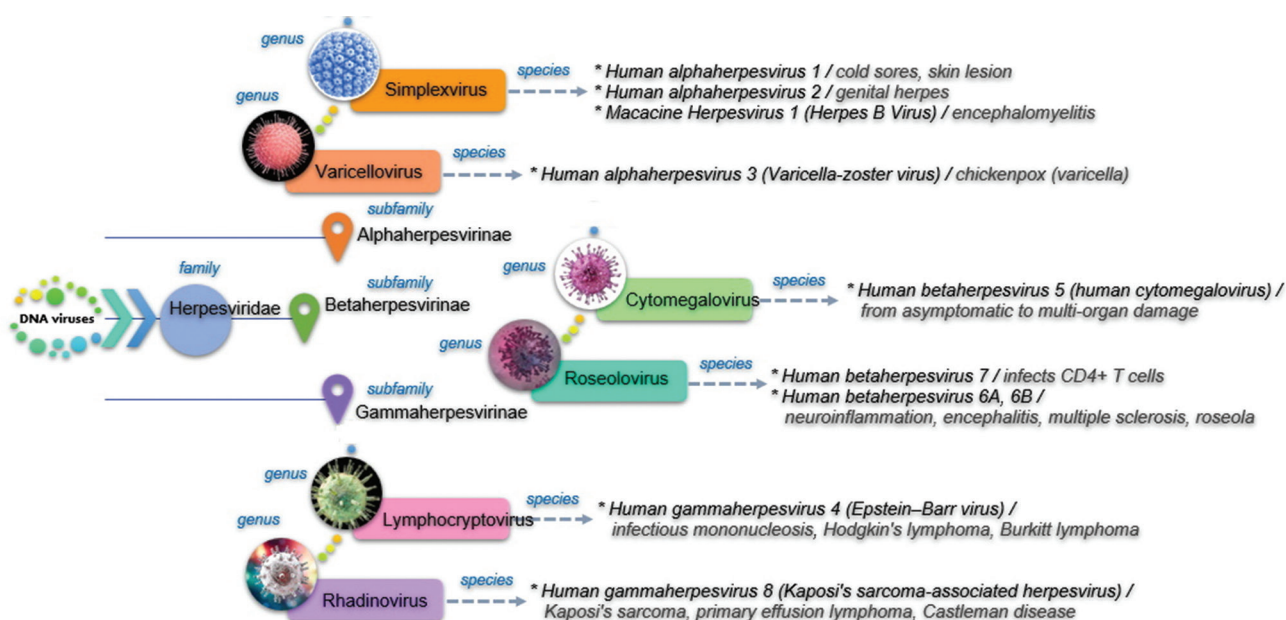


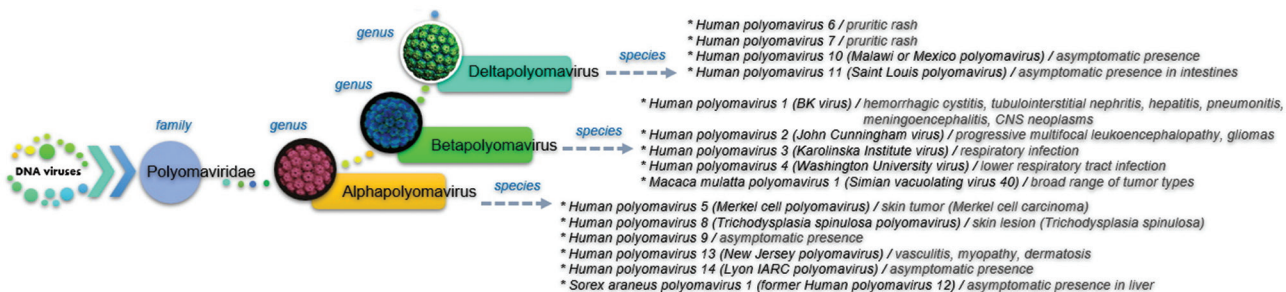
REVIEW ARTICLE

# From digital to quantum epidemiology: The Quantum Data Lake concept for big data related to viral infectious diseases

## Supplementary File



**Figure S1.** Data on the *Herpesviridae* family were collected and analyzed from the databases, The International Committee on Taxonomy of Viruses and The National Center for Biotechnology Information (NCBI). The ontology with symptoms and diseases was established after reviewing articles from NCBI, PubMed, and ScienceDirect.



**Figure S2.** Data on the *Polyomaviridae* family were collected and analyzed from the databases, The International Committee on Taxonomy of Viruses and The National Center for Biotechnology Information (NCBI); The ontology with symptoms and diseases was established after reviewing articles from NCBI, PubMed, and ScienceDirect.

1	2	3	4	5	6	7	8	9	10
11	12	13	14	15	16	17	18	19	20
21	22	23	24	25	26	27	28	29	30
31	32	33	34	35	36	37	38	39	40
41	42	43	44	45	46	47	48	49	50
51	52	53	54	55	56	57	58	59	60
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71	72	73	74	75	76	77	78	79	80
81	82	83	84	85	86	87	88	89	90
91	92	93	94	95	96	97	98	99	100
101	102	103	104	105	106	107	108	109	110
111	112	113	114	115	116	117	118	119	120
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131	132	133	134	135	136	137	138	139	140
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161	162	163	164	165	166	167	168	169	170
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181	182	183	184	185	186	187	188	189	190
191	192	193	194	195	196	197	198	199	200
201	202	203	204	205	206	207	208	209	210
211	212	213	214	215	216	217	218	219	220
221	222	223	224	225	226	227	AZ1_1	HANO464	ICPX1
JEB2	mCG2	mCG3	mCH2	mdo1c02	mdo1c232	mga2c01	mga2c70	mDysk1	mDysk2
mDysk3	mDysk5	mDysk6	me180	mEV03c05	mEV03c09	mEV03c40	mEV03c45	mEV03c60	mEV03c104
mEV03c188	mEV03c212	mEV03c434	mEV06c12b	mEV06c107	mEV06c118	mEV07c367	mEV07c382	mEV07c390	mFD1
mFD2	mF1864	mFS1	mHIVGc36	mHIVGc70	mICB1	mKC5	mKN1	mKN2	mKN3
mL55	mLCOSOc196	mm090c09	mm090c10	mm090c66	mm090c145	mm292c10	mm292c14	mm292c88	mm292c100
mMTS1	mMTS2	mSD2	mSE355	mSE379	mSE383	mTVMBSc09	mTVMBSc529	mTVMBSc2024	mTVMBSc2450
mTVMBShc13	mTVMBShc33	mTVMBShc141	mw02c24a	mw03c65	mw07c34d	mw07c68b	mw07c74b	mw11c13	mw11C24
mw11C39	mw11C51	mw15c111	mw18c07	mw18c11d	mw18c25	mw18c39	mw18c134	HPV-mw20c01a	mw20c01b
mw20c02c	mw20c03a	mw20c04	mw20c08a	mw20c09	mw20c10a	mw21c693	mw22c09	mw23c08c	mw23c77
mw23c101c	mw27c04c	mw27c39c	mw27c52c	mw27c157c	mw34c04a	mw34c11a	mw34c14a	mw34c28a	mw34c34a
mwg1c05	mwg1c09	mZJ01	RTRX1	RTRX2	RTRX3	RTRX4	RTRX5	RTRX6	RTRX7
RTRX8	RTRX9	RTRX10	Xc	Xd	Xf	Xg	Xh		

Figure S3. Visualization of the genera classification of human papillomaviruses based on the number of virus types. The color identification is as follows: pink: genus *Alphapapillomavirus*; blue: genus *Betapapillomavirus*; green: genus *Gammapapillomavirus*; yellow: genus *Mupapillomavirus*; violet: genus *Nupapillomavirus*; dark grey: unclassified *Papillomaviridae*; light gray: no information; white: withdrawn numbers.

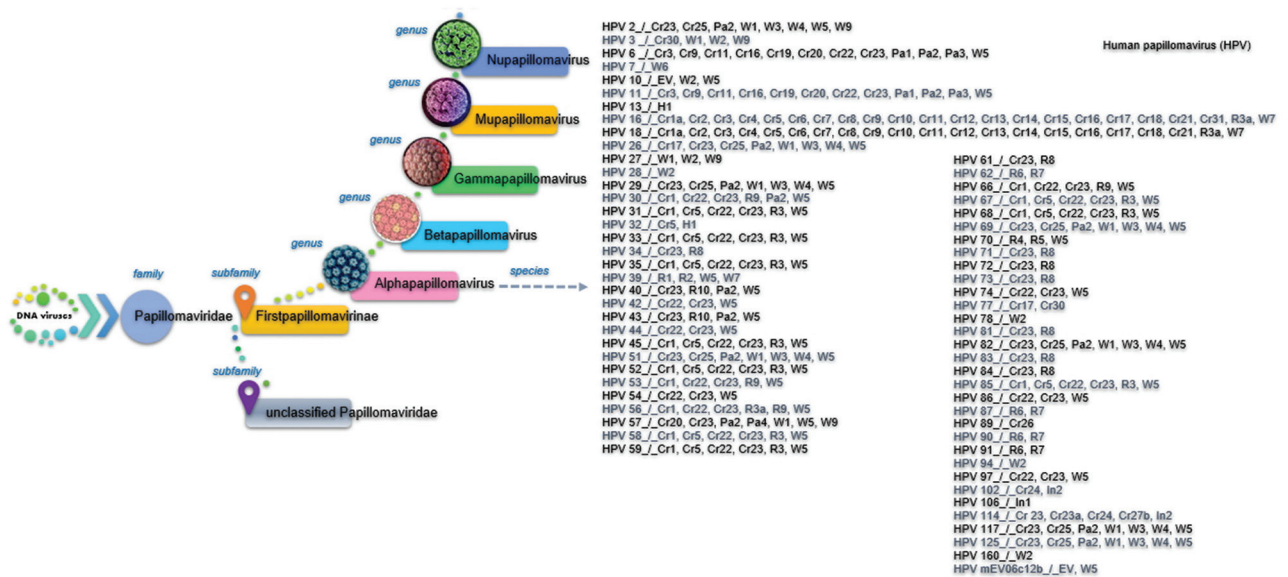


Figure S4a. Data on the *Papillomaviridae* family (genus *Alphapapillomavirus*) were collected and analyzed from the databases. The International Committee on Taxonomy of Viruses and The National Center for Biotechnology Information (NCBI). The ontology with symptoms and diseases was established after reviewing articles from NCBI, PubMed, and ScienceDirect.

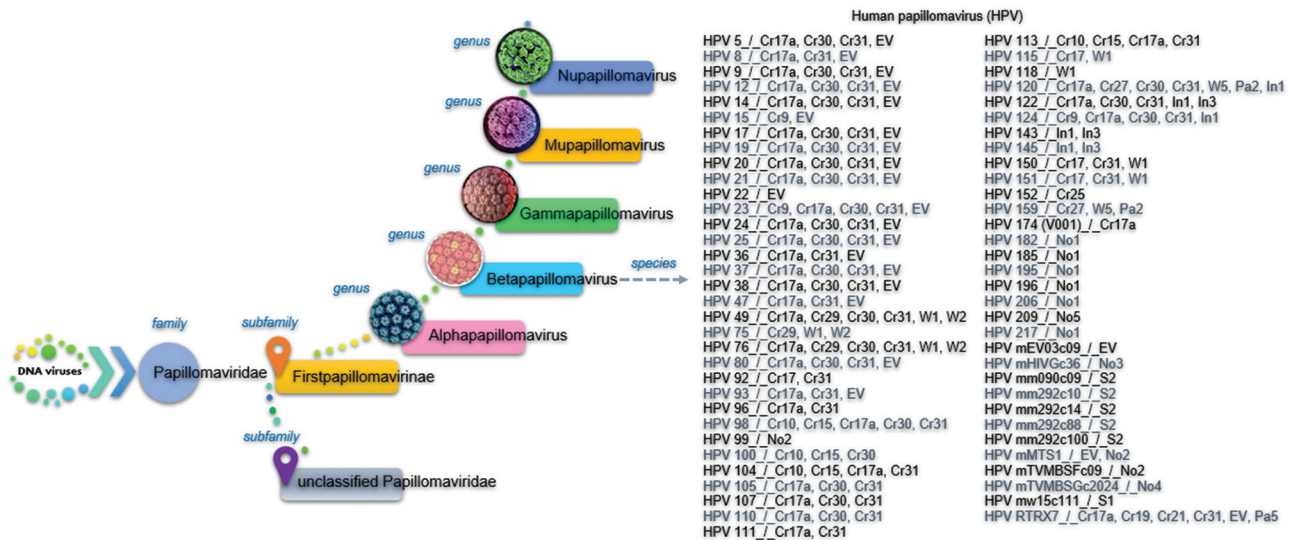


Figure S4b. Data on the *Papillomaviridae* family (genus *Betapapillomavirus*) were collected and analyzed from the databases, The International Committee on Taxonomy of Viruses and The National Center for Biotechnology Information (NCBI). The ontology with symptoms and diseases was established after reviewing articles from NCBI, PubMed, and ScienceDirect.

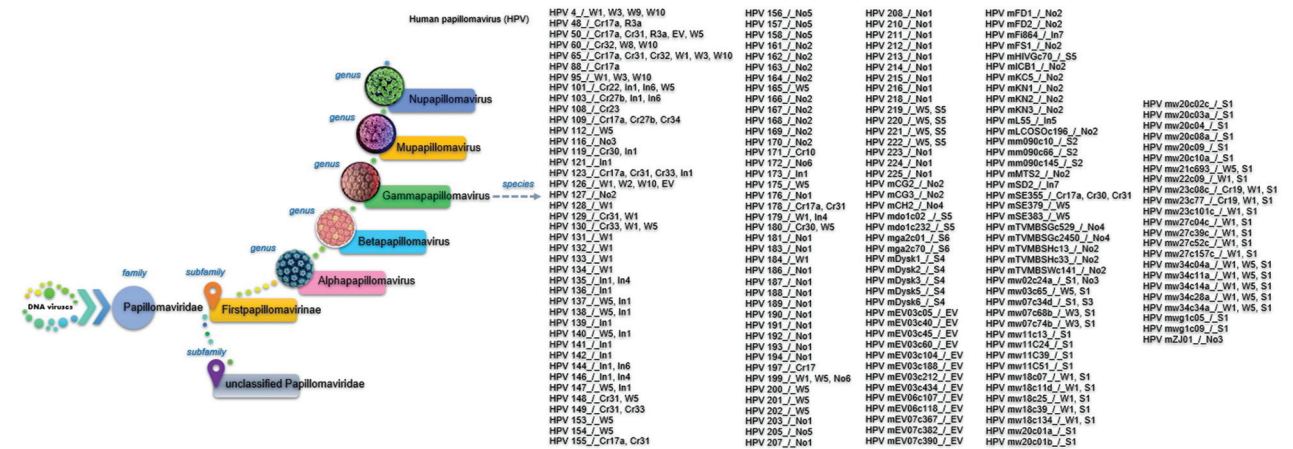


Figure S4c. Data on the *Papillomaviridae* family (genus *Gammapapillomavirus*) were collected and analyzed from the databases, The International Committee on Taxonomy of Viruses and The National Center for Biotechnology Information (NCBI). The ontology with symptoms and diseases was established after reviewing articles from NCBI, PubMed, and ScienceDirect.

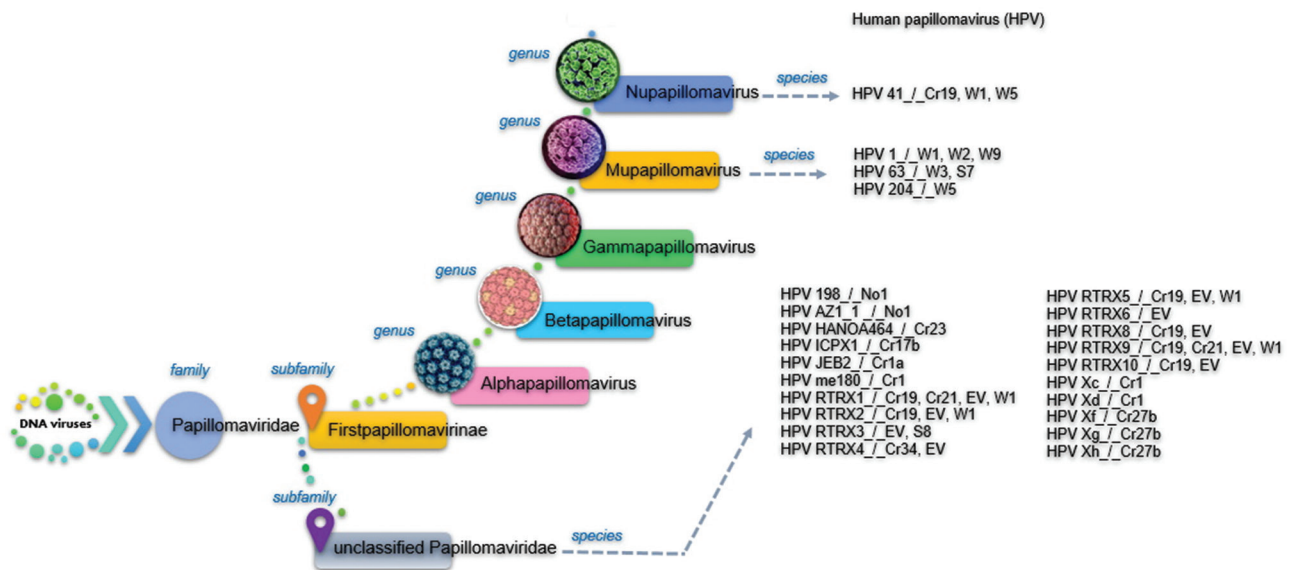


Figure S4d. Data on the Papillomaviridae family (genera Mupapillomavirus, Nupapillomavirus, and unclassified Papillomaviridae) were collected and analyzed from the databases, The International Committee on Taxonomy of Viruses and The National Center for Biotechnology Information (NCBI). The ontology with symptoms and diseases was established after reviewing articles from NCBI, PubMed, and ScienceDirect.

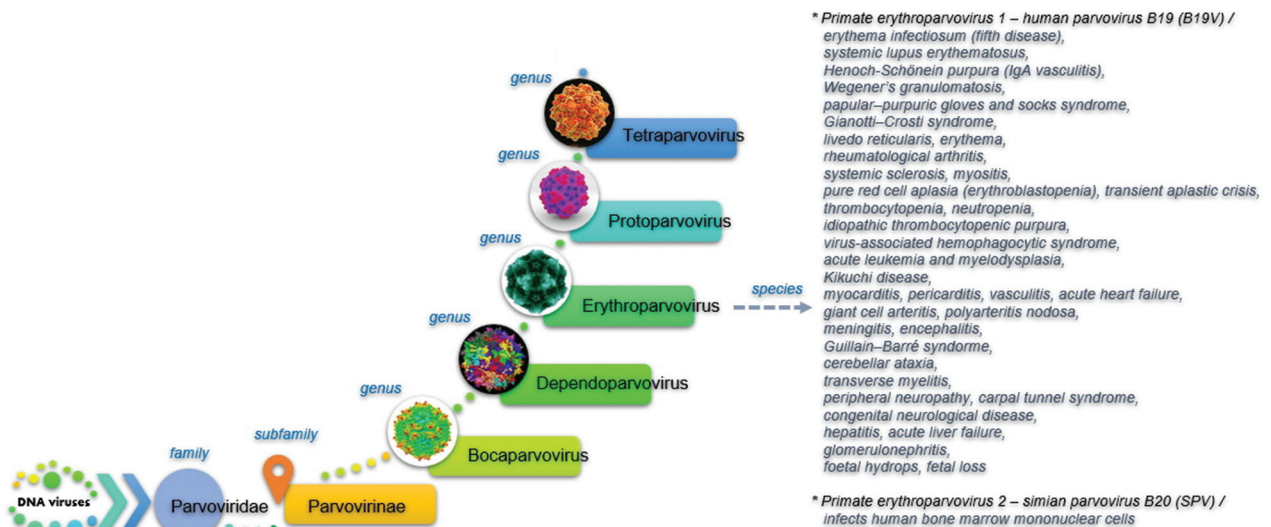
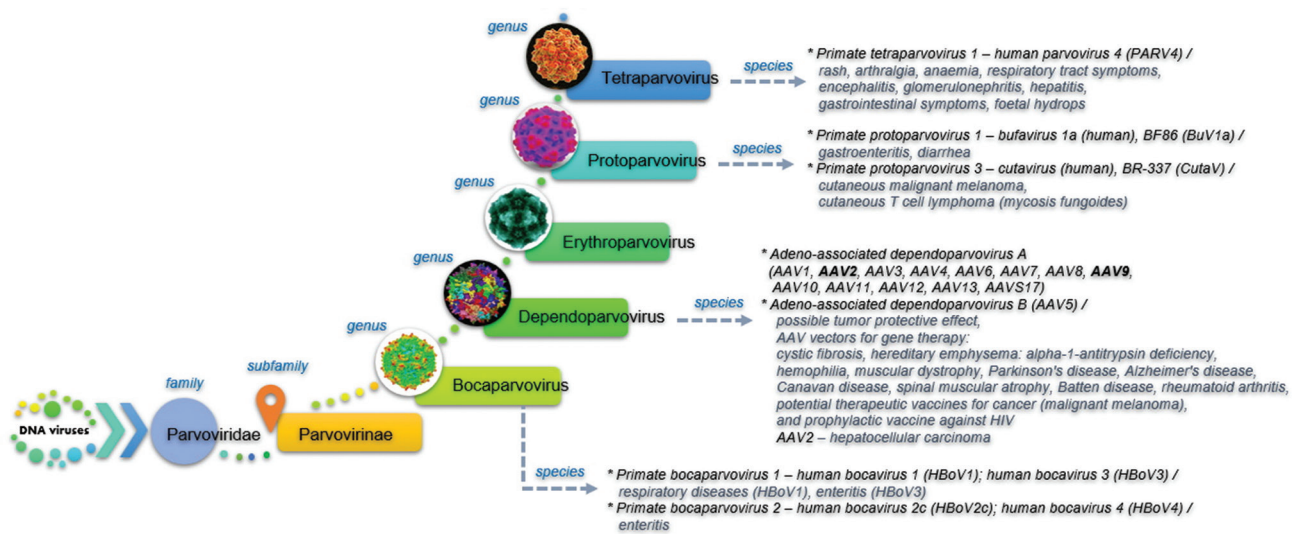
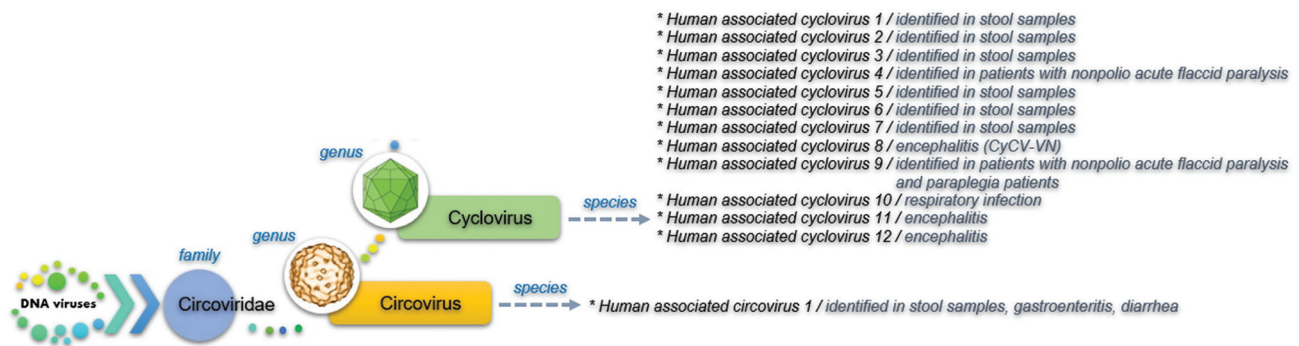


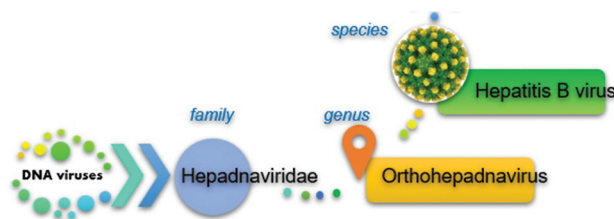
Figure S5a. Data on the Parvoviridae family (genus Erythroparvovirus) were collected and analyzed from the databases, The International Committee on Taxonomy of Viruses and The National Center for Biotechnology Information (NCBI). The ontology with symptoms and diseases was established after reviewing articles from NCBI, PubMed, and ScienceDirect.



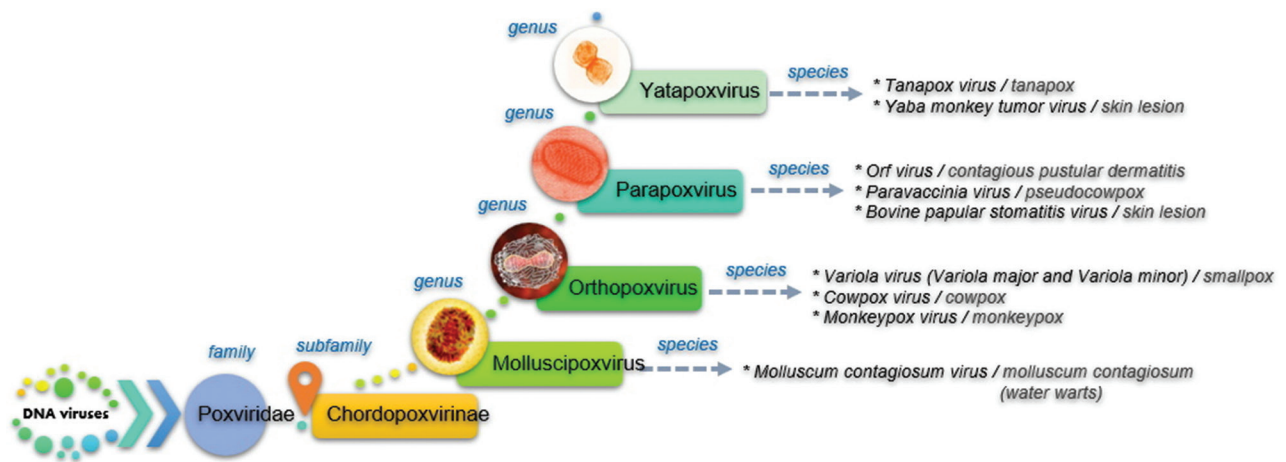
**Figure S5b.** Data on the *Parvoviridae* family (genera *Bocaparvovirus*, *Dependoparvovirus*, *Protoparvovirus*, and *Tetraparvovirus*) were collected and analyzed from the databases, The International Committee on Taxonomy of Viruses and The National Center for Biotechnology Information (NCBI). The ontology with symptoms and diseases was established after reviewing articles from NCBI, PubMed, and ScienceDirect.



**Figure S6.** Data on the *Circoviridae* family were collected and analyzed from the databases, The International Committee on Taxonomy of Viruses and The National Center for Biotechnology Information (NCBI). The ontology with symptoms and diseases was established after reviewing articles from NCBI, PubMed, and ScienceDirect.



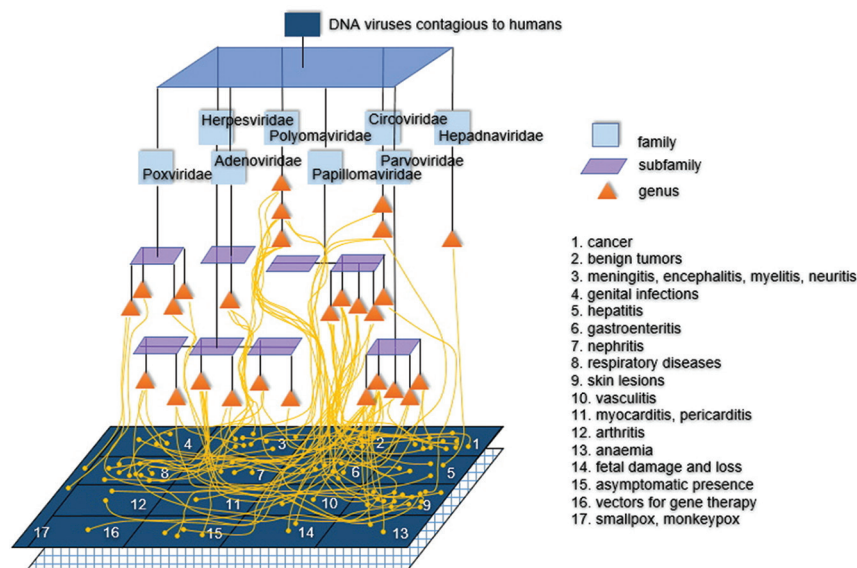
**Figure S7.** Data on the *Hepadnaviridae* family were collected and analyzed from the databases, The International Committee on Taxonomy of Viruses and The National Center for Biotechnology Information (NCBI). The ontology with symptoms and diseases was established after reviewing articles from NCBI, PubMed, and ScienceDirect.



**Figure S8.** Data on the *Poxviridae* family were collected and analyzed from the databases, The International Committee on Taxonomy of Viruses and The National Center for Biotechnology Information (NCBI). The ontology with symptoms and diseases was established after reviewing articles from NCBI, PubMed, and ScienceDirect.



**Figure S9.** Data on the *Adenoviridae* family were collected and analyzed from the databases, The International Committee on Taxonomy of Viruses and The National Center for Biotechnology Information (NCBI). The ontology with symptoms and diseases was established after reviewing articles from NCBI, PubMed, and ScienceDirect.



**Figure S10.** A neural tensor network of the main groups of symptoms and diseases caused by DNA viruses.

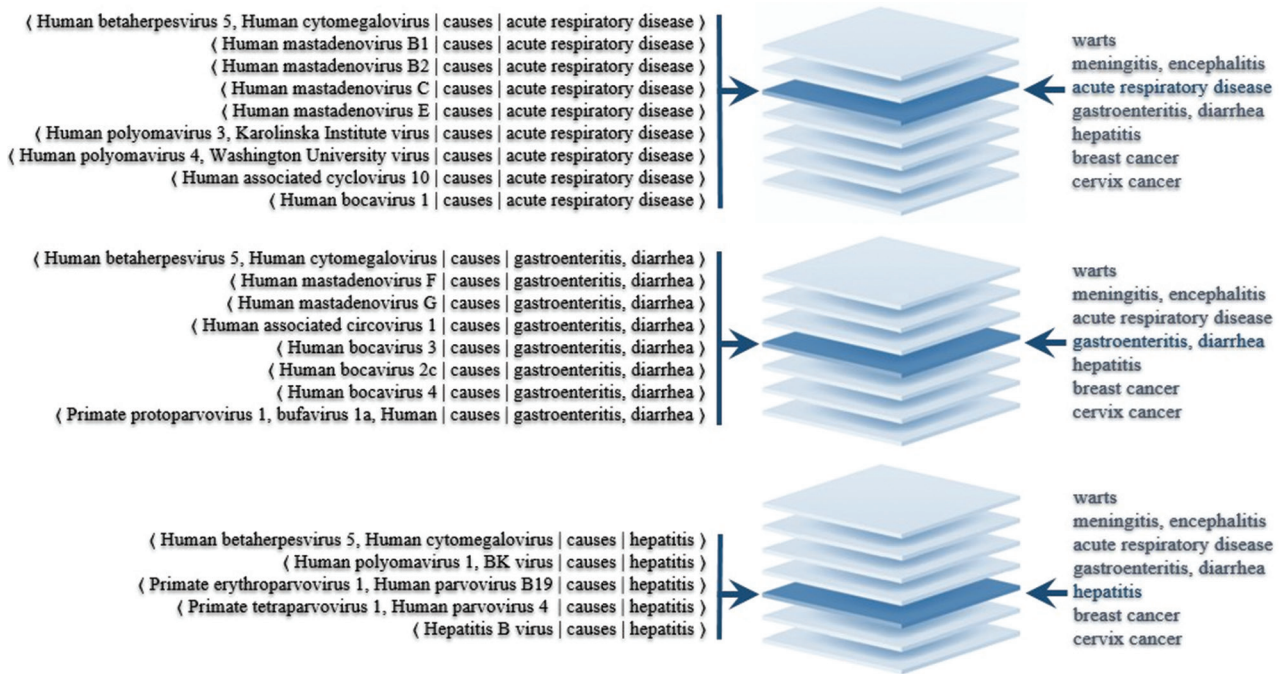


Figure S11. The Robson semantic triples for storing information on similar symptoms, syndromes, and diseases caused by different DNA viruses.

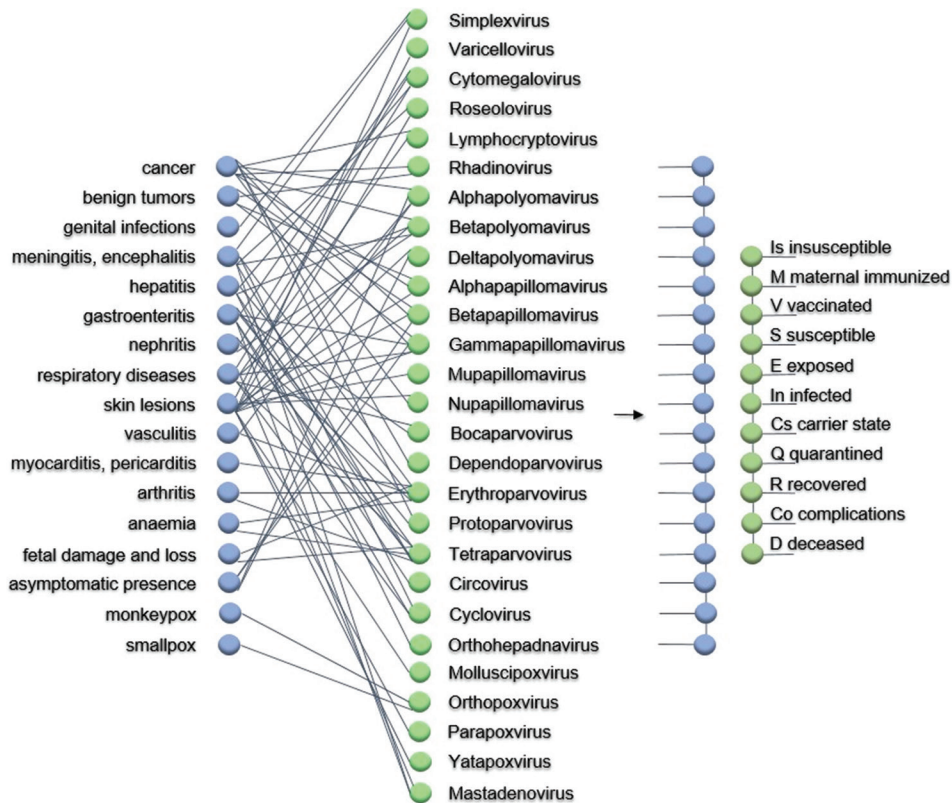


Figure S12. The main groups of symptoms and diseases caused by DNA viruses, and the compartmental susceptible-infectious-recovered model data presented as matrix product states.

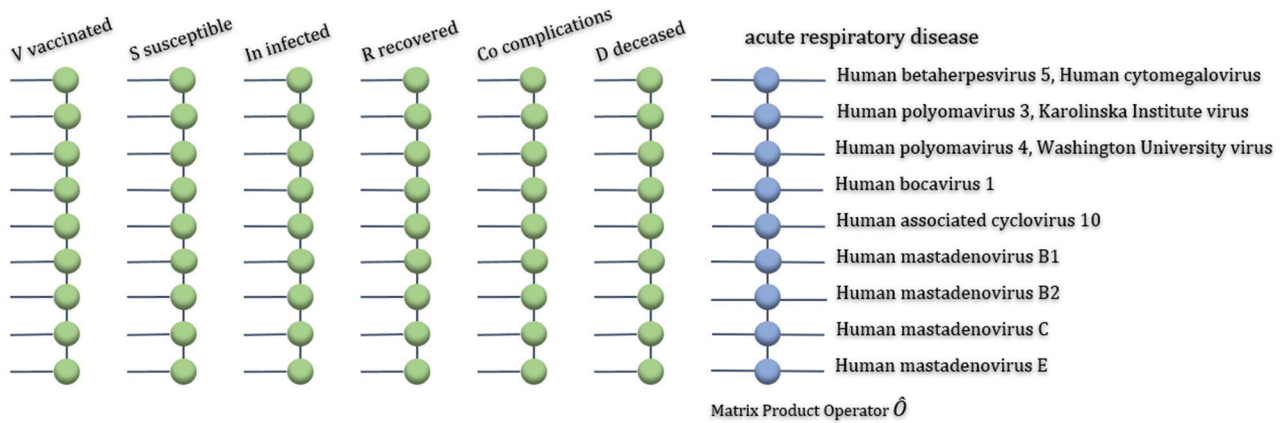


Figure S13. Matrix product state presentation of the compartmental susceptible-infectious-recovered model data and acute respiratory disease cases caused by different DNA viruses.

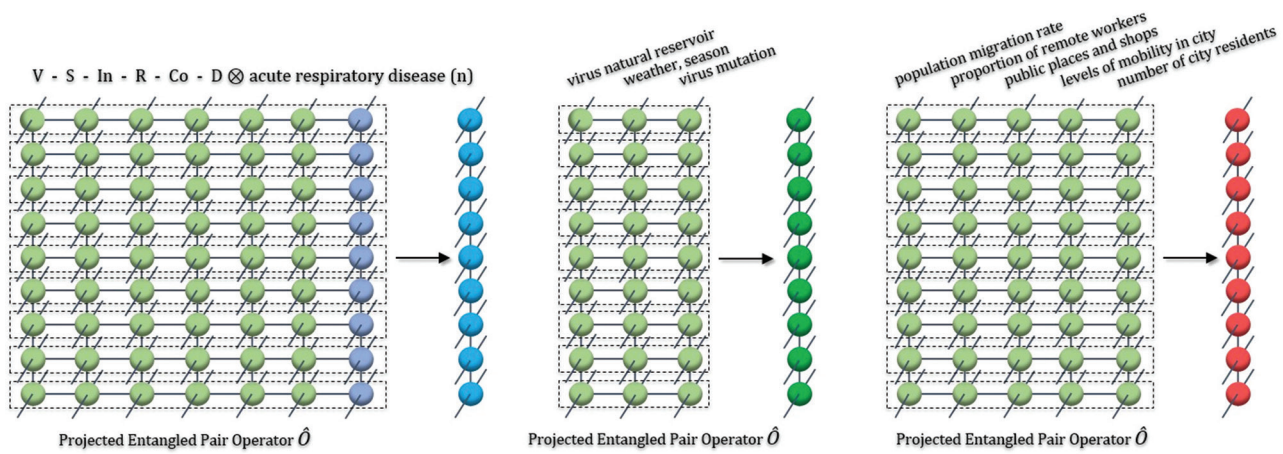


Figure S14. Compartmental susceptible-infectious-recovered model data, environmental data, and social data presented as projected entangled pair states and matrix product states.

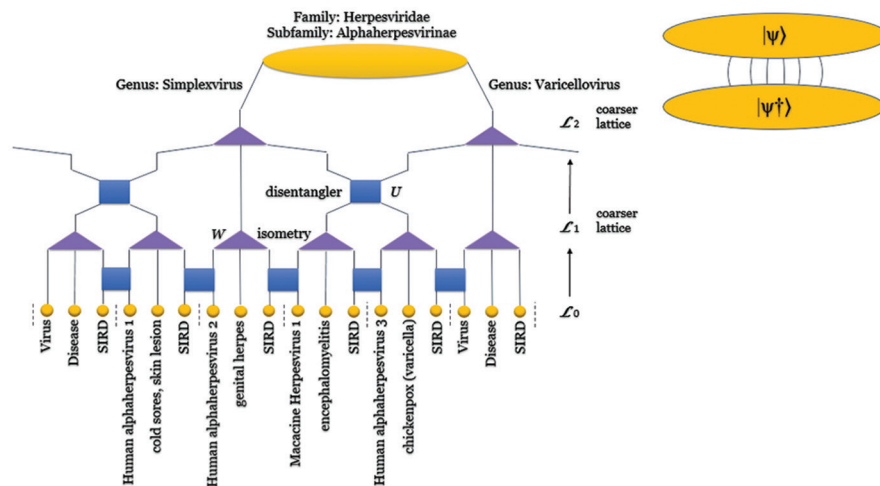


Figure S15. Ternary (three-site blocks) multi-scale entanglement renormalization ansatz with lattice length corresponding to the calculated cases caused by viruses of the subfamily *Alphaherpesvirinae*, family *Herpesviridae* (symptoms and diseases data, compartmental susceptible-infectious-recovered model).

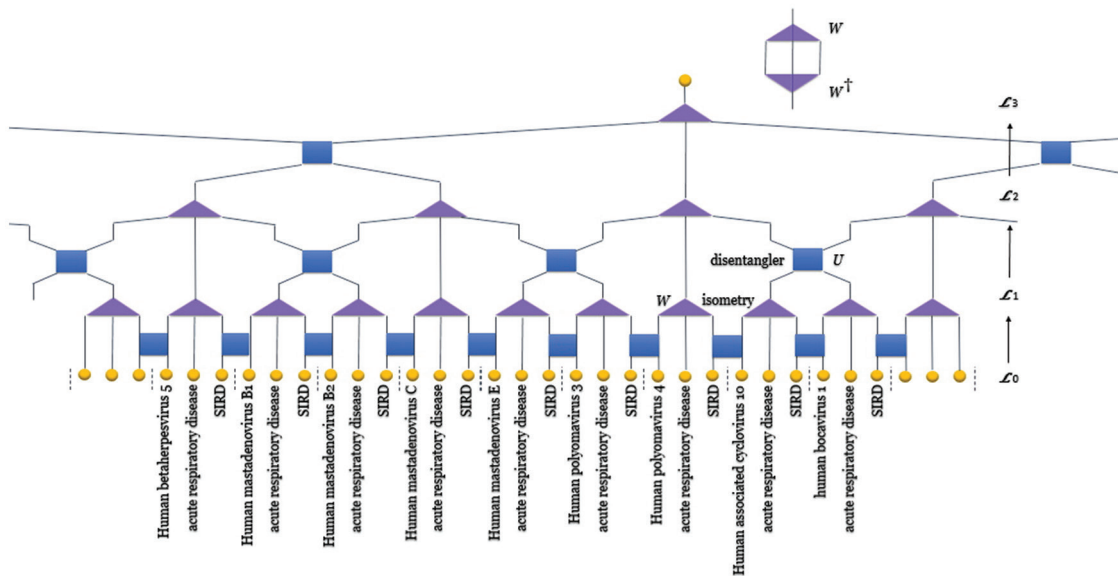


Figure S16. Ternary (three-site blocks) multi-scale entanglement renormalization ansatz with lattice length corresponding to the calculated cases of acute respiratory disease caused by different DNA viruses (symptoms and diseases data, compartmental susceptible-infectious-recovered model data).

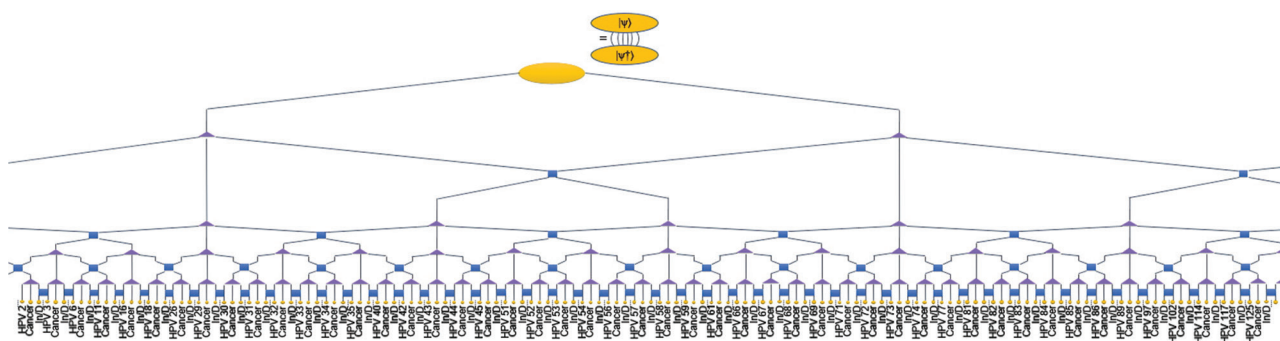


Figure S17. Ternary (three-site blocks) multi-scale entanglement renormalization ansatz with lattice length corresponding to the calculated cases of cancer caused by the *Human papillomavirus* of genus *Alphapapillomavirus*, subfamily *Firstpapillomavirinae*, family *Papillomaviridae* (compartmental infectious/deceased [In/D] model data).

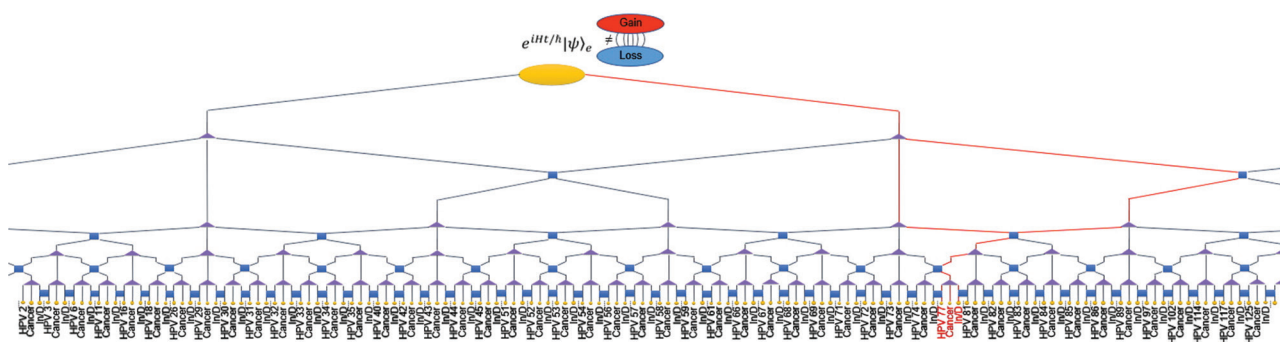


Figure S18. Ternary (three-site blocks) multi-scale entanglement renormalization ansatz with lattice length corresponding to the calculated cases of cancer caused by the *Human papillomavirus* of genus *Alphapapillomavirus*, subfamily *Firstpapillomavirinae*, family *Papillomaviridae* (compartmental infectious/deceased [In/D] model data). The assumed version of quantum non-Hermitian many-body system with violation of the entanglement monotonicity and appearance of local entanglement gain due to spontaneous PT-symmetry breaking, leading to a non-reversible coarse-graining transformation. There is indication of a possible increase in skin cancer cases.