Supplementary Appendix

Methods appendix

Model Covariates

The cause of death ensemble modelling (CODEm) approach used in GBD allows us to try multiple covariates that we believe to be significant with the rate of snakebite death, and CODEm uses feature selection to pick out only the best combinations of covariates based on out-of-sample RMSE validation.

The covariates used in the GBD 2019 venomous animal contact CODEm model and their prior direction are below in Table 1, along with the same covariates and their direction used in the species-specific models. Directions differ for some priors because of uncertainty that a prior direction would be true for all five venomous species models. For example, we have a strong prior that the rate of scorpion bites would decrease with rainfall, but we do not have this strong negative prior for snakes and believe it could be a positive association.

Appendix Table 1. Covariates used in the five ST-GPR models and the general GBD 2019 model. Directions represent priors set on the beta coefficients to ensure their direction is as expected.

Covariate	GBD 2019 direction	Species-specific direction
Healthcare Access and Quality Index	-1	-1
Rainfall population-weighted (mm/yr)	1	0
Urbanicity	-1	-1
Proportion of population involved in agricultural activities	1	1
Population-weighted mean temperature	1	0
Socio-demographic Index	-1	-1
Absolute value of average latitude	-1	0
Education (years per capita)	-1	-1
Elevation over 1500m (proportion)	-1	0
Elevation under 100m (proportion)	-1	0
Log-transformed age-standardised SEV scalar: venom	1	1
Population density (over 1000 ppl/sqkm, proportion)	-1	-1
Population density (under 150 ppl/sqkm, proportion)	1	1
LDI (I$ per capita)	-1	-1
Proportion of population vulnerable to venomous snakebites[a]	1	1
Mean number of venomous snake species[a]	1	1

a: These covariates were only used in the mortality from venomous snakes model, not the other four species. They were extracted from data used by Longbottom et al.[1] LDI=lag-distributed income. SEV=summary exposure value. ST-GPR=spatiotemporal Gaussian process regression.

Years of life lived residual life expectancy

Years of life lived (YLLs) are defined as the difference between life expectancy and the age at which a death occurs, based on life tables used in GBD 2019 that estimate the remaining life expectancy for each five-year age group in all populations greater than 5 million in GBD 2019. Table 2 shows the life expectancy used in YLL calculations for GBD 2019.

Appendix Table 2. Residual years of life lost from a death for each age group. Residual life expectancy is based on the maximum life expectancy globally.

Age	Residual life expectancy (years)
0	87.9
1	87.0
5	83.0
10	78.1
15	73.1
20	68.1
25	63.2
30	58.2
35	53.3
40	48.4
45	43.5
50	38.7
55	34.0
60	29.3
65	24.7
70	20.3
75	16.1
80	12.2
85	8.8
90	6.1
95	3.9
100	2.2
105	1.6
110	1.4

Venom-specific ICD codes

The ICD codes used for data extraction of vital registration and verbal autopsy data are in Table 3. The table includes the garbage codes used for redistribution, which were either not coded in enough detail to indicate a species (E905) or coded for “Contact with unspecified venomous animal or plant” (E905.9x and X29.x). These codes were redistributed based on the distribution of correctly coded deaths in a country, sex, or age group.

Appendix Table 3: ICD codes used for venomous species-specific analysis. Trailing x's represent any value that trails the non-x characters, because every ICD code within the ICD categories was used.

Venomous animal	ICD-9	ICD-10
Snake	E905.0x	X20.x
Spider	E905.1x	X21.x
Scorpion	E905.2x	X22.x
Bees	E905.3x	X23.x
Other	E905.4x; E905.5x; E905.6x; E905.7x; E905.8x	X24.x; X25.x; X26.x; X27.x; X28.x
Unspecified venomous animal (Considered as garbage codes for redistribution)	E905; E905.9x;	X29.x

Garbage code redistribution

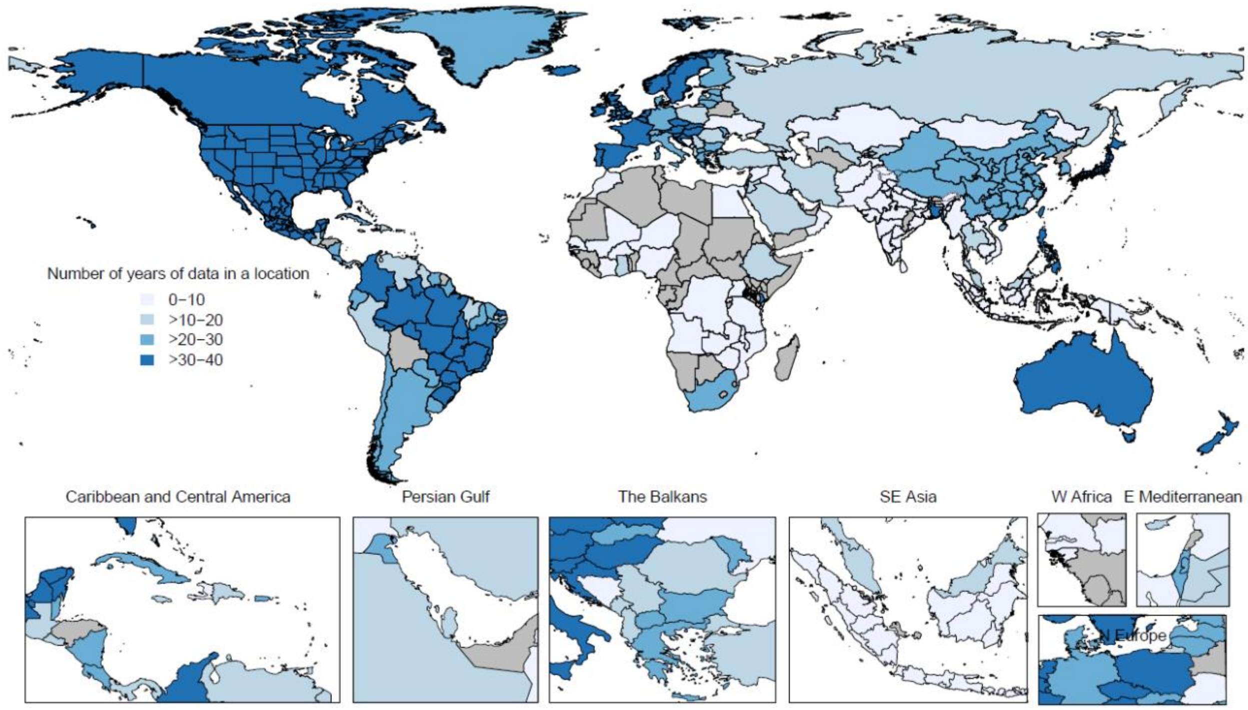
Deaths due to unspecified venomous animals were redistributed to each animal category above based on the distribution of animal-specific deaths by age, sex, and location. Out of 69,097 deaths that could be coded to the ICD codes above, 5,711 (8.3%) were coded to unspecified venomous animal contact and needed to be redistributed. Redistribution was done by aggregating all properly coded deaths by location, age, sex, and animal, and applying the proportion of correctly coded deaths due to each animal to the number of deaths coded for unspecified venomous animal contact. These redistributed animal deaths were added onto the number of properly coded deaths for each animal.

If a location-age-sex group had more incorrectly coded deaths that needed to be redistributed than properly coded deaths across all five animal groups, then we aggregated based on a broader demographic in order to have a more stable proportion for redistribution. First, we aggregated the codes by only location and age, and applied these proportions to the location-age-sex groups where there were sufficiently properly coded deaths by location and age, but not when stratified by sex. If there were still insufficient deaths when disregarding sex, we aggregated across all ages and both sexes within a location and applied that proportion. If there were still more deaths needed for redistribution than properly coded deaths in a location, we aggregated deaths over GBD region to estimate the proportion of deaths due to each animal and applied that proportion to the redistributed deaths.

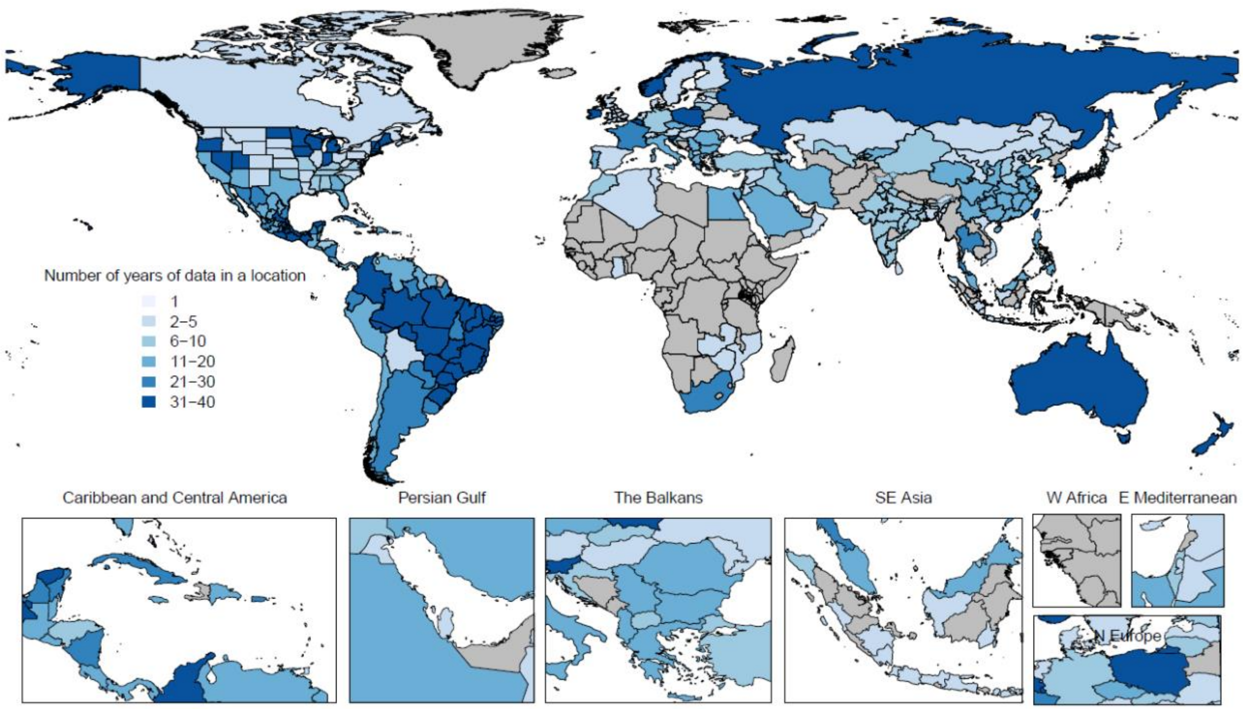
There were 27,020 deaths properly coded for snakebites. After redistribution, there were 29,040 deaths attributable to snakebites, an increase of 7.5%.

Input data sources

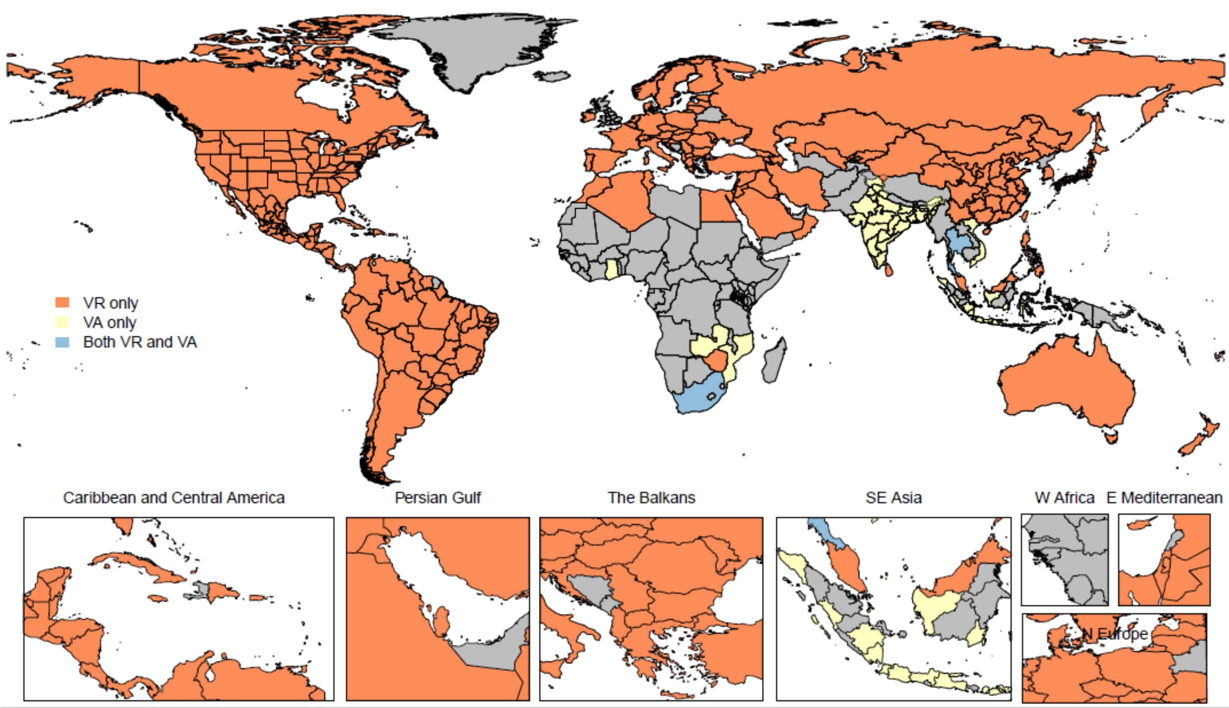
Supplementary appendix Figure 1 shows the coverage of vital registration and verbal autopsy used in this analysis. Verbal autopsy has been shown to have high sensitivity and specificity for snakebites and venomous animal contact deaths.[2] We also used the WHO Venomous Snake Distribution maps[3] to decrease the proportion of deaths due to venomous snakebite to zero in countries without endemic venomous snakes of medical importance (Supplementary appendix Table 4).



Appendix Figure 1: Data used in the venomous animal contact CODEm model. Gray represents countries with no data.



Appendix Figure 2: Count of unique location-years of data by location, used in the snakebite-specific model.



Appendix Figure 3: Map of vital registration (VR) and verbal autopsy (VA) data coverage used in the snakebite-specific model. Locations in gray do not have a single source of data.

Appendix Table 4: Locations where there are no endemic venomous snakes. Proportions in these locations were decreased to zero.

American Samoa
Antigua and Barbuda
Barbados
Bermuda
Cape Verde
Chile
Comoros
Cook Islands
Cuba
Dominica
Dominican Republic
Federated States of Micronesia
Fiji
Greenland
Grenada
Guam
Haiti
Iceland
Ireland
Jamaica
Kiribati
Madagascar
Maldives
Malta
Marshall Islands
Mauritius
Monaco
Nauru
New Zealand
Niue
Northern Mariana Islands
Palau
Puerto Rico
Saint Kitts and Nevis
Saint Vincent and the Grenadines
Samoa
Seychelles
Solomon Islands

The Bahamas
Tokelau
Tonga
Tuvalu
Vanuatu
Virgin Islands

ST-GPR parameters

Spatiotemporal Gaussian process regression (ST-GPR) has three different hyperparameters that are set to control the amount of temporal, age, and spatial smoothing. Time smoothing follows Equation 1, where j is the observed data point and I is the country-year-age-sex to be predicted. We set λ to be equal to 0.1, causing a high amount of smoothing over time due to a prior expectation that the burden of snakebite would not have significant change year to year.

$$Eq.1:\ w_t = e^{-\lambda|time_i - time_j|}$$

Age weighting follows equation 2, where j is an observed data point, I is a country-year-age-sex point to be predicted, and ω is the set hyperparameter. We set omega to be 0.5, establishing a medium rate of smoothing over age to allow some effect while also giving ST-GPR the flexibility to follow data points closely.

$$Eq.2:\ age\ weight_{i,j} = 0$$

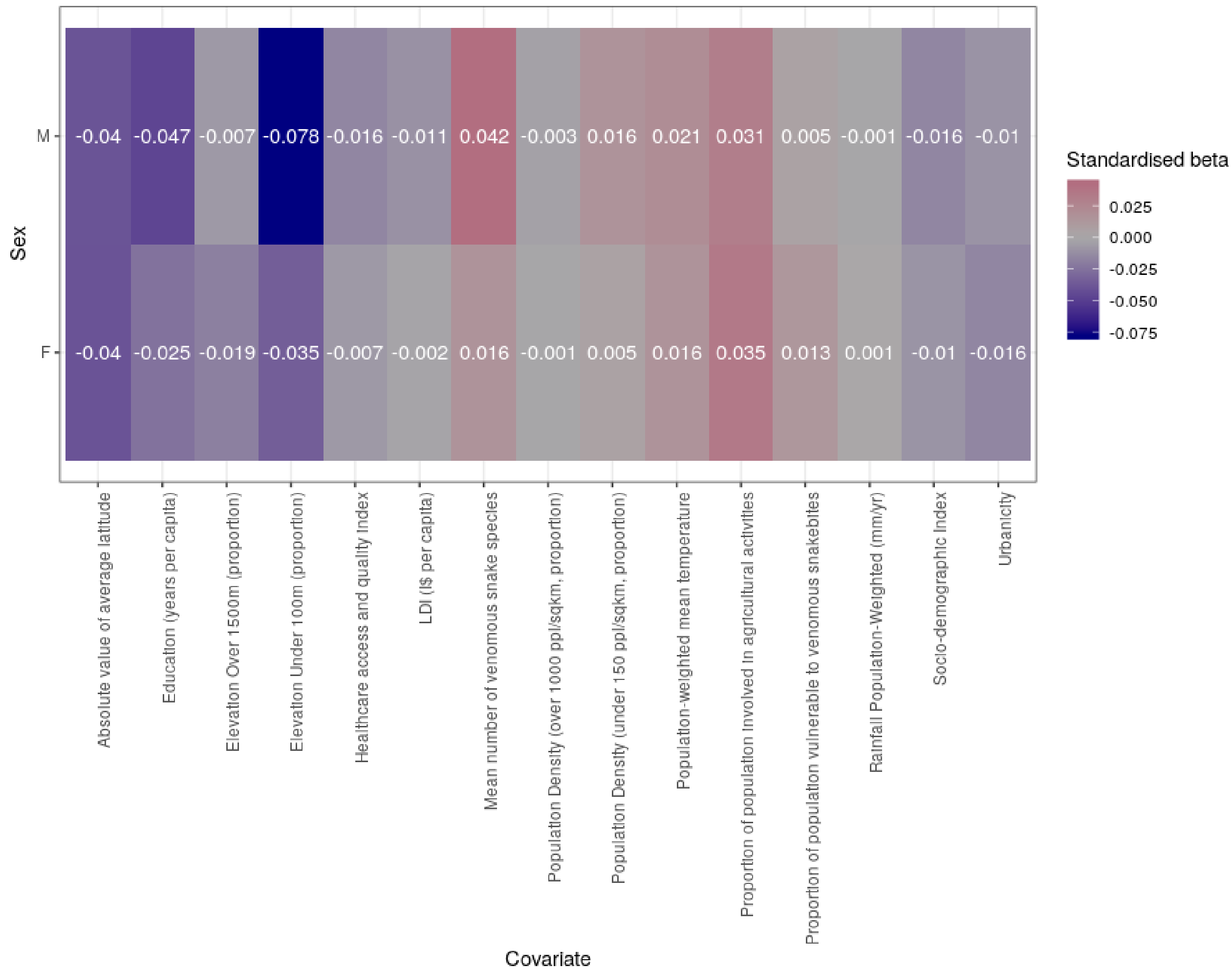
Space weighting follows Eq. 3 below. We set zeta equal to 0.01, creating very little smoothing between countries and subnational locations. We believed there would be significant variation between countries due to ecology, health system strength, and other characteristics, and we allowed ST-GPR to follow the trends in a given location when provided with data to do so.

$$\textit{Eq. 3: Space weight} = \begin{cases} \zeta^0 = 1 & for\ residuals\ within\ country\ i \\ \zeta^1 & for\ residuals\ within\ region\ j\ but\ not\ country\ i \\ \zeta^2 & for\ residuals\ not\ in\ region\ j \end{cases}$$

ST-GPR ensemble model hybridization results for covariate selection

The covariates and their resulting coefficient of the ensemble model are shown below. Each sex is modeled independently. Standardised coefficients allow easy comparisons between covariates on very different scales. The mixed-effects model with nested random effects using GBD regions and data input locations is described below:

$$Snakebite\ mortality\ rate\ per\ 100{,}000 \sim covariates + (1|GBD\ region/location)$$

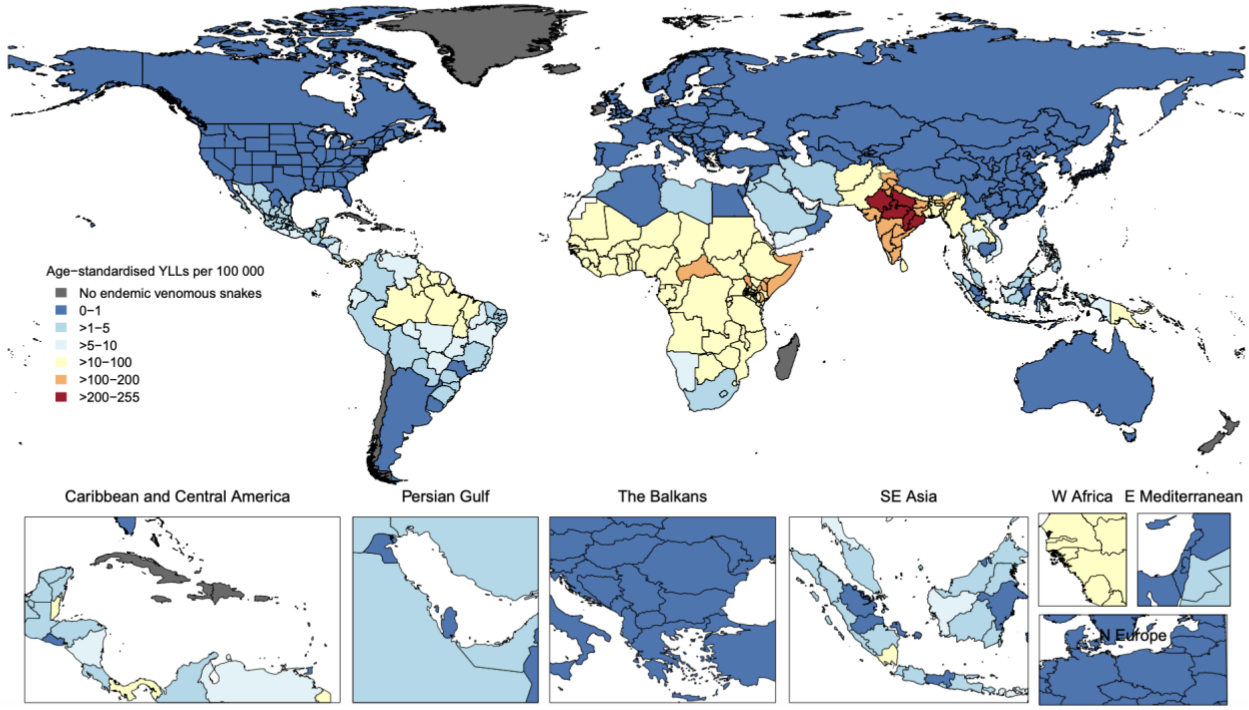


Appendix Figure 4: Standardised weighted beta coefficients of the 16 covariates used in the ensemble modelling approach. Standardised coefficients are equal to the beta coefficient per unit of the variable times the standard deviation of the covariates over the standard deviation of the input data:

$$\beta_{standardized} = \frac{\beta_{untransformed} * \sigma_{covariate}}{\sigma_{snakebite\ mortality\ rate\ per\ 100{,}000}}$$

Supplementary results

Appendix Figure 5: Age-standardised YLLs due to snakebites in 2019 for both sexes combined. GBD 2019 did not publish state-level estimates for China, and each state is colored the estimate of the rate of China's national estimate. Endemic habitat of venomous snakes of medical importance was looked up from the WHO venomous snake distribution maps: https://apps.who.int/bloodproducts/snakeantivenoms/database/default.htm.



Appendix Table 5: Venomous snakebite deaths and YLLs in India and its states in 2019.

Location	Deaths - Count, 2019	Deaths - Age-standardised rate, 2019	YLLs - Count, 2019	YLLs - Age-standardised rate, 2019
Andhra Pradesh	2,310 (1,190 to 3,110)	4.19 (2.15 to 5.63)	89,300 (47,800 to 122,000)	163 (87 to 223)
Arunachal Pradesh	21 (15 to 42)	1.68 (1.22 to 3.27)	1,030 (718 to 2,100)	66 (46 to 131)
Assam	768 (605 to 1,000)	2.44 (1.92 to 3.14)	37,500 (29,200 to 49,900)	107 (84 to 141)
Bihar	3,760 (1,570 to 5,290)	3.63 (1.53 to 5.05)	190,000 (76,500 to 276,000)	160 (65 to 229)
Chhattisgarh	1,810 (962 to 2,370)	6.50 (3.52 to 8.42)	80,700 (44,300 to 108,000)	263 (143 to 349)
Delhi	211 (148 to 275)	1.22 (0.86 to 1.58)	9,530 (6,860 to 12,600)	50 (36 to 67)
Goa	19 (14 to 25)	1.11 (0.81 to 1.48)	673 (487 to 910)	41 (30 to 55)
Gujarat	2,730 (1,490 to 3,440)	4.23 (2.29 to 5.34)	124,000 (69,000 to 158,000)	178 (99 to 228)

Haryana	710 (535 to 891)	2.62 (1.99 to 3.30)	33,300 (25,500 to 42,400)	116 (88 to 148)
Himachal Pradesh	268 (157 to 339)	3.52 (2.04 to 4.44)	10,600 (6,170 to 13,500)	138 (81 to 175)
Jammu & Kashmir and Ladakh	478 (172 to 623)	3.97 (1.41 to 5.15)	21,800 (8,000 to 28,700)	163 (59 to 214)
Jharkhand	1,040 (580 to 1,480)	3.20 (1.78 to 4.44)	46,600 (26,200 to 67,700)	129 (73 to 186)
Karnataka	2,100 (1,590 to 2,600)	3.19 (2.40 to 3.94)	92,800 (70,800 to 115,000)	136 (104 to 168)
Kerala	307 (238 to 453)	0.74 (0.58 to 1.13)	10,700 (8,230 to 17,100)	28 (21 to 45)
Madhya Pradesh	4,390 (2,470 to 5,790)	5.68 (3.08 to 7.39)	215,000 (125,000 to 289,000)	249 (141 to 332)
Maharashtra	4,010 (2,390 to 5,070)	3.25 (1.95 to 4.08)	172,000 (106,000 to 214,000)	136 (85 to 170)
Manipur	35 (25 to 59)	1.19 (0.85 to 2.00)	1,560 (1,090 to 2,620)	47 (33 to 78)
Meghalaya	33 (22 to 63)	1.29 (0.92 to 2.50)	1,580 (1,070 to 3,080)	51 (35 to 97)
Mizoram	11 (6 to 29)	1.05 (0.63 to 2.86)	490 (293 to 1,290)	41 (25 to 107)
Nagaland	22 (17 to 31)	1.49 (1.12 to 2.06)	1,060 (769 to 1,530)	59 (44 to 83)
Odisha	2,250 (1,360 to 3,030)	5.00 (3.01 to 6.69)	103,000 (61,800 to 141,000)	222 (132 to 306)
Other Union Territories	33 (22 to 49)	0.94 (0.65 to 1.38)	1,310 (882 to 2,000)	35 (24 to 53)
Punjab	881 (633 to 1,110)	2.78 (2.00 to 3.51)	37,100 (26,900 to 47,000)	117 (85 to 146)
Rajasthan	4,070 (2,440 to 5,230)	5.80 (3.48 to 7.44)	205,000 (122,000 to 265,000)	261 (151 to 336)
Sikkim	7 (4 to 10)	1.18 (0.77 to 1.71)	270 (175 to 411)	44 (29 to 65)
Tamil Nadu	2,780 (1,720 to 3,530)	3.40 (2.13 to 4.30)	111,000 (74,700 to 141,000)	135 (91 to 171)
Telangana	1,550 (780 to 2,180)	4.38 (2.19 to 6.05)	64,900 (34,200 to 91,100)	171 (89 to 239)
Tripura	26 (17 to 68)	0.69 (0.46 to 1.77)	1,080 (700 to 2,860)	27 (18 to 70)
Uttar Pradesh	12,000 (5,230 to 16,100)	6.02 (2.60 to 7.99)	566,000 (252,000 to 784,000)	247 (109 to 337)
Uttarakhand	423 (231 to 591)	3.91 (2.16 to 5.46)	17,800 (10,200 to 24,700)	153 (86 to 213)
West Bengal	2,090 (1,220 to 2,730)	2.16 (1.23 to 2.81)	91,600 (54,200 to 120,000)	92 (54 to 122)
India	**51,100 (29,600 to 64,100)**	**4.00 (2.31 to 5.01)**	**2,340,000 (1,350,000 to 2,970,000)**	**171 (99 to 218)**

Appendix Table 6: Regional forecast mortality forecasted to 2030, 2040, and 2050.

Region	Deaths (Absolute number)					Age-standardized mortality rate per 100,000				
	2019*	2020	2030	2040	2050	2019*	2020	2030	2040	2050
Andean Latin America	47 (16 to 60)	68 (15 to 83)	86 (12 to 112)	106 (10 to 149)	129 (7 to 199)	0.08 (0.03 to 0.10)	0.11 (0.02 to 0.13)	0.11 (0.02 to 0.15)	0.12 (0.01 to 0.16)	0.12 (0.01 to 0.18)
Australasia	1 (1 to 2)	1 (1 to 1)	1 (1 to 1)	1 (1 to 1)	1 (0 to 1)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)
Caribbean	12 (9 to 15)	18 (14 to 21)	35 (24 to 44)	70 (42 to 94)	149 (74 to 216)	0.02 (0.02 to 0.03)	0.04 (0.03 to 0.04)	0.06 (0.04 to 0.07)	0.10 (0.06 to 0.14)	0.18 (0.09 to 0.26)
Central Asia	9 (8 to 10)	10 (9 to 11)	9 (8 to 11)	8 (7 to 11)	8 (6 to 10)	0.01 (0.01 to 0.01)	0.01 (0.01 to 0.01)	0.01 (0.01 to 0.01)	0.01 (0.01 to 0.01)	0.01 (0.00 to 0.01)
Central Europe	5 (4 to 6)	6 (5 to 6)	5 (5 to 6)	5 (4 to 5)	4 (3 to 5)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)
Central Latin America	210 (174 to 255)	189 (170 to 206)	147 (127 to 168)	112 (92 to 133)	83 (65 to 102)	0.09 (0.07 to 0.11)	0.07 (0.07 to 0.08)	0.05 (0.04 to 0.05)	0.03 (0.03 to 0.04)	0.02 (0.02 to 0.02)
Central Sub-Saharan Africa	791 (507 to 1,355)	883 (564 to 1,579)	1,164 (656 to 2,416)	1,535 (752 to 3,840)	2,039 (853 to 6,028)	1.25 (0.83 to 1.82)	1.26 (0.84 to 2.05)	1.18 (0.68 to 2.40)	1.13 (0.57 to 2.71)	1.09 (0.47 to 3.09)
East Asia	230 (176 to 280)	145 (128 to 191)	85 (69 to 159)	48 (35 to 124)	26 (17 to 90)	0.01 (0.01 to 0.01)	0.01 (0.01 to 0.01)	0.00 (0.00 to 0.01)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)
Eastern Europe	22 (19 to 26)	19 (18 to 21)	13 (12 to 15)	9 (8 to 10)	6 (5 to 7)	0.01 (0.01 to 0.01)	0.01 (0.01 to 0.01)	0.01 (0.00 to 0.01)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)
Eastern Sub-Saharan Africa	2,102 (1,573 to 3,002)	2,208 (1,634 to 3,116)	2,591 (1,819 to 3,955)	3,109 (2,051 to 5,205)	3,738 (2,268 to 6,771)	1.19 (0.83 to 1.61)	1.10 (0.79 to 1.54)	0.90 (0.62 to 1.36)	0.74 (0.48 to 1.22)	0.61 (0.37 to 1.09)
High-income Asia Pacific	9 (7 to 11)	8 (6 to 9)	6 (4 to 7)	4 (3 to 5)	3 (2 to 4)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)
High-income North America	17 (16 to 19)	16 (14 to 17)	16 (14 to 17)	15 (14 to 17)	15 (13 to 17)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)
North Africa and Middle East	350 (243 to 485)	379 (272 to 493)	326 (226 to 478)	283 (180 to 468)	246 (140 to 460)	0.06 (0.05 to 0.09)	0.06 (0.05 to 0.08)	0.05 (0.03 to 0.07)	0.04 (0.02 to 0.06)	0.03 (0.02 to 0.05)
Oceania	69 (40 to 108)	77 (42 to 116)	90 (47 to 140)	106 (54 to 171)	125 (59 to 217)	0.65 (0.38 to 1.03)	0.64 (0.36 to 1.00)	0.63 (0.34 to 0.99)	0.62 (0.31 to 1.00)	0.61 (0.29 to 1.06)
South Asia	54,588 (31,838 to 68,321)	60,538 (34,100 to 75,645)	58,433 (32,577 to 85,624)	56,447 (30,908 to 95,744)	54,241 (28,352 to 106,833)	3.37 (1.96 to 4.19)	3.64 (2.06 to 4.56)	3.03 (1.70 to 4.45)	2.55 (1.41 to 4.33)	2.17 (1.14 to 4.27)

Southeast Asia	801 (581 to 961)	840 (603 to 968)	689 (500 to 870)	557 (395 to 791)	438 (287 to 693)	0.14 (0.10 to 0.16)	0.14 (0.10 to 0.16)	0.09 (0.07 to 0.12)	0.06 (0.04 to 0.09)	0.04 (0.03 to 0.07)
Southern Latin America	3 (3 to 4)	5 (4 to 5)	8 (6 to 9)	12 (10 to 15)	18 (14 to 24)	0.00 (0.00 to 0.01)	0.01 (0.01 to 0.01)	0.01 (0.01 to 0.01)	0.01 (0.01 to 0.02)	0.02 (0.01 to 0.02)
Southern Sub-Saharan Africa	71 (56 to 90)	78 (62 to 98)	90 (68 to 122)	107 (76 to 152)	127 (84 to 200)	0.12 (0.09 to 0.15)	0.12 (0.10 to 0.15)	0.11 (0.09 to 0.15)	0.11 (0.08 to 0.15)	0.10 (0.07 to 0.16)
Tropical Latin America	240 (224 to 261)	204 (188 to 220)	185 (165 to 208)	164 (141 to 192)	140 (115 to 171)	0.11 (0.10 to 0.12)	0.09 (0.08 to 0.09)	0.06 (0.06 to 0.07)	0.05 (0.04 to 0.06)	0.04 (0.03 to 0.04)
Western Europe	14 (12 to 15)	14 (13 to 15)	14 (13 to 15)	14 (12 to 16)	14 (12 to 15)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)	0.00 (0.00 to 0.00)
Western Sub-Saharan Africa	3,822 (2,682 to 6,000)	3,903 (2,756 to 5,900)	4,808 (3,093 to 8,106)	5,922 (3,548 to 10,915)	7,222 (3,935 to 14,706)	1.42 (1.03 to 2.06)	1.42 (1.01 to 2.10)	1.24 (0.81 to 2.03)	1.09 (0.65 to 1.97)	0.97 (0.53 to 1.95)
Global	**63,415 (38,930 to 78,633)**	**69,608 (42,094 to 86,040)**	**68,799 (41,372 to 97,613)**	**68,633 (40,347 to 111,231)**	**68,771 (39,108 to 125,599)**	**0.81 (0.50 to 1.00)**	**0.87 (0.53 to 1.08)**	**0.75 (0.45 to 1.07)**	**0.66 (0.39 to 1.08)**	**0.59 (0.34 to 1.08)**

*: 2019 data are our snakebite mortality estimates, while 2020, 2030, 2040, and 2050 estimates are the results of the forecasting model.

GATHER checklist

Item #	Checklist item	Reported on page #
Objectives and funding		
1	Define the indicator(s), populations (including age, sex, and geographic entities), and time period(s) for which estimates were made.	Main text (Methods)
2	List the funding sources for the work.	Abstract (Funding), Acknowledgments
Data Inputs		
For all data inputs from multiple sources that are synthesized as part of the study:		
3	Describe how the data were identified and how the data were accessed.	Main manuscript methods and appendix
4	Specify the inclusion and exclusion criteria. Identify all ad-hoc exclusions.	Main manuscript methods and appendix
5	Provide information on all included data sources and their main characteristics. For each data source used, report reference information or contact name/institution, population represented, data collection method, year(s) of data collection, sex and age range, diagnostic criteria or measurement method, and sample size, as relevant.	Main manuscript methods and appendix Sections 3-4. Detailed data sources for each component available online at GBD Input Data Sources Tool (http://ghdx.healthdata.org/gbd-2019/data-input-sources)
6	Identify and describe any categories of input data that have potentially important biases (e.g., based on characteristics listed in item 5).	Main manuscript methods and appendix
For data inputs that contribute to the analysis but were not synthesized as part of the study:		
7	Describe and give sources for any other data inputs.	Main manuscript methods and appendix
For all data inputs:		
8	Provide all data inputs in a file format from which data can be efficiently extracted (e.g., a spreadsheet rather than a PDF), including all relevant meta-data listed in item 5. For any data inputs that cannot be shared because of ethical or legal reasons, such as third-party ownership, provide a contact name or the name of the institution that retains the right to the data.	Detailed data sources for each component available online (https://ghdx.healthdata.org/gbd-2019)
Data analysis		
9	Provide a conceptual overview of the data analysis method. A diagram may be helpful.	Manuscript methods and appendix
10	Provide a detailed description of all steps of the analysis, including mathematical formulae. This description should cover, as relevant, data cleaning, data pre-processing, data adjustments and weighting of data sources, and mathematical or statistical model(s).	Manuscript methods and appendix
11	Describe how candidate models were evaluated and how the final model(s) were selected.	Manuscript methods and appendix
12	Provide the results of an evaluation of model performance, if done, as well as the results of any relevant sensitivity analysis.	

13	Describe methods for calculating uncertainty of the estimates. State which sources of uncertainty were, and were not, accounted for in the uncertainty analysis.	Manuscript methods and appendix
14	State how analytic or statistical source code used to generate estimates can be accessed.	Statistical code used in GBD is published on GitHub, including core modelling code for ST-GPR and CODEm
Results and Discussion		
15	Provide published estimates in a file format from which data can be efficiently extracted.	Main text, and GBD 2019 venomous animal contact are publicly available from the GHDx online results tool (http://ghdx.healthdata.org/gbd-results-tool)
16	Report a quantitative measure of the uncertainty of the estimates (e.g. uncertainty intervals).	Main text estimates include 95% uncertainty intervals
17	Interpret results in light of existing evidence. If updating a previous set of estimates, describe the reasons for changes in estimates.	Main text discussion
18	Discuss limitations of the estimates. Include a discussion of any modelling assumptions or data limitations that affect interpretation of the estimates.	Main text discussion

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