40.5% as high risk, compared to 79.5% and 84.9% using the SIRS criteria and CURB65 respectively.

Conclusions All three scoring systems can stratify according to risk of 30 day mortality, though none of them are particularly accurate. qSOFA has poor sensitivity, and may underestimate severity and risk of 30 day mortality in CAP. New assessment tools to accurately identify CAP patients at increased risk of poor outcomes are urgently required.

<table>
<thead>
<tr>
<th>Score</th>
<th>Sensitivity (%)</th>
<th>Specificity (%)</th>
<th>NPV (%)</th>
<th>PPV (%)</th>
<th>Negative LR</th>
<th>Positive LR</th>
</tr>
</thead>
<tbody>
<tr>
<td>CURB65</td>
<td>84.9</td>
<td>40</td>
<td>91.5</td>
<td>25.9</td>
<td>0.38</td>
<td>1.42</td>
</tr>
<tr>
<td>SIRS</td>
<td>79.5</td>
<td>32.5</td>
<td>87.3</td>
<td>21.4</td>
<td>0.63</td>
<td>1.18</td>
</tr>
<tr>
<td>qSOFA</td>
<td>40.5</td>
<td>79.5</td>
<td>84.3</td>
<td>32.9</td>
<td>0.75</td>
<td>1.98</td>
</tr>
</tbody>
</table>

NPV – negative predictive value, PPV – positive predictive value, LR – Likelihood ratio

Introduction
The presence of respiratory pathogens on oral surfaces is a risk factor for pneumonia. Understanding why non-oral respiratory pathogens appear is crucial in planning interventions to manipulate the oral microbiota to prevent pneumonia. We sought to understand whether respiratory pathogens were associated with reduction in oral bacterial diversity (invasion hypothesis) or no change in diversity (overgrowth hypothesis).

Methods
We analysed extracted DNA from 167 throat samples from 53 hospitalised older patients with hip fracture using next generation sequencing (Lib-L chemistry, mothur). Occurrence of respiratory tract infection (RTI, clinician-initiated antibiotic for chest infection) within 3 months of discharge was noted via case notes and telephone call to General Practitioner. We used linear mixed effect modelling in R (nlme package) to investigate the association between relative abundance of respiratory pathogens and species richness, with patient as the random effect. We used correspondence analysis (CA) to analyse beta-diversity (vegan package).

Results
Respiratory pathogens (Haemophilus influenzae, Staphylococcus aureus, Enterobacteriaceae) were present in 38/167 samples (23%). Higher relative abundances of respiratory pathogens were not significantly associated with sample diversity (t=−1.400575, p=0.1641). Moreover, mixed effect models demonstrated no increase in relative abundances of respiratory pathogens over time in individual patients whilst in hospital (t=−0.206605, p=0.8367). While RTI was associated with higher relative abundances of respiratory pathogens (t=1.9502718, p=0.0567), there was no association between RTI and oropharyngeal species richness (t=−0.361164, p=0.7195).

Conclusions
There was no association between detection of respiratory pathogens and oropharyngeal species diversity. These Results support the overgrowth, rather than the invasion, hypothesis, and larger studies to explore frequency of oral clearance in conjunction with the oral microbiota are warranted. In addition, the lack of change over time in relative abundances of respiratory pathogens suggests that the exposure to the hospital environment is not a major driver in the appearance of these organisms.

References