

Files for calculation of SARS-CoV-2 transmission characteristics in Australia

1. Github_case_sequence_input.m: loads in the case data and sequence information. Adds longitude and latitude to each resident postcode. Also specifies probabilities for time differences, age, age_group, gender, distance.
2. Github_NSW_labs.m: specifies the sites for each pathology provider in NSW. Must also load spreadsheets containing the Lat and Long for each site.
 - a. '4Cyte Pathology_Pathology_Coordinates_googleAPI_217_NSW_JM.xlsx'
 - b. 'NSW_postcodes_LHD.xlsx'
 - c. Austech Medical Laboratories_Coordinates_googleAPI_5_NSW.xlsx'
 - d. Australian Clinical Labs_Coordinates_googleAPI_NSW_377_withDups_JM.xlsx'
 - e. 'Douglass_Hanly_Moir_Pathology_Coordinates_googleAPI_208_JM.xlsx'
 - f. 'Lavery_Pathology_Coordinates_googleAPI_370_towns_with_dups.xlsx'
 - g. 'NSW_Health_Pathology_googleAPI_NSW_157.xlsx'
 - h. 'SEALS_Coordinates_googleAPI_46.xlsx'
 - i. 'SYDPATH_googleAPI_Australia_24.xlsx'
3. Github_Westmead_children_link.m: estimate linkages for Westmead hospital
 - a. Calls prob_link_child_noany.m
4. Create the link sets for each state/territory:
 - a. Github_Links_ACT.m
 - i. Calls prob_link_state.m
 - b. Github_Links_NSW.m
 - i. Calls prob_link_NSW_noany.m
 - ii. Github_links_NSW_geo.m: incorporates geo info into the NSW linkage set
 1. Calls prob_link_NSW_geo.m
 - c. Github_Links_NT.m
 - d. Github_Links_QLD.m
 - e. Github_links_SA.m
 - i. Calls prob_link_state_SA.m
 - f. Github_Links_TAS.m
 - g. Github_Links_VIC.m
 - i. Calls prob_link_VIC_noany.m
 - h. Github_Links_WA.m
5. Github_seq_case_opt.m: run the optimization routine on each state/territory to estimate the optimal linkages between the cases and sequences
 - a. Calls bipartite_prob.m to set up the bipartite problem
6. Github_all_matches.m: collect all matches across the states
7. Github_LHD_trans_MC.m: load in the Local Health District information for NSW.
 - a. Calls NSW_postcodes_LHD.xlsx

8. Github_aligned_clone2seqs_linked_all_geo_shortb_MC.m: Connect the linked cases to the nodes in the transmission networks, running Monte Carlo on within-clone network calculations over the ranges of age and distance preference.
 - a. Calls clone2seqs_geo.m: to generate network of sequences from network of clones
 - i. Calls within_clone_network_geo.m: generates the optimal network within a given clone for a set value of λ_a and λ_d .
 1. Calls CLE_optimal.m
 - a. Calls CLE_calc1.m
9. Github_analyse2b_MC.m: analyse the MC results.