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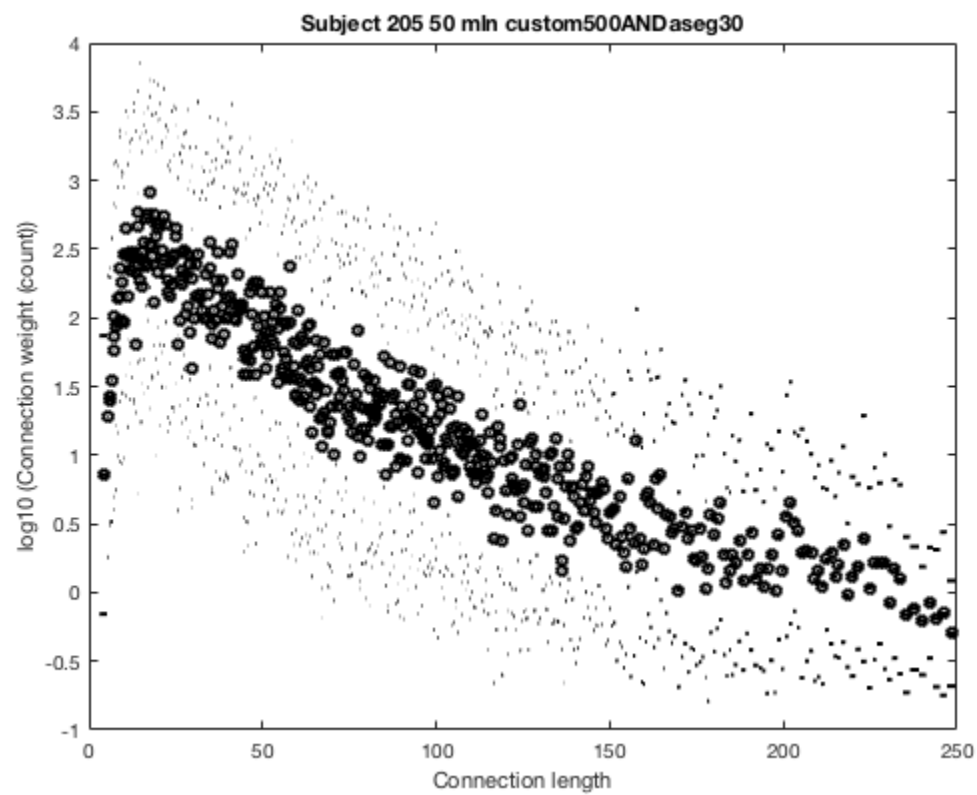
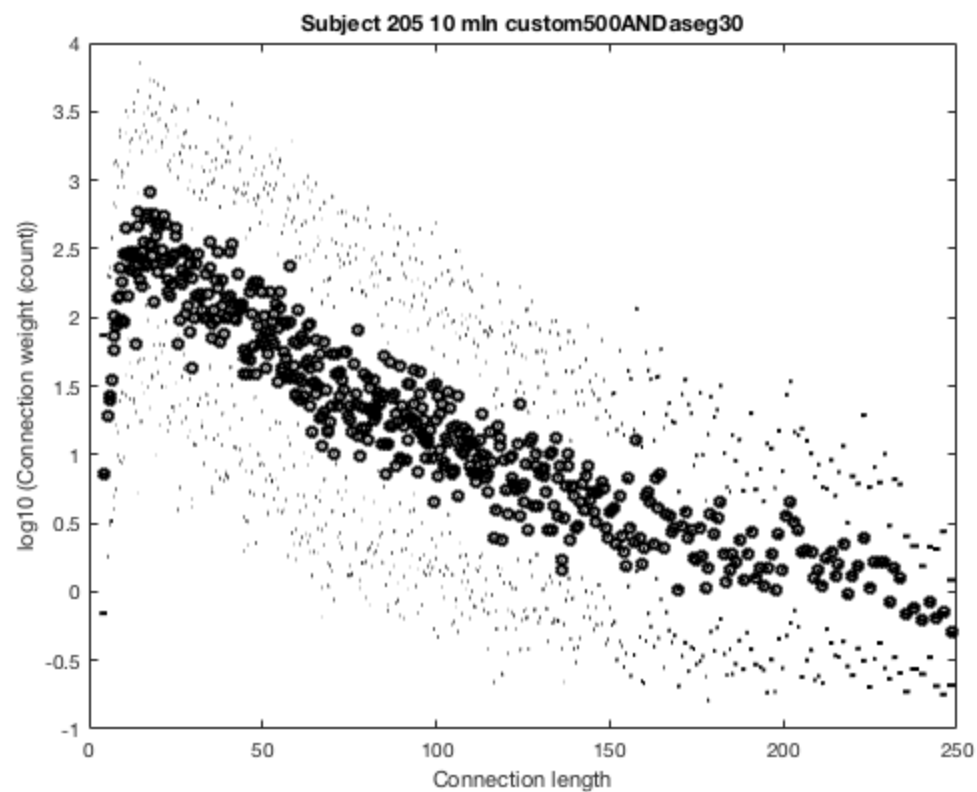
% differences between 10 and 50 mln streamlines
% clear all; close all;
% cd ('/Users/Aurina/GoogleDrive/Genetics_connectome/Gen_Cog/Data/
Connectomes/10_50_mlnStreamlines/');
% load('FACT_custom500ANDaseg30_10_mil.mat');
% density10 = density;
% len10 = len;
% count10 = count;
% deg10 = zeros(length(density10), size(density10{1},1));
% NumNodes = size(density{1},1);
% for i=1:length(density10)
%     deg10(i,:) = degrees_und(density10{i});
% end
% load('FACT_custom500ANDaseg30_50_mil.mat');
% density50 = density;
% len50 = len;
% count50 = count;
% deg50 = zeros(length(density), size(density{1},1));
% for i=1:length(density)
%     deg50(i,:) = degrees_und(density50{i});
% end
% dif = deg50-deg10;
% for i=1:length(density)
%     FigHandle = figure('Position', [100, 100, 1200, 1200]);
%     subplot(3,2,5);
%     scatter(deg10(i,:), deg50(i,:));
%     xlabel('10 mil streamlines degrees'); ylabel('50 mil streamlines
degrees');
%     hold on;
%     x = linspace(1,size(density{1},1), size(density{1},1));
%     y = x;
%     plot(x,y);
%
%     subplot(3,2,6); bar(x,dif(i,:)); title('Difference between
degrees (50mln - 10mln streamlines)');
%     xlabel('Node');
%     ylabel('Difference in degrees');
%     Matrix10 = fRandom2AnatomicalParcellations_annot('custom500',
'ANDaseg30', density10{i});
%     Matrix50 = fRandom2AnatomicalParcellations_annot('custom500',
'ANDaseg30', density50{i});
%     subplot(3,2,1); imagesc(log(Matrix10)); axis square; title
('Connectome 10 mil streamlines');
%     subplot(3,2,2); imagesc(log(Matrix50)); axis square; title
('Connectome 50 mil streamlines');
%
%     subplot(3,2,3); histogram(deg10(i,:), 20); title('Degree
distribution 10 mil'); xlabel('Degree');
%     subplot(3,2,4); histogram(deg50(i,:), 20); title('Degree
distribution 50 mil'); xlabel('Degree');
%
% end

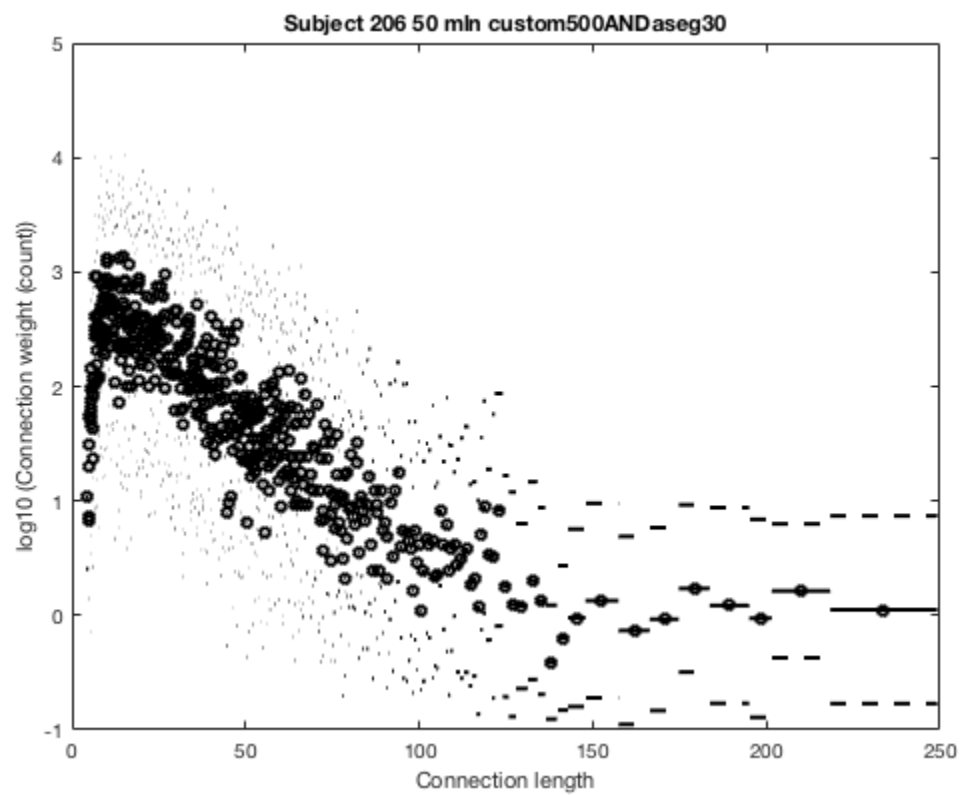
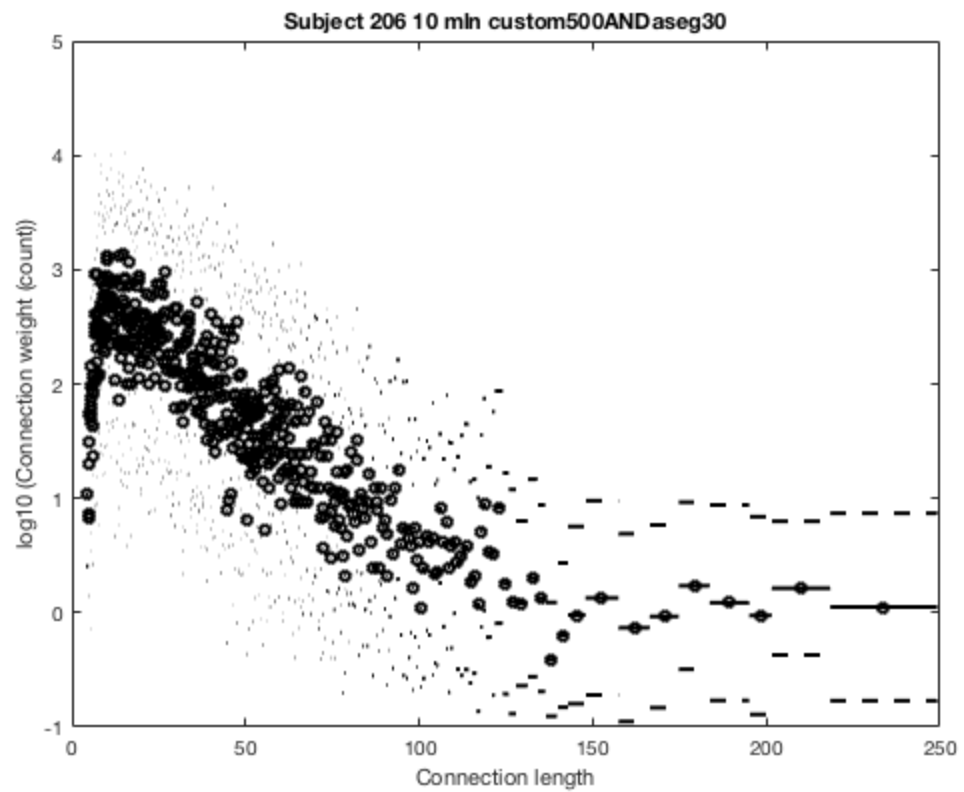
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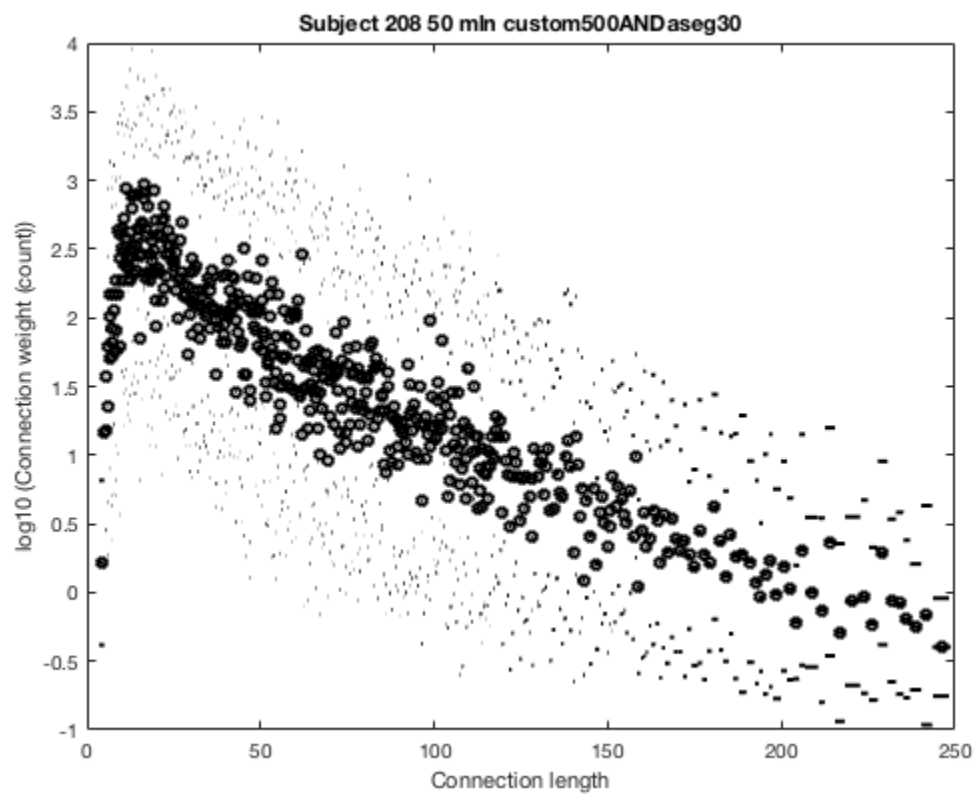
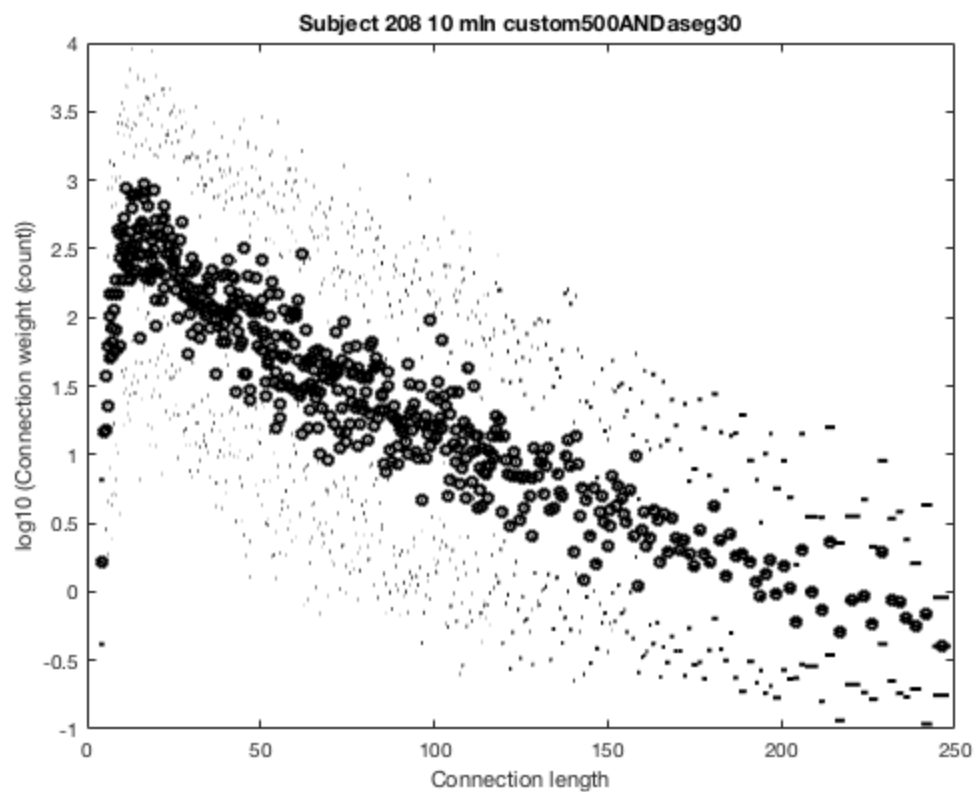
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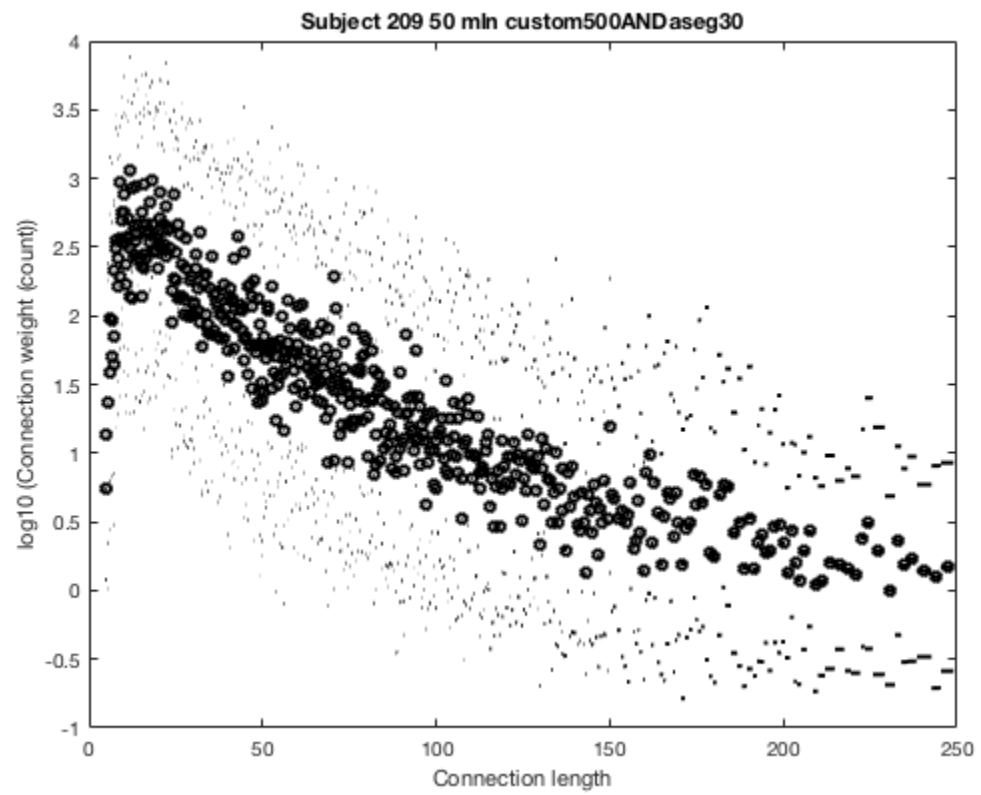
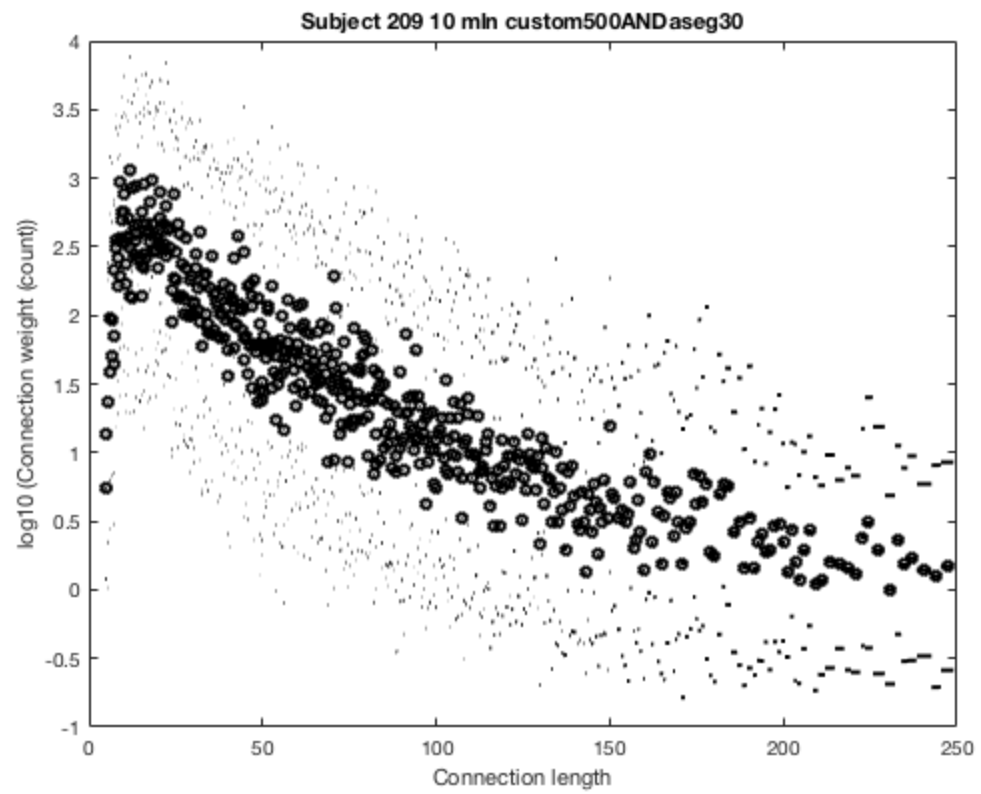
% A = mean(dif,1);
% figure; bar(x,A);
%
% Ranks10 = zeros(length(density),NumNodes);
% Ranks50 = zeros(length(density),NumNodes);
%
% for i=1:length(density)
%     [ignore, idx10] = sort( deg10(i,:) , 'descend');
%     [ignore, idx50] = sort( deg50(i,:) , 'descend');
%     Ranks10(i,idx10 ) = 1:numel(idx10);
%     Ranks50(i,idx50 ) = 1:numel(idx50);
% end
%
% R = zeros(length(density),NumNodes);
% for i=1:length(density)
%     R10 = Ranks10(i,:);
%     R50 = Ranks50(i,:);
%     Ra = R50-R10;
%     R(i,:) = Ra;
% figure;
% %FigHandle = figure('Position', [100, 100, 1200, 1200]);
% subplot(1,2,1); bar(Ra); title(sprintf('%d subj Difference
    between ranks 50mln - 10mln\ncustom500 parcellation',
    sub_id(i))); xlabel('Node'); ylabel('Rank difference'); axis square;
% subplot(1,2,2); scatter(R10, R50); title(sprintf('%d subj 50mln
    and 10mln rank correlation\ncustom500 parcellation', sub_id(i)));
%     xlabel('10 mln rank'); ylabel('50 mln rank');axis square;
% hold on;
% x = linspace(1,size(density{1},1), size(density{1},1));
% y = x;
% plot(x,y);
% end
%mean rank difference with SD for each ROI across subjects
% weight and distance correlation
for i=1:length(density)
    Weights10 = count10{i}(:);
    Length10 = len10{i}(:);
    Weights50 = count50{i}(:);
    Length50 = len50{i}(:);
    A10 = [Length10 Weights10];
    A50 = [Length50 Weights50];
    A10( ~any(A10,2), : ) = []; %rows
    A50( ~any(A50,2), : ) = []; %rows
    BF_PlotQuantiles(A10(:,1),log10(A10(:,2)),500,0,1)
    title (sprintf('Subject %d 10 mln custom500ANDaseg30',
sub_id(i))); xlabel('Connection length'); ylabel('log10 (Connection
weight (count))');
    BF_PlotQuantiles(A50(:,1),log10(A50(:,2)),500,0,1)
    title (sprintf('Subject %d 50 mln custom500ANDaseg30',
sub_id(i))); xlabel('Connection length'); ylabel('log10 (Connection
weight (count))');
end

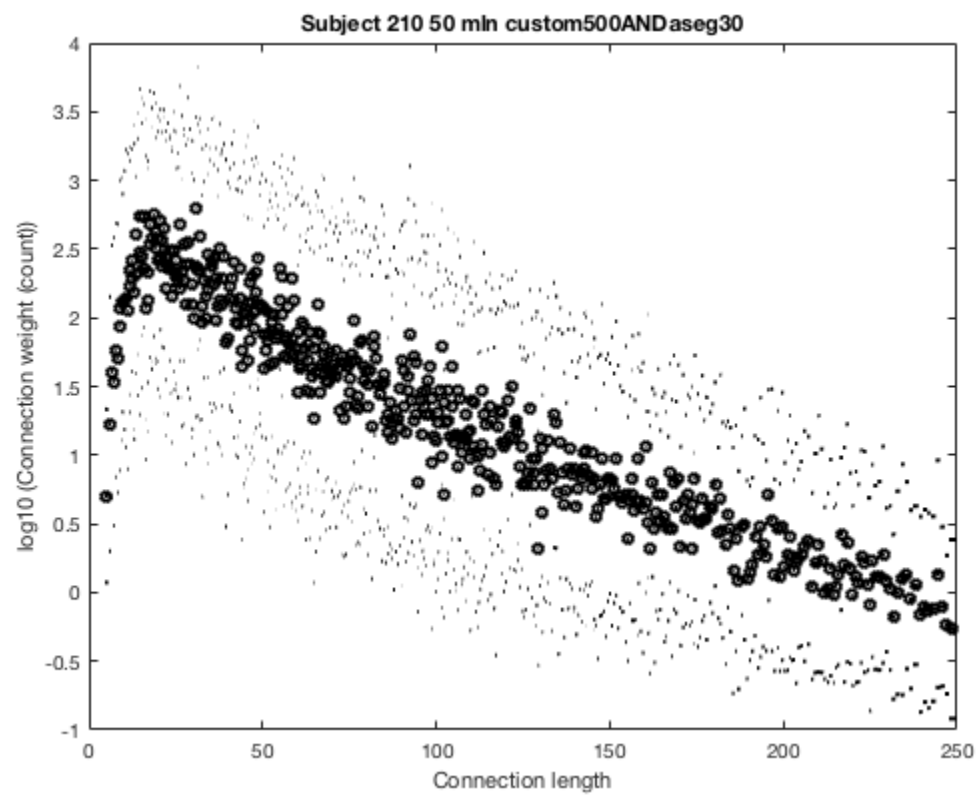
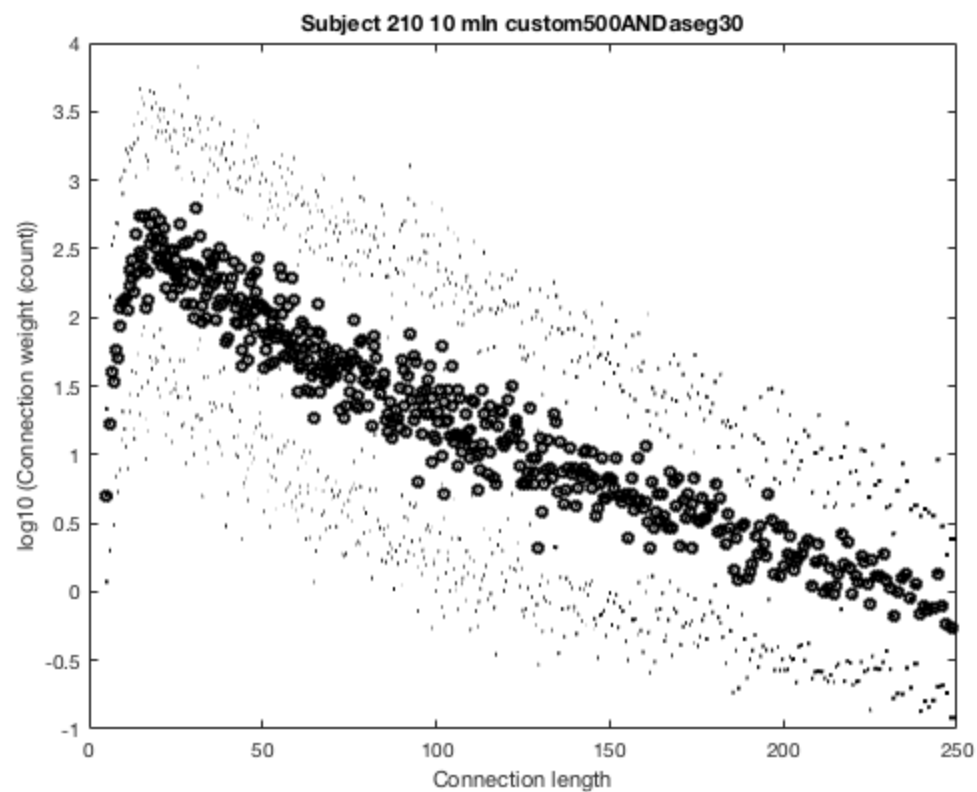
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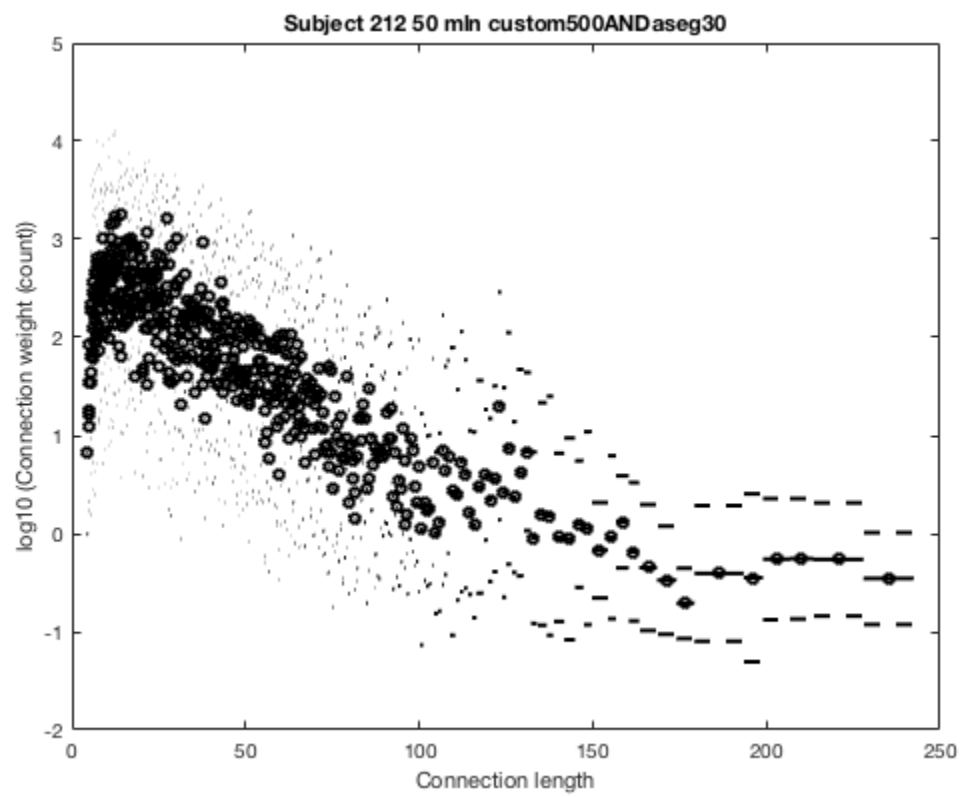
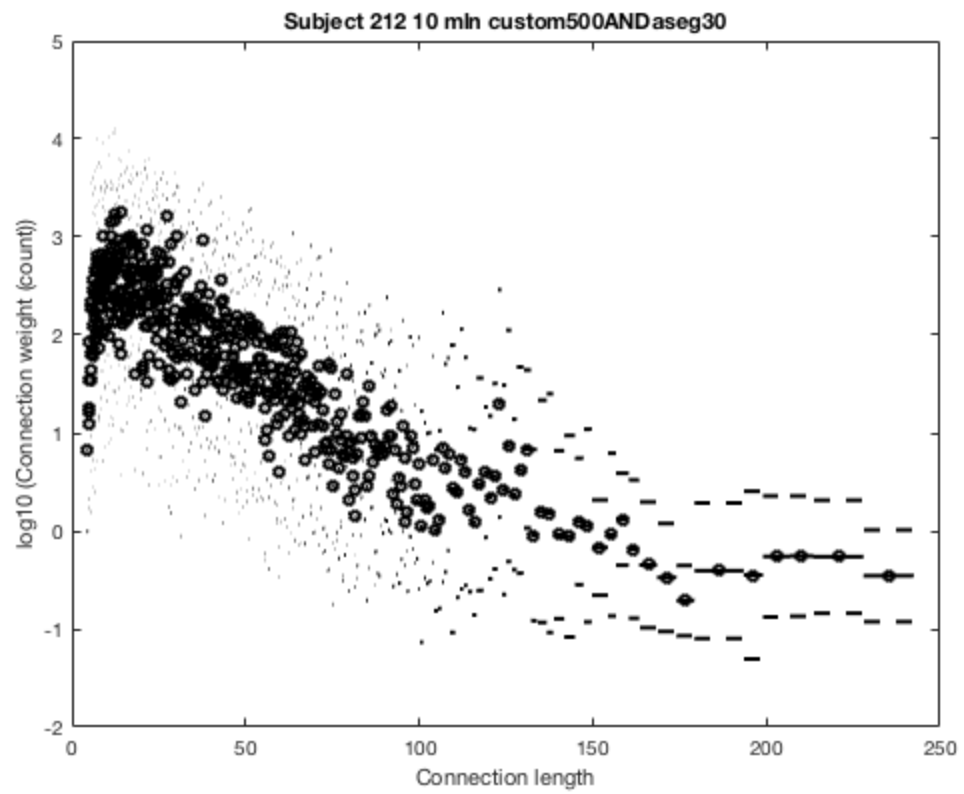


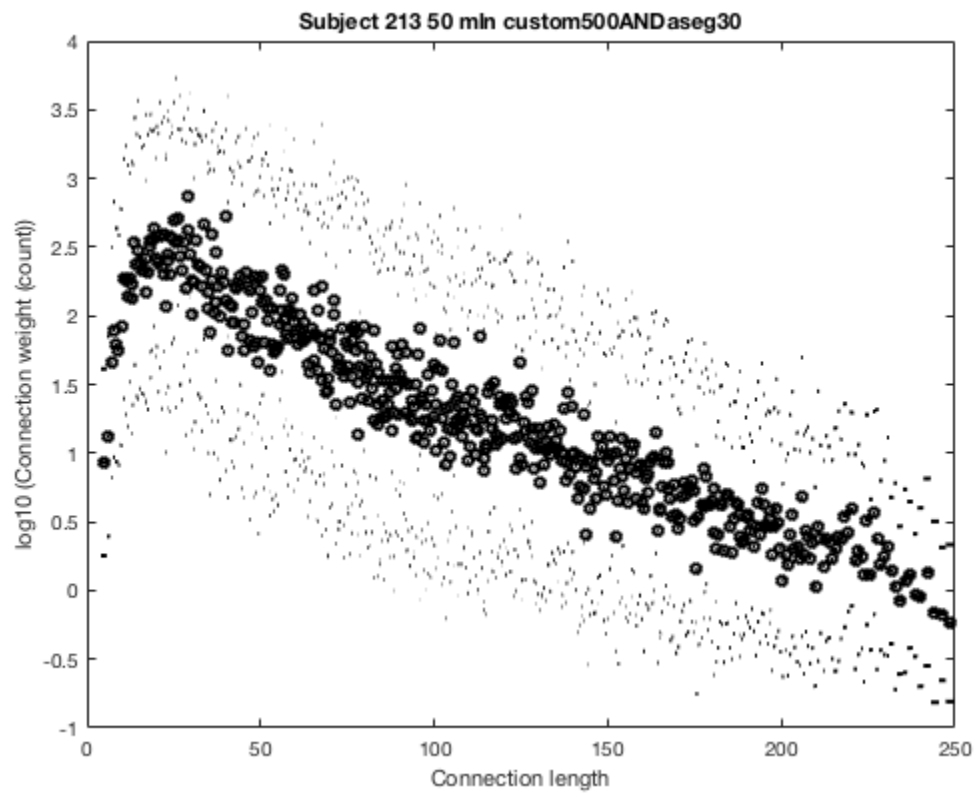
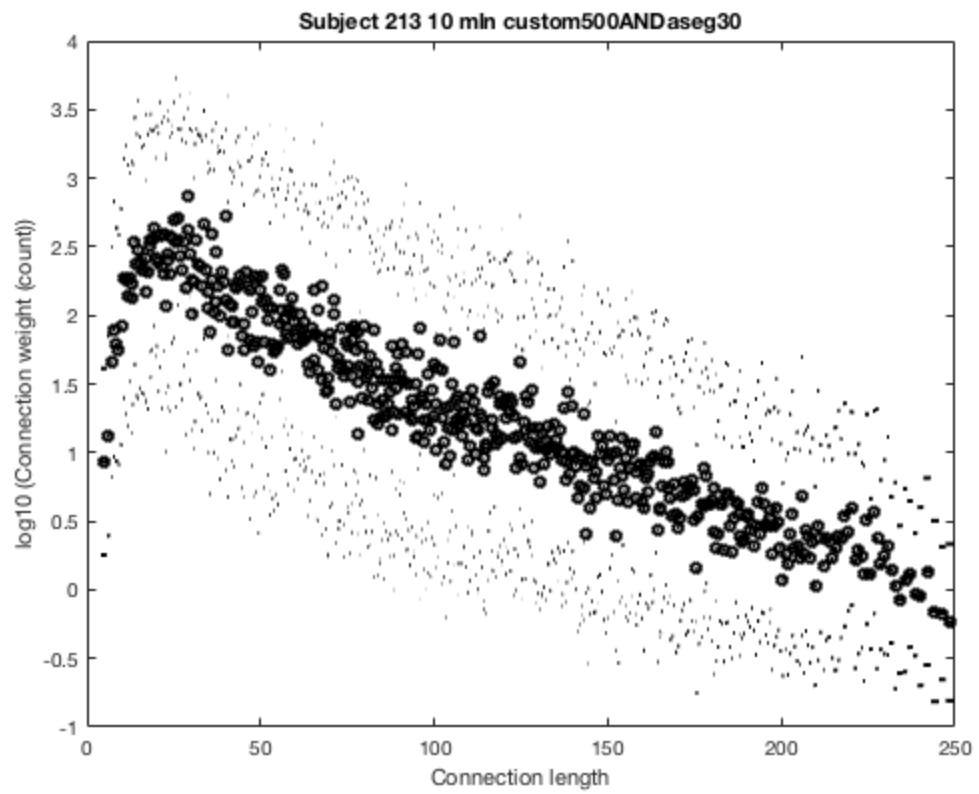


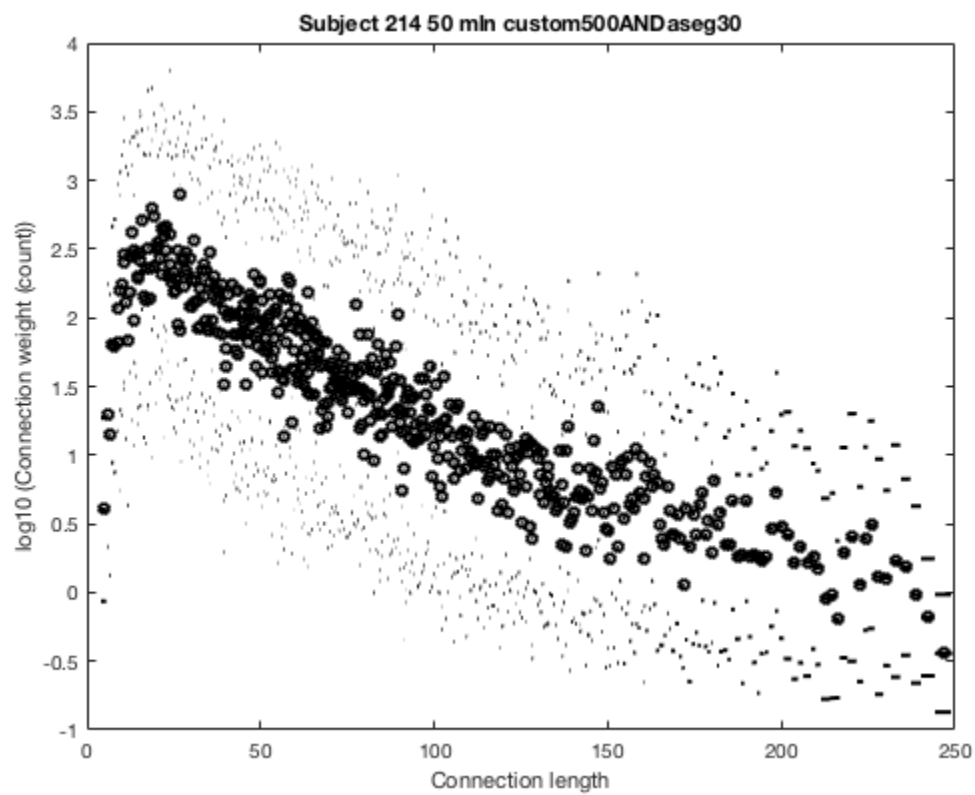
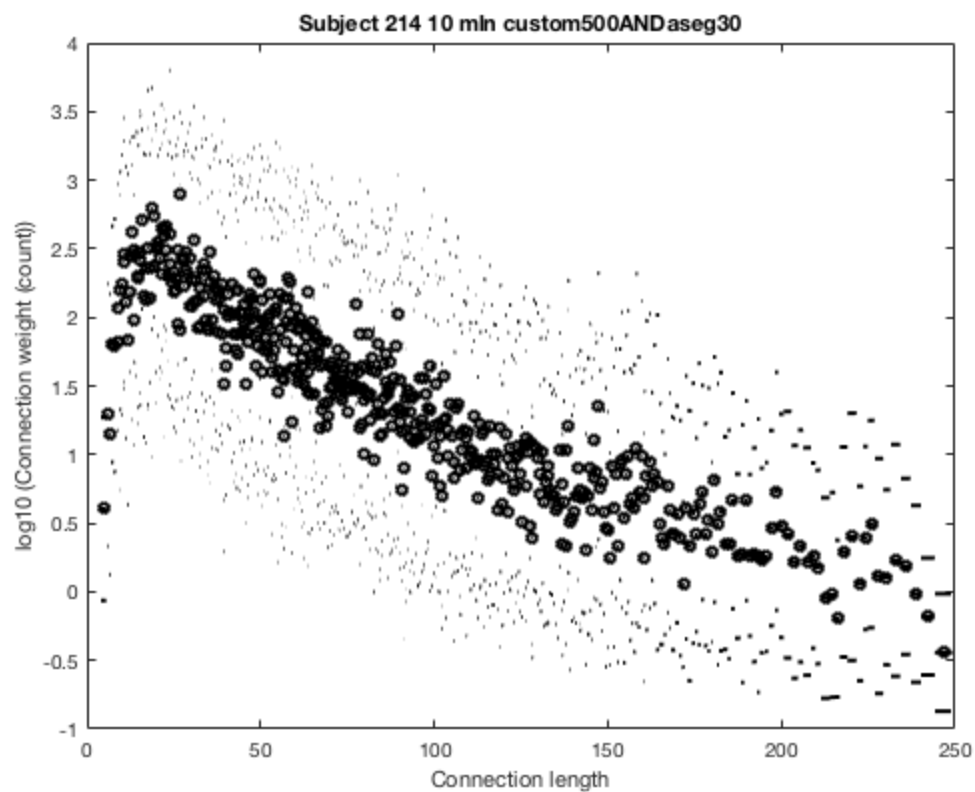


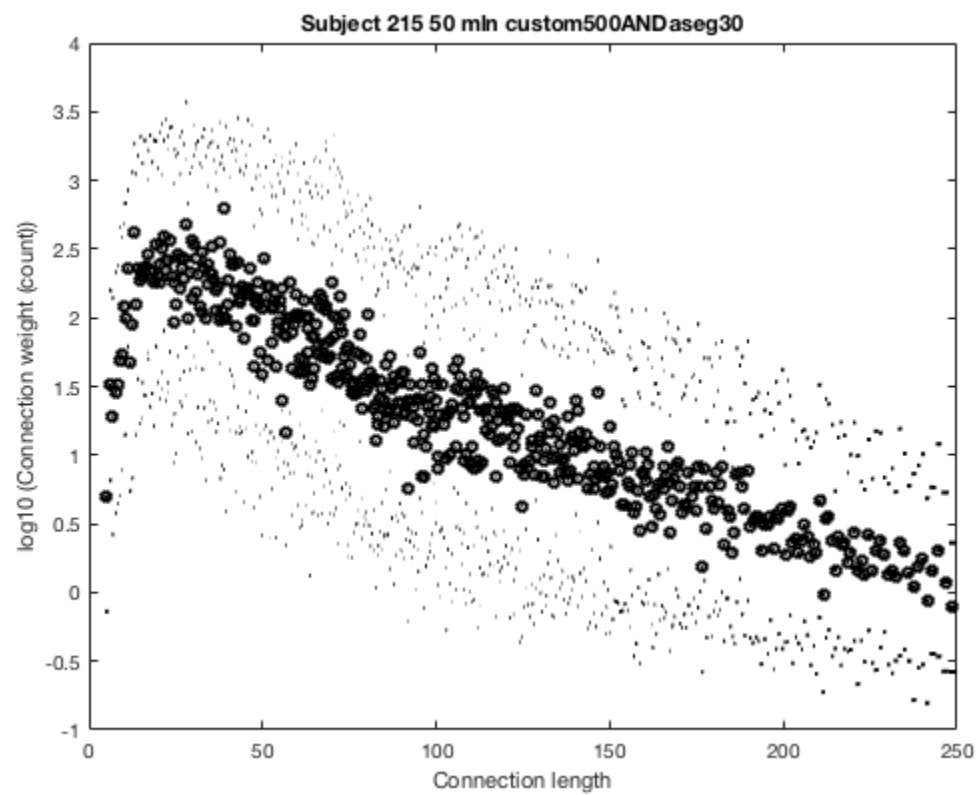
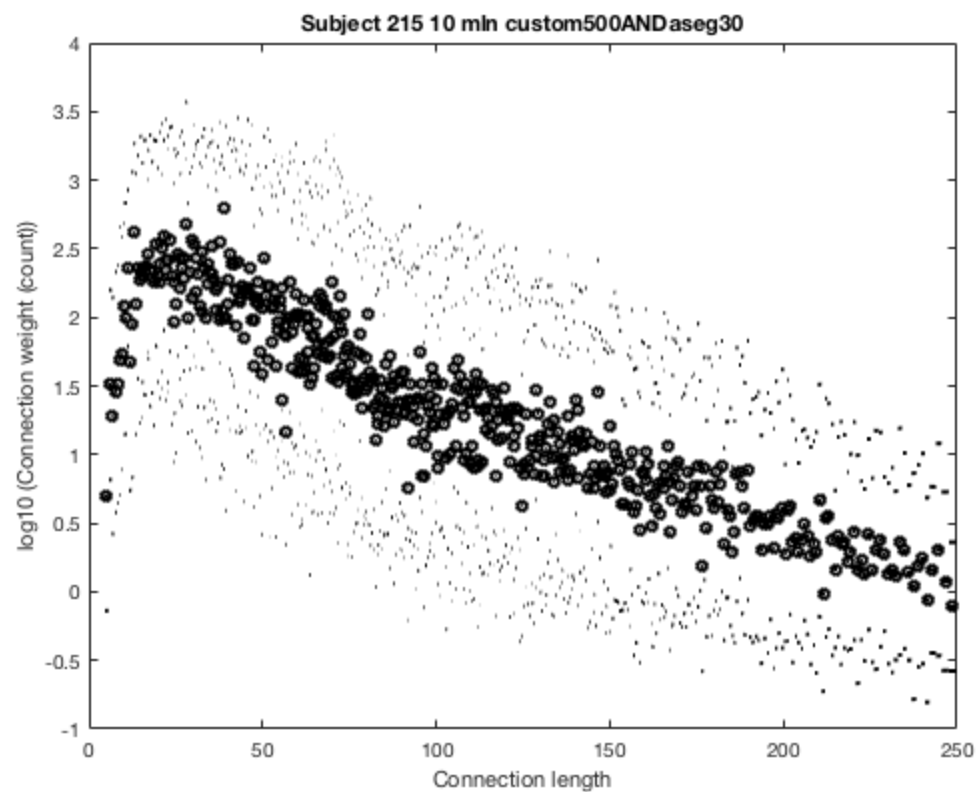


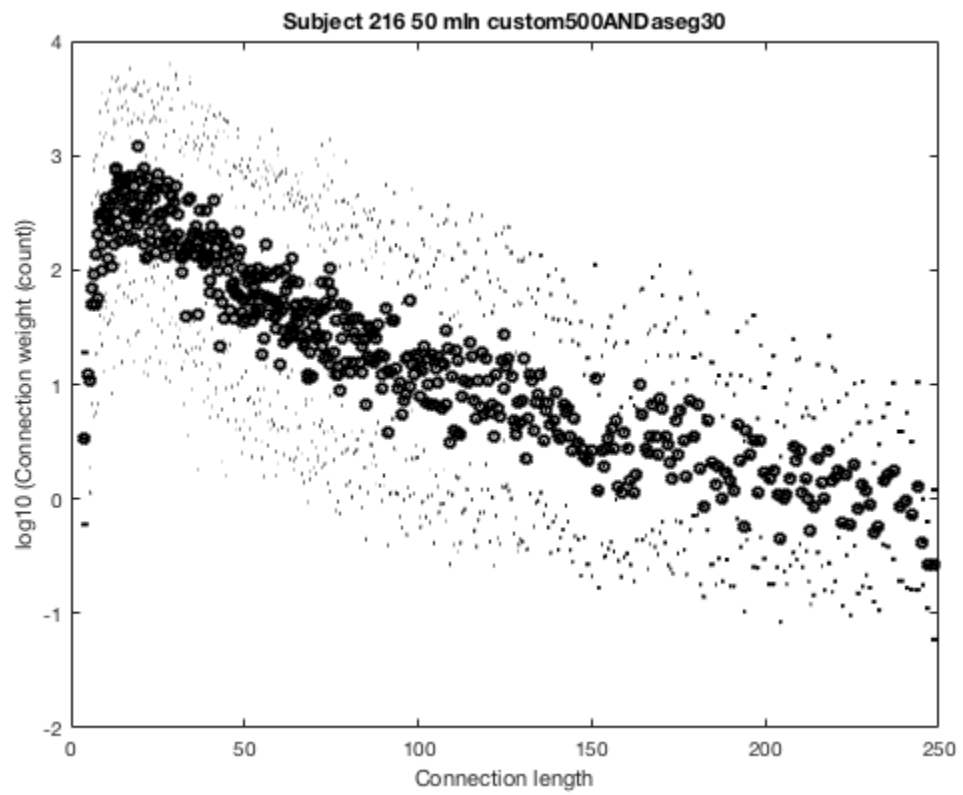
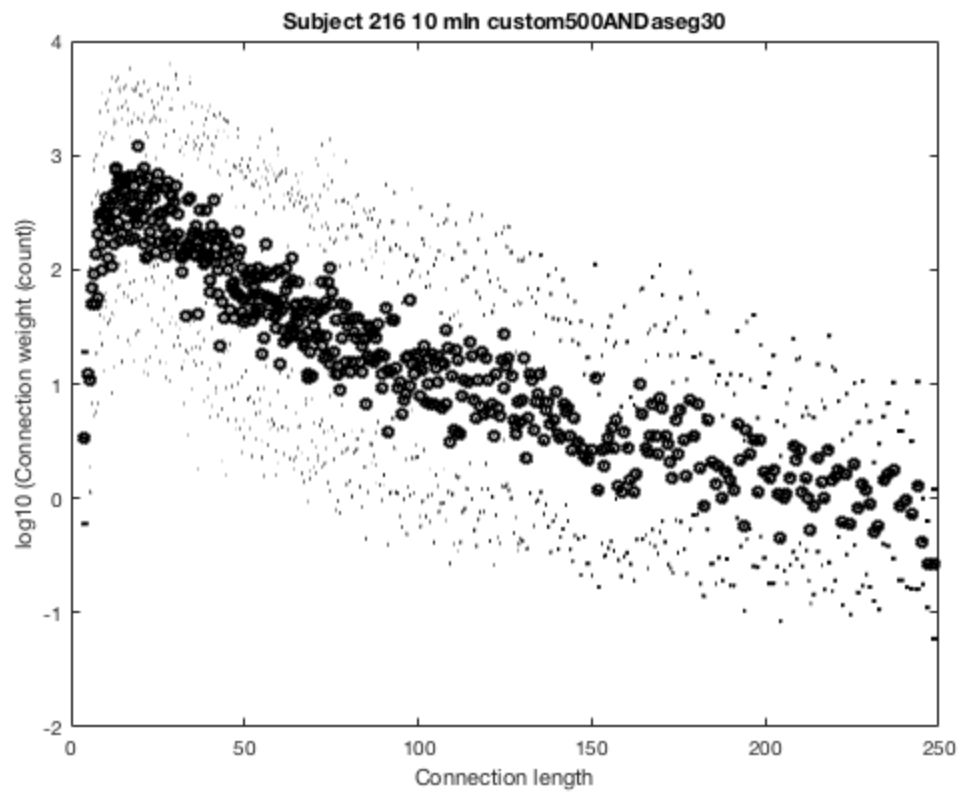












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