spatially explicit models are good for simulating disease transmissions [3]. The results from the simulation allow us to determine whether there is a significant relationship between prevalence of CWD and land access for localized culling. Additionally, through the simulation we can avoid costly real-life testing and other hazards in the field.

Research goals

For this project, the main goals that were set up and accomplished were gaining an in depth understanding of Chronic Wasting Disease, learning R in order to understand the R script and the Monte Carlo simulation that was used, figuring out how parameters influence the four pieces of output from the model, and matching those four pieces with the field data the MN DNR supplied by having the closest parameter picks. After these initial goals, our subsequent goals were to use the baseline parameter choices to understand and predict the output for different land access management scenarios and gather our findings for a final presentation and report.

Methodology

Our first approach to finding a good baseline involved changing the resolution of the simulation. We wanted to simulate a 28 x 28-mile area; however, a complete simulation of that resolution takes 2 – 3 days to complete (a complete simulation is one that was run 100 times). Keeping all other variables the same and just decreasing the resolution we realized drastically decreased the simulation time; however, it provided inaccurate results due to dear density and other variables not scaling down properly well as time constraints on figuring out how to properly scale the other variables down to correspond to the resolution. There were 3 variables that were completely adjustable within this simulation: Eta as Whether transmission is density (eta = 0) or frequency (eta = 1) dependent, B.d as the Direct transmission coefficient, and B.i as the Indirect transmission coefficient. See appendix 6 for how it translated to the model code.

Once we figured out that it was necessary to simulate in the 28 x 28 space instead of trying random values and letting the computer run for 3 days, we conducted a Design of Experiment (DOE). Within this DOE 72 tests for plausible variable combinations were come up with and ran a single time. Based on the results, we filtered out combinations that produced poor results and focused on the tests that yielded results close to the field data given by the MN DNR (figure 1). Figure 1 shows the 4 main output our model also gives as number of deer harvested and tested positive, and number of culled and from the culled positive. From the DOE we found 15 potential combinations of the 3 variables, and from there were further able to get the number down to 7 using different statistical measures such as RMSE, MAE, MAPE, and R – squared. With the 7 combinations with the best results, we ran these simulations multiple times and took the average of the best one to form our baseline. Once we decided on the baseline we decided to run 4 scenarios of 0% management area, 10% area, 50% area, and 100% area and given the results decide if there was an impact in controlling the disease based on land access.

Harvest and Sample Numbers for DPAs 603, 347/647, and 348/648

Year	Number of deer harvested	Number of Hunter harvested deer tested	Number of Hunter Harvested deer positive	Shooting Permits	Shooting Permits Positive	Number of deer Culled and Sampled	Number of culled deer positive	Percent of acres accessable for culling
2016	3578	1239	6	214	2	238	2	UNK
2017	3167	1665	6	19	0	0	0	NA
2018	2269	2018	14	328	0	455	12	18.30%
2019	3096	2991	16	9	0	214	4	9.80%
2020	3206	1105	9	18	0	282	3	6.70%
2021	2814	1586	16	21	0	189	8	9.10%
2022	2647	908	9	0	0	402	16	7.70%

Figure 1: MN DNR Field Data

Results

We agreed on a baseline set of parameters that we would not change at all but instead change the amount of land access the spatially explicit model has available to cull deer. Our main 3 parameters eta, B.d, B.i we chose as the numbers 0.0004, 0.002, and 0.0002 respectively. See appendix 6 and 7 for the expanded code version of the full list of parameters such as mortality rates and number of sick deer introduced that still was relevant to our 4-piece output goal. B.d and B.i were important due to being direct and indirect transmission components about how they are semi based on literature as direct transmission has a 100 times greater chance to spread a disease rather than indirect means like in this case prion deposits in carcasses and in the environment. However, these numbers are still unknown on the correct parameter choices, so our choices did not reflect 100 times increase but ten times increase. From our baseline we got a rough estimate of the graph in appendix 2 that corresponded to positive deer prevalence as one of the main outputs but was not the very best we could find if we had more time. From figure 3 we can also see that the number of deer hunted is close on average to figure1 and the number culled is close. However, it is hard to tell if the proportion of deer positive is close to field data, but this is where our checking prevalence graphs (appendix 1) tells us if we are on track with field data.

For the first management scenario as the worst-case scenario for MN DNR to have 0% access of the land to form a localized culling solution in appendix 3 we saw a sharp increase in the average prevalence of the disease over the 26 simulations ran with a 95% confidence interval over the recorded years. The second management scenario is if the MN DNR had slightly more than the usual 8.5% pre given by our model for an increase to 10% land access. If we consult appendix 4, we can see the prevalence is being controlled slightly better than the original 8.5% baseline in appendix 2 with a 95% confidence interval shaded in red for the multiple simulations. The third scenario is if the MN DNR had half the land in the study zone (figure 2) as appendix 4 showed slight peaks in prevalence within the confidence interval range but overall was lower than field data. Finally, the management scenario with 100% access as appendix 5 shows a similar trend that appendix 4 has but there are no peaks of increased prevalence. These results tell the MN DNR that the baseline and model are useful in matching reality (figure 1) and can be used to help convince landowners that more land access can help drop the increase of CWD prevalence.

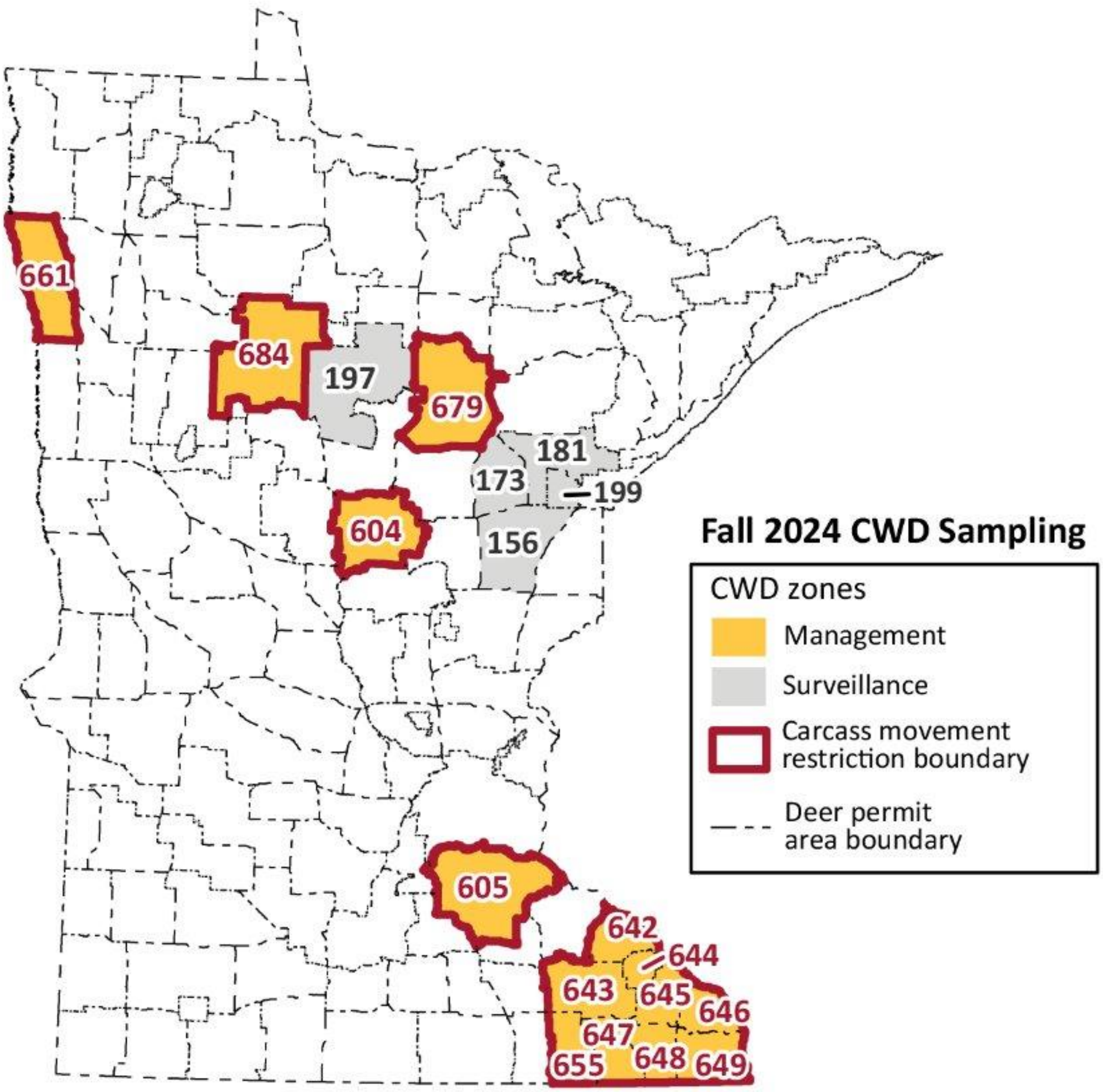


Figure 2: study zone of MN DNR field work

N_Hunt_1	N_Hunt_2	N_Hunt_3	N_Hunt_4	N_Hunt_5	N_Hunt_6	N_Hunt_7	P_Hunt_1	P_Hunt_2	P_Hunt_3	P_Hunt_4	P_Hunt_5	P_Hunt_6	P_Hunt_7	N_Cull_1	N_Cull_2	N_Cull_3	N_Cull_4	N_Cull_5	N_Cull_6	N_Cull_7	P_Cull_1	P_Cull_2	P_Cull_3	P_Cull_4	P_Cull_5	P_Cull_6	P_Cull_7
NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
3286	3528	3725	4192	4588	5023	5717	0.002062	0.002924	0.001823	0.002457	0.001541	0.003546	0	174	380	190	131	149	336	0	0.005747	0.071053	0.1	0.21374	0.147651	0.08631	NA
2965	3109	3491	3760	3985	4351	4892	0.001195	0.00107	0.00198	0.008219	0.003549	0.006279	0.002185	158	97	286	638	465	389	210	0.025316	0.020619	0.122378	0.109718	0.148387	0.143959	0.080952
3022	3013	3367	3670	4041	4520	4832	0.004505	0	0.00207	0	0.003478	0.007886	0.003644	435	0	296	0	239	626	403	0.013793	NA	0.060811	NA	0.079498	0.095847	0.141439
3004	3152	3388	3697	4044	4495	4907	0.002288	0.002081	0.003049	0.001918	0.003578	0.006061	0.007215	278	282	241	97	289	754	709	0	0.021277	0.074689	0.134021	0.141869	0.098143	0.124118
3086	3238	3548	3881	4136	4542	5131	0.002188	0.001007	0.003749	0.002703	0.003384	0	0.002007	225	181	332	254	363	0	260	0.026667	0.016575	0.057229	0.086614	0.057851	NA	0.111538
3017	3139	3504	3663	4043	4537	4831	0.002186	0	0.004032	0.002705	0.001779	0.003165	0.004342	235	0	332	339	143	329	394	0.029787	NA	0.114458	0.097345	0.153846	0.06079	0.045685
3003	3028	3419	3731	4028	4236	4708	0.001221	0.001064	0.003984	0.00543	0.005008	0.004115	0.002948	148	131	238	537	792	407	353	0.02027	0.015267	0.105042	0.065177	0.074495	0.137592	0.087819
3047	3081	3426	3776	4027	4570	4962	0.001203	0.002137	0.002022	0.001847	0.005259	0.003065	0.002837	173	219	122	165	311	423	264	0.028902	0.013699	0.057377	0.09697	0.115756	0.061466	0.151515
3175	3509	3663	4031	4472	4957	5429	0.004171	0.003895	0.004625	0.00265	0.001586	0.002051	0.002483	372	307	512	248	57	301	291	0.034946	0.068404	0.109375	0.133065	0.175439	0.07309	0.034364
3040	3199	3408	3868	4131	4347	4826	0.00232	0	0.002039	0.003537	0.012017	0.004	0.002939	277	0	126	560	1096	421	344	0.025271	NA	0.039683	0.069643	0.092153	0.104513	0.087209
3044	3214	3457	3792	4157	4569	5022	0.003394	0.002112	0.001929	0.005464	0.005004	0.00236	0.001432	341	124	192	382	192	68	20	0.02346	0.024194	0.020833	0.162304	0.067708	0.088235	0.2
2941	3136	3484	3760	4075	4436	4816	0.002548	0	0	0.002765	0.005141	0.007053	0.005185	185	0	0	319	770	799	313	0.032432	NA	NA	0.144201	0.050649	0.051314	0.105431
3040	3099	3403	3757	4122	4405	4679	0.001192	0	0.006054	0.002828	0.004219	0.004754	0.003802	198	0	593	199	430	731	378	0.025253	NA	0.084317	0.145729	0.125581	0.082079	0.132275
3088	3282	3488	3714	4011	4550	5100	0.001153	0	0.001951	0.00188	0	0.003928	0.003336	182	0	275	153	0	353	654	0.005495	NA	0.029091	0.202614	NA	0.172805	0.074924
3005	3196	3377	3686	4010	4501	4883	0.002317	0.004082	0.002112	0.000962	0.001759	0.006354	0.001416	329	359	204	71	172	313	186	0.006079	0.036212	0.039216	0.056338	0.02907	0.076677	0.05914
3068	3134	3366	3767	4092	4621	4791	0.001156	0.003049	0.002058	0.004488	0.004382	0.003882	0.002926	108	321	126	359	489	363	305	0.009259	0.024922	0.119048	0.052925	0.141104	0.140496	0.068852
3184	3127	3466	3698	4046	4479	4789	0.003286	0	0.005128	0.007463	0.001736	0.005435	0.004277	431	0	425	540	73	340	285	0.013921	NA	0.063529	0.144444	0.109589	0.061765	0.077193
2988	3170	3485	3832	4192	4483	5184	0.001115	0.003243	0.002927	0.00641	0.004288	0.001577	0.002766	90	244	185	444	269	81	496	0.022222	0	0.086486	0.087838	0.193309	0.148148	0.08871
3053	3160	3367	3678	4213	4623	5027	0.005708	0.001082	0	0.002846	0.000827	0.003717	0.002761	437	104	0	252	87	469	223	0.016018	0.019231	NA	0.039683	0.183908	0.044776	0.107623
3017	3220	3501	3917	4024	4531	4931	0.00114	0.000992	0.001009	0.009778	0.007491	0.005439	0.003484	173	80	129	872	371	194	221	0.023121	0.05	0.007752	0.084862	0.180593	0.268041	0.095023
2989	3171	3528	3749	4132	4546	4782	0.001244	0.002101	0.000994	0.001797	0.004223	0.011398	0.001451	181	274	134	393	329	702	200	0.022099	0.040146	0.089552	0.040712	0.130699	0.108262	0.045
3043	3035	3398	3846	3987	4596	4824	0.001119	0.001099	0.001038	0.002671	0.000859	0.003805	0.002214	127	86	116	153	180	468	183	0.015748	0.046512	0.025862	0.267974	0.072222	0.098291	0.202186
3545	3780	4059	4442	4837	5374	5889	0.007576	0.006233	0.006728	0.002387	0.003584	0.003139	0.001192	593	501	490	185	217	444	496	0.08769	0.161677	0.07551	0.091892	0.050691	0.06982	0.020161
2987	3180	3452	3665	3922	4256	4668	0.001202	0.000974	0.004826	0.004826	0.004344	0.003292	0.00078	222	162	349	564	255	201	97	0.009009	0.006173	0.083095	0.049645	0.180392	0.079602	0.072165
3080	3063	3473	3866	4167	4413	4827	0.001104	0	0.003883	0.011111	0.004219	0.00464	0.002235	129	0	562	747	307	354	238	0.015504	NA	0.072954	0.123159	0.068404	0.19209	0.151261

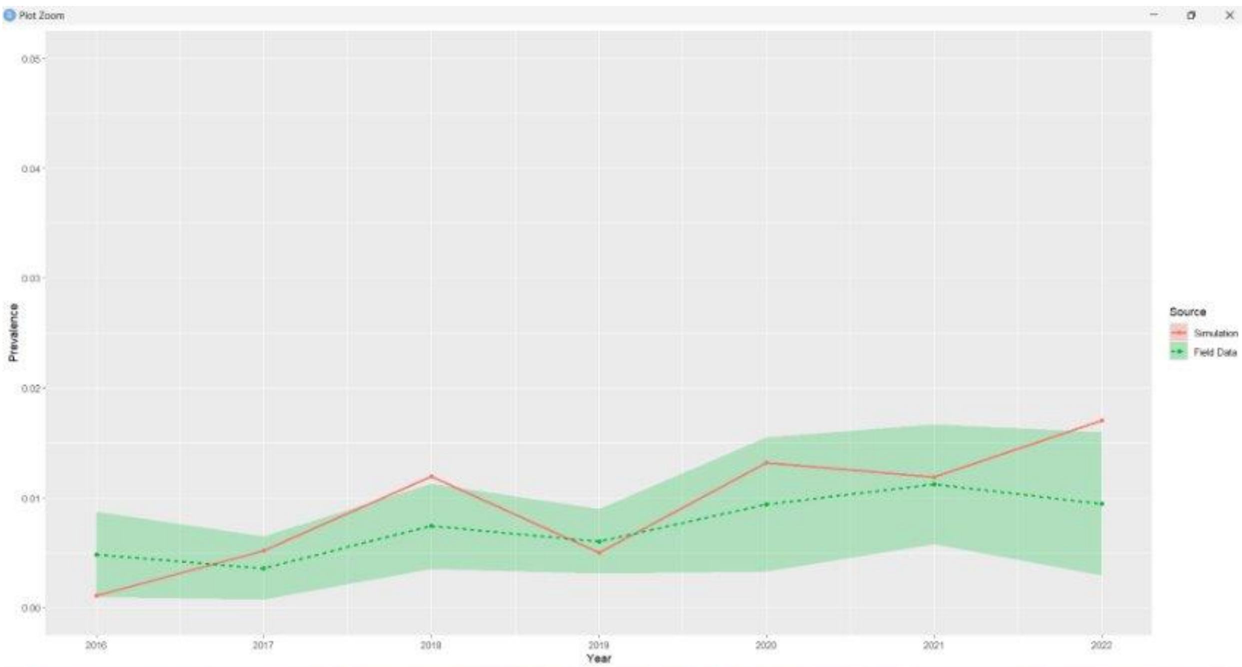
Figure 3: baseline output

Conclusion

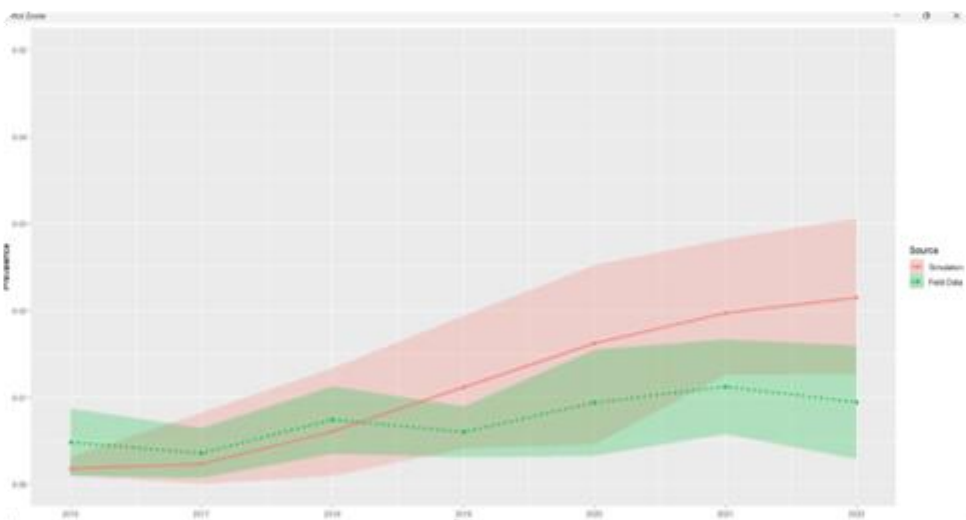
In conclusion, we achieved our main goals of better understanding the parameters that make the model, finding a baseline to match the field data as close to reality and getting results for management scenarios. However, there were some limitations in the process that hampered the work regarding time constraints because finding parameters for the baseline takes days, thus it isn't perfect. However we saw a significant decrease in prevalence of the management graphs and can apply this work to MN DNR work by achieving three things: helping the organization save time and money due to the simulation being useful, give findings to convince land owners to increase land access, and finally helping the MN DNR understand where to allocate more resources such as testing, culling, or projects that help communicate with landowners about the disease management. For future goals for further work on the project we could use the expanded time to better optimize the code for faster run times, test out better baseline parameters with help from statistical measures and explore more specific management scenarios.

Appendix

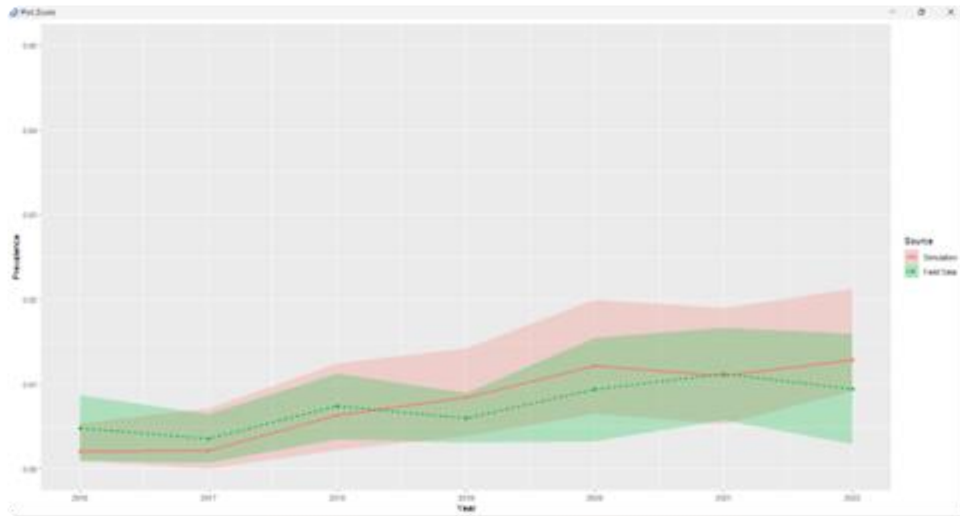
Appendix 1: Baseline parameter output graph



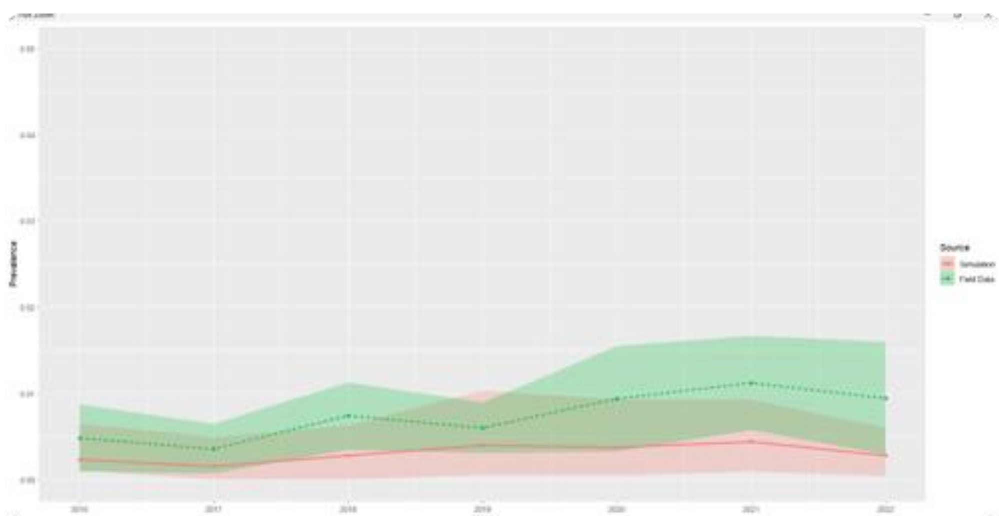
Appendix 2: Baseline parameter output graph with 0% land access



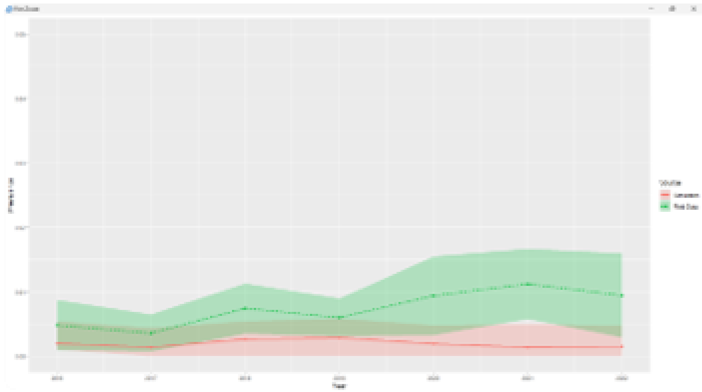
Appendix 3: Baseline parameter output graph with 10% land access



Appendix 4: Baseline parameter output graph with 50% land access



Appendix 5: Baseline parameter output graph with 100% land access



Appendix 6: Code snippets of main general changeable parameters

```
{
  deer.dens <- 25 # Deer per square mile                  # MINORLY ADJUSTABLE

  simulationAreaDims <- 1760 * 28.0 # In denominations of 1 mile = 1760 yards
  managementCellSize <- 1760 * 1.00 # In denominations of 1 mile = 1760 yards
  cellularResolution <- 1760 * 0.25 # In denominations of 1 mile = 1760 yards
  originatedAreaDims <- 1760 * 5.00 # In denominations of 1 mile = 1760 yards
}

# Define parameters for disease transmission (ALL FULLY ADJUSTABLE)
{
  eta <- 0.0004  ## Whether transmission is density (eta = 0) or frequency (eta = 1) dependent
  B.d <- 0.002  ## Direct transmission coefficient (100x larger than indirect)
  B.i <- 0.0002  ## Indirect transmission coefficient
```

Appendix 7: Code snippets of general changeable parameters continued

```
  numberOfIntroduced <- 25                               # FULLY ADJUSTABLE
  yearsOfManagement <- 7

  managementThreshold <- c(0.001, 0.008) # Desiring a mean of 0.0048

  probabilityOfTesting <- 0.400 # Excludes fawns because they were not tested
  probabilityOfCulling <- 0.850
  probabilityOfAccess  <- 0.1 #0.085

  ## Establish priority and marginal cull rates across eight-week periods
  {
    priorityCullRate <- 1 - (1 - probabilityOfCulling) ^ (1 / 8)
    marginalCullRate <- 1 - (1 - probabilityOfCulling) ^ (1 / 8)
  }
}

# Define parameters for mortality (ALL MINORLY ADJUSTABLE)
{
  naturalMortalityRate <- c(0.55, 0.10, 0.05) # Non-harvest mortality for juveniles, yearlings, adults
  hunt.antl <- 0.15 # Proportion of bucks that get harvested #0.25 og
  hunt.less <- 0.10 # Proportion of does/fawns that get harvestetd #0.20 og
```

References

[1] Thompson, N. E. (2023). *Management of free-ranging white-tailed deer with chronic wasting disease in Michigan* (dissertation).

[2] Almberg, Emily S., Cross, Paul C., Johnson, Christopher J., Heisey, Dennis M., & Richards, Bryan J. (2011). *Modeling routes of Chronic Wasting Disease Transmission: Environmental prion persistence promotes deer population decline and extinction* (dissertation).

[3] Kjaer, L. J. (2010). *Individual-based modeling of white-tailed deer (Odocoileus virginianus) movements and epizootiology* (dissertation).