

Interface <div>DatasetReader</div>	
<ul style="list-style-type: none"><li>read</li></ul>	<ul style="list-style-type: none"><li>filepath</li></ul>

GFF3DatasetReader <div>DatasetReader</div>	
<ul style="list-style-type: none"><li>read</li></ul>	<ul style="list-style-type: none"><li>filepath</li></ul>

Dataset <div>GGF3Dataset</div>	
<ul style="list-style-type: none"><li>create</li><li>get_df</li><li>get_active_operations</li></ul>	<ul style="list-style-type: none"><li>df : pd.DataFrame</li></ul>

GFF3Dataset <div>Dataset</div>	
<ul style="list-style-type: none"><li>get_information</li><li>unique_seq_IDs</li><li>type_of_operations</li><li>same_source</li><li>entries_for_each_type_of_operation</li><li>get_chromosomes</li><li>fraction_of_unassembles_seq</li><li>ensembl_havana</li><li>entries_for_each_type_of_operation_ensemblhavana</li><li>get_gene_names</li></ul>	<ul style="list-style-type: none"><li>df : pd.DataFrame</li><li>Dataset</li></ul>